

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 28, 2004, 17:51:02 ; Search time 3.97883 Seconds  
(without alignments)  
2975.262 Million cell updates/sec

Title: US-10-019-823B-2  
Perfect score: 194  
Sequence: 1 GKICTPAGVKCPAALPCCGLICIGGVNNKVC 33

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:\*  
1: Geneseq1980s:\*  
2: Geneseq1990s:\*  
3: Geneseq2000s:\*  
4: Geneseq2001s:\*  
5: Geneseq2002s:\*  
6: Geneseq2003as:\*  
7: Geneseq2003bs:\*  
8: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	194	100.0	33	4	AAB66900 Insectici
2	194	100.0	33	6	AAB66900 Paecilomy
3	194	100.0	34	6	AAB66900 Insectici
4	194	100.0	34	6	AAB66900 Insectici
5	194	100.0	34	6	AAB66900 Insectici
6	194	100.0	34	6	AAB66900 Insectici
7	194	100.0	34	6	AAB66900 Insectici
8	194	100.0	34	6	AAB66900 Insectici
9	194	100.0	34	6	AAB66900 Insectici
10	194	100.0	34	6	AAB66900 Insectici
11	194	100.0	34	6	AAB66900 Insectici
12	194	100.0	34	6	AAB66900 Insectici
13	194	100.0	34	6	AAB66900 Insectici
14	194	100.0	34	6	AAB66900 Insectici
15	194	100.0	34	6	AAB66900 Insectici
16	194	100.0	34	6	AAB66900 Insectici
17	194	100.0	34	6	AAB66900 Insectici
18	194	100.0	34	6	AAB66900 Insectici
19	194	100.0	34	6	AAB66900 Insectici
20	194	100.0	34	6	AAB66900 Insectici
21	194	100.0	34	6	AAB66900 Insectici
22	194	100.0	34	6	AAB66900 Insectici
23	194	100.0	34	6	AAB66900 Insectici
24	194	100.0	34	6	AAB66900 Insectici
25	194	100.0	35	6	AAB66900 Insectici

AAB66900 standard; peptide; 33 AA.  
XX  
AC AAB66900;  
DT 12-APR-2001 (first entry)  
DE Insecticidal protein #2.  
XX  
XX Insecticide; transgenic plant; insect-resistance.  
XX Paecilomyces sp.  
XX  
XX WO200100841-A1.  
XX 04-JAN-2001.  
XX  
PF 23-JUN-2000; 2000WO-GB002457.  
PR 29-JUN-1999; 99GB-00015215.  
PR 23-DEC-1999; 99GB-00030536.  
XX  
PA (ZENE ) ZENECA LTD.  
XX Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;  
PI Vincent JL, Lee MD;  
XX  
XX WPI; 2001-123015/13.  
XX Novel insecticidal protein obtained from species of Paecilomyces for  
PT controlling insects, and for insect-resistant transgenic plant  
PT production.  
XX  
XX Claim 3; Page 30; 72pp; English.  
XX The present invention relates to novel insecticidal proteins obtained  
CC from Paecilomyces sp. (see AAB66900 to AAB66901 and AAB66913). The  
CC insecticidal proteins can be used to produce transgenic plants, which are  
CC insect-resistant. Also, the insecticidal proteins are useful for  
CC controlling insects by providing them at a locus where insects feed  
XX  
XX Sequence 33 AA;  
XX  
XX Query Match 100.0%; Score 194; DB 4; Length 33;  
XX Best Local Similarity 100.0%; Pred. No. 9.6e-15;  
XX Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## ALIGNMENTS

RESULT 1  
AAB66900  
ID AAB66900 standard; peptide; 33 AA.  
XX  
AC AAB66900;  
DT 12-APR-2001 (first entry)  
DE Insecticidal protein #2.  
XX  
XX Insecticide; transgenic plant; insect-resistance.  
XX Paecilomyces sp.  
XX  
XX WO200100841-A1.  
XX 04-JAN-2001.  
XX  
PF 23-JUN-2000; 2000WO-GB002457.  
PR 29-JUN-1999; 99GB-00015215.  
PR 23-DEC-1999; 99GB-00030536.  
XX  
PA (ZENE ) ZENECA LTD.  
XX Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;  
PI Vincent JL, Lee MD;  
XX  
XX WPI; 2001-123015/13.  
XX Novel insecticidal protein obtained from species of Paecilomyces for  
PT controlling insects, and for insect-resistant transgenic plant  
PT production.  
XX  
XX Claim 3; Page 30; 72pp; English.  
XX The present invention relates to novel insecticidal proteins obtained  
CC from Paecilomyces sp. (see AAB66900 to AAB66901 and AAB66913). The  
CC insecticidal proteins can be used to produce transgenic plants, which are  
CC insect-resistant. Also, the insecticidal proteins are useful for  
CC controlling insects by providing them at a locus where insects feed  
XX  
XX Sequence 33 AA;  
XX  
XX Query Match 100.0%; Score 194; DB 4; Length 33;  
XX Best Local Similarity 100.0%; Pred. No. 9.6e-15;  
XX Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

26 194 100.0 35 6 AAB66900 Insectici  
27 194 100.0 35 6 AAB66900 Insectici  
28 183 94.3 33 4 AAB66900 Insectici  
29 82 42.3 36 5 AAB66900 Insectici  
30 79 40.7 36 5 AAB66900 Insectici  
31 75 38.7 36 2 AAB66900 Insectici  
32 75 38.7 37 2 AAB66900 Insectici  
33 73 37.6 35 5 AAB66900 Insectici  
34 73 37.6 82 5 AAB66900 Insectici  
35 72.5 37.4 37 5 AAB66900 Insectici  
36 72.5 37.4 37 7 AAB66900 Insectici  
37 72 37.1 33 7 AAB66900 Insectici  
38 69.5 35.8 30 5 AAB66900 Insectici  
39 69.5 35.8 77 5 AAB66900 Insectici  
40 69 35.6 31 5 AAB66900 Insectici  
41 69 35.6 39 5 AAB66900 Insectici  
42 69 35.6 67 5 AAB66900 Insectici  
43 69 35.6 2020 8 AAB66900 Insectici  
44 67 34.5 32 5 AAB66900 Insectici  
45 67 34.5 32 5 AAB66900 Insectici

QY 1 GKICTPAGVKCPAALPCCPGLCIGGVNNKVC 33  
 DB 1 GKICTPAGVKCPAALPCCPGLCIGGVNNKVC 33

RESULT 2  
 AAE36283  
 ID AAE36283 standard; peptide; 33 AA.  
 AC AAE36283;  
 XX 26-JUN-2003 (first entry)  
 DE Paecilomyces farinosus insecticidal protein.  
 XX Insecticidal protein; pesticide.  
 XX Paecilomyces farinosus.  
 XX WO200298911-A2  
 PD 12-DEC-2002.  
 PF 30-MAY-2002; 2002WO-GB002666.  
 XX 07-JUN-2001; 2001GB-00013900.  
 PA (SYGN ) SYNGENTA LTD.  
 XX Vincent JL, Viner R;  
 DR WPI; 2003-175137/17.  
 PT New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.  
 XX Claim 6; Page 23; 67pp; English.

XX The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects. Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is insecticidal protein  
 XX SQ Sequence 34 AA;

Query Match 100.0%; Score 194; DB 6; Length 34;  
 Best Local Similarity 100.0%; Pred. No. 9.9e-15;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GKICTPAGVKCPAALPCCPGLCIGGVNNKVC 33  
 DB 1 GKICTPAGVKCPAALPCCPGLCIGGVNNKVC 33

RESULT 3  
 AAE36261  
 ID AAE36261 standard; peptide; 34 AA.  
 AC AAE36261;  
 XX 26-JUN-2003 (first entry)  
 DE Insecticidal protein #3.  
 XX Insecticidal protein; pesticide.  
 XX Unidentified.  
 XX WO200298911-A2.  
 PD 12-DEC-2002.  
 PF 30-MAY-2002; 2002WO-GB002666.  
 XX 07-JUN-2001; 2001GB-00013900.  
 PA (SYGN ) SYNGENTA LTD.  
 XX Vincent JL, Viner R;  
 DR WPI; 2003-175137/17.  
 PT New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.  
 XX Example 1; Page 66; 67pp; English.

XX The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects. Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is Paecilomyces farinosus insecticidal protein  
 XX SQ Sequence 33 AA;

Query Match 100.0%; Score 194; DB 6; Length 33;  
 Best Local Similarity 100.0%; Pred. No. 9.6e-15;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GKICTPAGVKCPAALPCCPGLCIGGVNNKVC 33  
 DB 1 GKICTPAGVKCPAALPCCPGLCIGGVNNKVC 33

RESULT 3  
 AAE36261  
 ID AAE36261 standard; peptide; 34 AA.  
 AC AAE36261;  
 XX 26-JUN-2003 (first entry)  
 DE Insecticidal protein #3.  
 XX Insecticidal protein; pesticide.  
 XX Unidentified.  
 XX WO200298911-A2.

XX 12-DEC-2002.  
 PD 30-MAY-2002; 2002WO-GB002666.  
 PF 07-JUN-2001; 2001GB-00013900.  
 PR (SYGN ) SYNGENTA LTD.  
 PA Vincent JL, Viner R;  
 PI WPI; 2003-175137/17.  
 DR New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.  
 PT Claim 6; Page 23; 67pp; English.

XX The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects. Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is insecticidal protein  
 XX SQ Sequence 34 AA;

XX Query Match 100.0%; Score 194; DB 6; Length 34;  
 Best Local Similarity 100.0%; Pred. No. 9.9e-15;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GKICTPAGVKCPAALPCCPGLCIGGVNNKVC 33  
 DB 2 GKICTPAGVKCPAALPCCPGLCIGGVNNKVC 34

RESULT 4  
 AAE36295  
 ID AAE36295 standard; peptide; 34 AA.  
 AC AAE36295;  
 XX 26-JUN-2003 (first entry)  
 DE Insecticidal protein #25.  
 XX Insecticidal protein; pesticide.  
 XX Unidentified.  
 XX WO200298911-A2.  
 PD 12-DEC-2002.  
 PF 30-MAY-2002; 2002WO-GB002666.  
 XX 07-JUN-2001; 2001GB-00013900.  
 PA (SYGN ) SYNGENTA LTD.  
 XX Vincent JL, Viner R;  
 DR WPI; 2003-175137/17.  
 PT New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.  
 XX Example 1; Page 66; 67pp; English.

XX The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the







XX 26-JUN-2003 (first entry)  
 DT Insecticidal protein #17.  
 DE Insecticidal protein; pesticide.  
 XX Unidentified.  
 OS WO200298911-A2.  
 XX 12-DEC-2002.  
 XX 30-MAY-2002; 2002WO-GB002666.  
 XX 07-JUN-2001; 2001GB-00013900.  
 XX (SYGN ) SYNGENTA LTD.  
 XX Vincent JL, Viner R;  
 XX WPI; 2003-175137/17.  
 XX New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.  
 XX Example 1; Page 63; 67pp; English.  
 XX The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects. Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is insecticidal protein

XX Query Match 100.0%; Score 194; DB 6; Length 34;  
 DT Best Local Similarity 100.0%; Pred. No. 9.9e-15;  
 DE Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX

XX 1 GKICTPAGVKCPAALPCCPGRLRCIGGVNNKYCR 33  
 DT 2 GKICTPAGVKCPAALPCCPGRLRCIGGVNNKYCR 34  
 DE

XX RESULT 11  
 DT AAE36289  
 DE ID AAE36289 standard; peptide; 34 AA.  
 XX AAE36289;  
 XX 26-JUN-2003 (first entry)  
 DT Insecticidal protein #19.  
 DE Insecticidal protein; pesticide.  
 XX Unidentified.  
 OS WO200298911-A2.  
 XX 12-DEC-2002.  
 XX 30-MAY-2002; 2002WO-GB002666.  
 XX 07-JUN-2001; 2001GB-00013900.  
 XX (SYGN ) SYNGENTA LTD.  
 XX Vincent JL, Viner R;  
 XX WPI; 2003-175137/17.  
 XX New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.  
 XX Example 1; Page 63; 67pp; English.  
 XX The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects. Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is insecticidal protein

XX Query Match 100.0%; Score 194; DB 6; Length 34;  
 DT Best Local Similarity 100.0%; Pred. No. 9.9e-15;  
 DE Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX

XX 1 GKICTPAGVKCPAALPCCPGRLRCIGGVNNKYCR 33  
 DT 2 GKICTPAGVKCPAALPCCPGRLRCIGGVNNKYCR 34  
 DE

XX RESULT 12  
 DT AAE36263  
 DE ID AAE36263 standard; peptide; 34 AA.  
 XX AAE36263;  
 XX 26-JUN-2003 (first entry)  
 DT Insecticidal protein #5.  
 DE Insecticidal protein; pesticide.  
 XX Unidentified.  
 OS WO200298911-A2.  
 XX 12-DEC-2002.  
 XX 30-MAY-2002; 2002WO-GB002666.  
 XX 07-JUN-2001; 2001GB-00013900.  
 XX (SYGN ) SYNGENTA LTD.  
 XX Vincent JL, Viner R;  
 XX WPI; 2003-175137/17.  
 XX New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.  
 XX Claim 40; Page 35; 67pp; English.  
 XX The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects. Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is insecticidal protein

XX Query Match 100.0%; Score 194; DB 6; Length 34;  
 DT Best Local Similarity 100.0%; Pred. No. 9.9e-15;  
 DE Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX

XX 1 GKICTPAGVKCPAALPCCPGRLRCIGGVNNKYCR 33  
 DT 2 GKICTPAGVKCPAALPCCPGRLRCIGGVNNKYCR 34  
 DE

XX WPI; 2003-175137/17.  
 XX New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.  
 XX Example 1; Page 64; 67pp; English.  
 XX The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects. Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is insecticidal protein

XX Query Match 100.0%; Score 194; DB 6; Length 34;  
 DT Best Local Similarity 100.0%; Pred. No. 9.9e-15;  
 DE Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX

XX 1 GKICTPAGVKCPAALPCCPGRLRCIGGVNNKYCR 33  
 DT 2 GKICTPAGVKCPAALPCCPGRLRCIGGVNNKYCR 34  
 DE

XX RESULT 12  
 DT AAE36263  
 DE ID AAE36263 standard; peptide; 34 AA.  
 XX AAE36263;  
 XX 26-JUN-2003 (first entry)  
 DT Insecticidal protein #5.  
 DE Insecticidal protein; pesticide.  
 XX Unidentified.  
 OS WO200298911-A2.  
 XX 12-DEC-2002.  
 XX 30-MAY-2002; 2002WO-GB002666.  
 XX 07-JUN-2001; 2001GB-00013900.  
 XX (SYGN ) SYNGENTA LTD.  
 XX Vincent JL, Viner R;  
 XX WPI; 2003-175137/17.  
 XX New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.  
 XX Claim 40; Page 35; 67pp; English.  
 XX The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects. Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is insecticidal protein

XX Query Match 100.0%; Score 194; DB 6; Length 34;  
 DT Best Local Similarity 100.0%; Pred. No. 9.9e-15;  
 DE Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX

XX 1 GKICTPAGVKCPAALPCCPGRLRCIGGVNNKYCR 33  
 DT 2 GKICTPAGVKCPAALPCCPGRLRCIGGVNNKYCR 34  
 DE



XX The invention relates to insecticidal protein comprising an X-glycine  
 CC motif at the amino-terminus. Polynucleotide or DNA constructs of the  
 CC invention are useful for producing plants or plant parts that are  
 CC resistant to insects. The protein or synergistic combination is useful as  
 CC an active ingredient of a pesticide or for controlling insects.  
 CC Antibodies raised to the insecticidal proteins can be used to identify  
 CC other proteins with insecticidal activity. The present sequence is  
 CC insecticidal protein  
 XX

SQ Sequence 34 AA;

Query Match 100.0%; Score 194; DB 6; Length 34;  
 Best Local Similarity 100.0%; Pred. NO. 9.9e-15;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GKICTPAGVKPCPALPCCGRLCTIGGVNNKVC 33  
 |||||  
 Db 2 GKICTPAGVKPCPALPCCGRLCTIGGVNNKVC 34  
 |||||

Search completed: October 28, 2004, 18:19:40  
 Job time : 4.97883 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 28, 2004, 18:05:43 ; Search time 0.88081 Seconds  
(without alignments)  
3604.811 Million cell updates/sec

Title: US-10-019-823b-2

Perfect score: 194  
Sequence: 1 GKICTAGVKCPAALPCCPLGICGVNNKVC 33

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79;.\*  
1: Piri.\*  
2: Piri2.\*  
3: Piri3.\*  
4: Piri4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query	Length	DB	ID	Description
1	64	33.0	1064	2	A40136	fibropellin Ia - s
2	60	30.9	422	2	S48564	probable membrane
3	60	30.9	570	2	A48836	fibropellin C prec
4	58.5	30.2	34	2	A31043	mu-conotoxin GS -
5	58	29.9	37	2	E44007	apoptoxin III - tr
6	57.5	29.6	417	2	T08724	hypothetical prote
7	57	29.4	1221	2	T23472	hypothetical prote
8	56.5	29.1	585	2	S43572	C05B5.5 protein (c
9	56.5	29.1	585	2	E88571	protein C05B5.5 [i
10	56.5	29.1	1390	2	T30346	insulin receptor -
11	56	28.9	197	2	T10091	sperm mitochondria
12	56	28.9	238	2	T04166	thauromatin-like pro
13	56	28.9	2352	2	T30201	Notch homolog prot
14	56	28.9	2531	2	S18188	notch protein homo
15	56	28.9	2531	2	A46019	notch-1 protein -
16	55	28.4	132	2	H75335	hypothetical prote
17	54.5	28.1	218	2	T03287	osmotin protein ho
18	54.5	28.1	601	2	T22035	hypothetical prote
19	54.5	28.1	601	2	D89711	protein F4DE10.4 [i
20	54.5	28.1	768	2	A87722	protein ZC123.1 [i
21	54.5	28.1	1207	1	EGHU	epidermal growth f
22	54.5	28.1	4543	1	A53102	alpha-2-macroglobu
23	54	27.8	73	2	A43019	platelet aggregati
24	54	27.8	74	2	S25773	testis-specific pr
25	54	27.8	269	2	T26972	hypothetical prote
26	54	27.8	283	2	S88597	protein Y47D38.6 [i
27	54	27.8	2318	2	S45306	notch 3 protein -
28	54	27.8	2321	2	S78549	notch3 protein - h
29	53	27.3	375	2	A41428	CEF-10 protein pre

## RESULT 1

A40136  
fibropellin Ia - sea urchin (Strongylocentrotus purpuratus)  
N;Alternate names: epidermal growth factor homolog precursor  
N;Contains: alternatively spliced fibropellin Ib (EGFI)  
C;Species: Strongylocentrotus purpuratus (purple urchin)  
C;Date: 13-May-1992 #sequence\_revision 17-Sep-1997 #text\_change 09-Jul-2004  
C;Accession: A40136; B40136; C40136; A29316; A43131  
R;Delgadillo-Reynoso, M.G.; Rollo, D.R.; Hursh, D.A.; Raff, R.A.  
J. Mol. Evol. 29, 314-327, 1989  
A;Title: Structural analysis of the ueGF gene in the sea urchin Strongylocentrotus purpuratus  
A;Reference number: A40136; MUID:90112459; PMID:2514273  
A;Accession: A40136  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-114 <DEL>  
A;Cross-references: UNIPROT:P10079; GB:X17530; NID:g10225; PID:g667061  
A;Accession: B40136  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: DNA  
A;Residues: 181-251,329-370, 'R', 372-408, 'RA', 411-441 <DE2>  
A;Accession: C40136  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: DNA  
A;Residues: 'K', 747-821, 898-978 <DE3>  
R;Hursh, D.A.; Andrews, M.E.; Raff, R.A.  
Science 237, 1487-1490, 1987  
A;Title: A sea urchin gene encodes a polypeptide homologous to epidermal growth factor.  
A;Reference number: A29316; MUID:87319677; PMID:3498216  
A;Accession: A29316  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 'S', 280-481, 786-1064 <HUR>  
A;Cross-references: GB:M17421; NID:g161474; PIDN:AAA30050.1; PID:g552260  
R;Hunt, L.T.; Barker, W.C.  
FASEB J. 3, 1760-1764, 1989  
A;Title: Avidin-like domain in an epidermal growth factor homolog from a sea urchin.  
A;Reference number: A43131; MUID:89196806; PMID:2784773  
A;Contents: annotation  
C;Comment: EGF homology repeats 10-17 are spliced out in the short form (fibropellin Ib).  
F;1-19/Domain: signal sequence #status predicted <SIG>  
F;20-1064/Product: fibropellin I #status predicted <FIB>  
F;23-54/Domain: EGF homology <EG01>  
F;57-175/Domain: C1r/C1s repeat homology <C1r>  
F;180-211/Domain: EGF homology <EG02>  
F;218-249/Domain: EGF homology <EG03>  
F;256-287/Domain: EGF homology <EG04>  
F;294-325/Domain: EGF homology <EG05>  
F;332-363/Domain: EGF homology <EG06>  
F;370-401/Domain: EGF homology <EG07>  
F;408-439/Domain: EGF homology <EG08>  
F;446-477/Domain: EGF homology <EG09>

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Delta-4 protein - f  
crumbs protein - f  
xotch protein - Af  
hypothetical prote  
alpha-2-macroglobu  
metalothionein A  
platelet aggregati  
conserved hypothet  
Motch B protein -  
E2 glycoprotein pr  
transmembrane prot  
pathogenesis-relat  
osmotin-like prote  
osmotin-like prote

## ALIGNMENTS

5522

F:484-515/Domain: EGF homology <EG10>  
 F:522-553/Domain: EGF homology <EG11>  
 F:560-591/Domain: EGF homology <EG12>  
 F:598-629/Domain: EGF homology <EG13>  
 F:636-667/Domain: EGF homology <EG14>  
 F:674-705/Domain: EGF homology <EG15>  
 F:712-743/Domain: EGF homology <EG16>  
 F:750-781/Domain: EGF homology <EG17>  
 F:788-819/Domain: EGF homology <EG18>  
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 F:864-895/Domain: EGF homology <EG20>  
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Query Match 29.9%; Score 58; DB 2; Length 37;  
 Best Local Similarity 37.1%; Pred. No. 2.3;  
 Matches 13; Conservative 1; Mismatches 15; Indels 6; Gaps 1;  
 QY 4 CTPAGVKCPAALPCPG-----LRCIGGVNNKVC 32  
 Db 1 CNSKGTCTNADECCGGKCAYNVWNCIGGGCKTC 35

RESULT 6  
 T08724  
 hypothetical protein DKFZp566D213.1 - human  
 C:Species: Homo sapiens (man)  
 C:Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004  
 C:Accession: T08724  
 R:Koehrer, K.; Beyer, A.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.  
 submitted to the Protein Sequence Database, May 1999  
 A:Reference number: 216468  
 A:Accession: T08724  
 A:Molecule type: mRNA  
 A:Residues: 1-417 <KOE>  
 A:CROSS-references: UNIPROT:Q9Y409; EMBL:AL050275  
 A:Experimental source: fetal kidney; clone DKFZp566D213  
 C:Genetics:  
 A:Note: DKFZp566D213.1

Query Match 29.6%; Score 57.5; DB 2; Length 417;  
 Best Local Similarity 31.1%; Pred. No. 18;  
 Matches 14; Conservative 4; Mismatches 14; Indels 13; Gaps 1;  
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RESULT 7  
 T23472  
 hypothetical protein K08E7.5 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
 C:Accession: T23472  
 R:Smyle, R.  
 submitted to the EMBL Data Library, July 1996  
 A:Reference number: Z19745  
 A:Accession: T23472  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-1221 <WIL>  
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 A:Experimental source: clone K08E7  
 C:Genetics:  
 A:Gene: CBSP:K08E7.5  
 A:Map position: 4  
 A:Introns: 26/1; 103/1; 170/1; 640/1; 802/2; 831/1; 864/3; 891/3; 908/1; 938/2; 980/1; 1

Query Match 29.4%; Score 57; DB 2; Length 1221;  
 Best Local Similarity 34.5%; Pred. No. 49;  
 Matches 10; Conservative 3; Mismatches 14; Indels 2; Gaps 1;  
 QY 4 CTPAGVKCPAALPCCPGLRCIGGVNNKVC 32  
 Db 971 CAPPAPCCLTIPCCPPIPC--PQPKIC 997

RESULT 8  
 S43572  
 C0585.5 protein (clone C0585) - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C:Date: 07-Sep-1994 #sequence\_revision 10-Nov-1995 #text\_change 10-Nov-1995  
 C:Accession: S43572  
 R:Mortimore, B.  
 submitted to the EMBL Data Library, April 1994

A:Reference number: S43570  
 A:Accession: S43572  
 A:Status: Preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-585 <MOR>  
 A:CROSS-references: EMBL:Z32679  
 C:Genetics:  
 A:Introns: 35/2; 218/3; 292/2; 328/1; 442/2

Query Match 29.1%; Score 56.5; DB 2; Length 585;  
 Best Local Similarity 30.4%; Pred. No. 31;  
 Matches 14; Conservative 2; Mismatches 11; Indels 19; Gaps 2;

QY 1 GKICT-----PAGVKC-----PAALPCCPGLRCIGGV 27  
 Db 531 GGYCSTSTQCTGYQCIDGKCKTKHFLAPPCVAECPPGTRCINGV 576

RESULT 9  
 E88571  
 protein C05B5.5 [imported] - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C:Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Jul-2004  
 C:Accession: E88571  
 R:Anonymous, The C. elegans Sequencing Consortium.  
 Science 282, 2012-2018, 1998  
 A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biology  
 A:Reference number: A75000; MUID:99069613; PMID:9851916  
 A:Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/projects/C.elegans/

A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and  
 A:Accession: E88571  
 A:Status: preliminary  
 A:Molecule type: DNA  
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 A:CROSS-references: UNIPROT:P34293; GB:chr\_III; PIDN:CAA83593.1; PID:g3873993; GSPDB:GN00  
 C:Genetics:  
 A:Gene: C05B5.5  
 A:Map position: 3

Query Match 29.1%; Score 56.5; DB 2; Length 585;  
 Best Local Similarity 30.4%; Pred. No. 31;  
 Matches 14; Conservative 2; Mismatches 11; Indels 19; Gaps 2;

QY 1 GKICT-----PAGVKC-----PAALPCCPGLRCIGGV 27  
 Db 531 GGYCSTSTQCTGYQCIDGKCKTKHFLAPPCVAECPPGTRCINGV 576

RESULT 10  
 T30346  
 insulin receptor - yellow fever mosquito  
 C:Species: Aedes aegypti (yellow fever mosquito)  
 C:Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 09-Jul-2004  
 C:Accession: T30346  
 R:Grat, R.; Neuenschwander, S.; Brown, M.R.; Ackermann, U.  
 Insect Mol. Biol. 6, 151-163, 1996  
 A:Title: Insulin mediated secretion of ecdysteroids from mosquito ovaries and molecular  
 A:Reference number: Z20834  
 A:Accession: T30346  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-1390 <GRA>  
 A:CROSS-references: UNIPROT:O93105; EMBL:U72939; NID:gi620749; PID:gi620750; PIDN:AAB1705

C:Superfamily: insulin receptor; protein kinase homology  
 Query Match 29.1%; Score 56.5; DB 2; Length 1390;  
 Best Local Similarity 36.6%; Pred. No. 62;  
 Matches 15; Conservative 2; Mismatches 11; Indels 13; Gaps 3;

QY 3 ICTPAGVKCPAALP-----CCPGLRCIGGV-----NKVCR 33  
 Db 228 ICPP---ECPPACSKTGYCCDAESCLGGCNLPNTSSCSVCR 265

RESULT 11  
T10081  
sperm mitochondrial capsule selenoprotein - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 16-Jul-1999 #sequence\_revision 04-Mar-2000 #text\_change 09-Jul-2004  
C:Accession: T10081; A37199  
R:Kleene, K.C.; Smith, J.; Bozorgzadeh, A.; Harris, M.; Hahn, L.; Karimpour, I.; Gerstel  
Dev. Biol. 137, 395-402, 1990  
A:Title: Sequence and developmental expression of the mRNA encoding the seleno-protein c  
A:Reference number: A37199; MUID:90152148; PMID:2303168  
A:Accession: T10081  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-6, 'X', 8-16, 'X', 18-33, 'X', 35-197 <KLE1>  
A:Cross-references: UNIPROT:P15265; EMBL:M29603; NID:G199088; PIDN:AAA53045.1; PID:G5672  
A:Experimental source: strain CD-1  
A>Note: in Genbank entry MUSMCS, release 113.0, PIDN:AAA53045.1, the selenocysteine UGA  
A:Accession: A37199  
A:Molecule type: mRNA  
A:Residues: 55-197 <KLE2>  
A:Cross-references: GB:M29603; NID:G199088  
A>Note: the authors translated the codon TGT for residue 112 as Pro  
C:Genetics:  
A:Gene: MCS  
A:Genome: nuclear  
A:Keywords: mitochondrion; selenocysteine; sperm  
C:Keywords: Modified site: selenocysteine #status predicted  
F,7,17,34/Modified site: selenocysteine #status predicted

Query Match 28.9%; Score 56; DB 2; Length 197;  
Best Local Similarity 45.0%; Pred. No. 15;  
Matches 9; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 4 CTPAGVKCPAALPCCPGRLC 23  
Db 87 CCKPSKPPKPPKPPKPPKPPK 106

RESULT 12  
T04166  
thau-matin-like protein - rice  
C:Species: Oryza sativa (rice)  
C>Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 09-Jul-2004  
C:Accession: T04166  
R:Colic, K.C.; Velazhahan, R.; Aunuratha, C.S.; Muthukrishnan, S.  
submitted to the EMBL Data Library, November 1996  
A:Description: Induction of thau-matin-like proteins (TLPs) in Rhizoctonia solani - infect  
A:Reference number: Z15250  
A:Accession: T04166  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-238 <CON>  
A:Cross-references: UNIPROT:O04364; EMBL:U77657; NID:G2062388; PIDN:AAB53368.1; PID:G206  
C:Superfamily: thau-matin I

Query Match 28.9%; Score 56; DB 2; Length 238;  
Best Local Similarity 45.2%; Pred. No. 17;  
Matches 14; Conservative 2; Mismatches 13; Indels 2; Gaps 2;

QY 1 GKICTPAGVKCPAAL-PCCPG-LRIGGWN 29  
Db 146 GAGCPKGGPRCATATPCCPSLRAPGCGN 176

RESULT 13  
T30201  
Notch homolog protein - sea squirt (Halocynthia roretzi)  
C:Species: Halocynthia roretzi  
C>Date: 02-Sep-2000 #sequence\_revision 02-Sep-2000 #text\_change 08-Sep-2002  
C:Accession: T30201  
R:Horii, S.; Saichoh, T.; Matsumoto, M.; Makabe, K.W.; Nishida, H.  
Dev. Genes Evol. 207, 371-380, 1997  
A:Title: Notch homologue from Halocynthia roretzi is preferentially expressed in the cer

A:Reference number: Z20775  
A:Accession: T30201  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-2352 <HOR>  
A:Cross-references: EMBL:AB001327; NID:d1204472; PID:d1026501; PIDN:BAA25571.1  
C:Genetics:  
C:Superfamily: notch protein; ankyrin repeat homology; EGF homology

Query Match 28.9%; Score 56; DB 2; Length 2352;  
Best Local Similarity 36.8%; Pred. No. 1.1e+02;  
Matches 14; Conservative 2; Mismatches 14; Indels 8; Gaps 2;

QY 4 CTP--AGVKCPAAL-----PCCPGLRIGGWNKVC 33  
Db 593 CTFPGTGEHCDTIDNECDSPCMGATCQNEVNFVQ 630

RESULT 14  
S18188  
notch protein homolog - rat  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 19-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 02-Aug-2002  
C:Accession: S18188  
R:Reinmaster, G.; Roberts, V.J.; Lemke, G.  
Development 113, 199-205, 1991  
A:Title: A homolog of Drosophila Notch expressed during mammalian development.  
A:Reference number: S18188; MUID:92111383; PMID:1764995  
A:Accession: S18188  
A:Molecule type: mRNA  
A:Residues: 1-2531 <WEI>  
A:Cross-references: EMBL:X57405; NID:G57634; PID:G57635  
C:Superfamily: notch protein; ankyrin repeat homology; EGF homology  
F;1025-1056/Domain: EGF homology <EGF1>  
F;1233-1264/Domain: EGF homology <EGF2>  
F;1917-1949/Domain: ankyrin repeat homology <AN1>  
F;1950-1982/Domain: ankyrin repeat homology <AN2>  
F;1984-2016/Domain: ankyrin repeat homology <AN3>  
F;2017-2049/Domain: ankyrin repeat homology <AN4>  
F;2050-2082/Domain: ankyrin repeat homology <AN5>

Query Match 28.9%; Score 56; DB 2; Length 2531;  
Best Local Similarity 36.8%; Pred. No. 1.1e+02;  
Matches 14; Conservative 2; Mismatches 14; Indels 8; Gaps 2;

QY 4 CTP--AGVKCPAALPCCPGRLR-----CIGGWNKVC 33  
Db 245 CLFPGAGQCNENVDPCGNNCKGACVDGVNTYNC 282

RESULT 15  
A46019  
notch-1 protein - mouse  
N:Alternate names: notch protein  
C:Species: Mus musculus (house mouse)  
C>Date: 22-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 16-Aug-2004  
C:Accession: A46019; S25144; C49175; B46438; PH1569; S32109  
R:del Amo, F.F.; Gendron-Maguire, M.; Swiatek, P.J.; Jenkins, N.A.; Copeland, N.G.; Grid  
Genomics 15, 259-264, 1993  
A:Title: Cloning, analysis, and chromosomal localization of Notch-1, a mouse homolog of I  
A:Reference number: A46019; MUID:93194170; PMID:8449489  
A:Accession: A46019  
A:Status: not compared with conceptual translation  
A:Molecule type: nucleic acid  
A:Residues: 1-2531 <DEL>  
A:Cross-references: UNIPROT:O01705; GB:Z11886; GB:S47228; NID:G288502; PIDN:CAA77941.1; I  
A>Note: sequence extracted from NCBI backbone (NCBIP:127318)  
R:Francisco del Amo, F.; Smith, D.E.; Swiatek, P.J.; Gendron-Maguire, M.; Greenspan, R.J.; N  
submitted to the EMBL Data Library, April 1992  
A:Description: Expression pattern of Notch, a mouse homolog of Drosophila Notch, suggests  
A:Reference number: S25144



A;Accession: S25144  
 A;Molecule type: mRNA  
 A;Residues: 1551-2108,'O',2110-2114,'ALP',2118-2170 <FRA>  
 A;Cross-references: EMBL:Z11886  
 R;Lardelli, M.; Lendahl, U.  
 Exp. Cell Res. 204, 364-372, 1993  
 A;Title: Notch A and Notch B--two mouse Notch homologues coexpressed in a wide variety of  
 A;Reference number: A49175; MUID:93178563; PMID:8440332  
 A;Accession: C49175  
 A;Status: preliminary; nucleic acid sequence not shown  
 A;Molecule type: mRNA  
 A;Residues: 1161-1547 <LAR>  
 A;Cross-references: EMBL:X68278; NID:G287987; PIDN:CAA48339.1; PID:G287988  
 A;Experimental source: embryo  
 A;Note: sequence extracted from NCBI backbone (NCBIP:126159)  
 R;Kopan, R.; Weintraub, H.  
 J. Cell Biol. 121, 631-641, 1993  
 A;Title: Mouse notch: expression in hair follicles correlates with cell fate determination  
 A;Reference number: A46438; MUID:93252998; PMID:8486742  
 A;Accession: B46438  
 A;Status: preliminary  
 A;Molecule type: nucleic acid  
 A;Residues: 1865-1932,'RR',1935-1937,'L',1938-1967,'I',1969-2044,'IE',2047-2052,'S',2054  
 A;Experimental source: embryo  
 A;Note: sequence extracted from NCBI backbone (NCBIN:131246, NCBIP:131247)  
 C;Comment: This protein has many EGF repeats and lin-12[1172]/Notch repeats.  
 C;Comment: This protein is one of the neurogenic proteins controlling the decision between  
 C;Genetics:  
 A;Gene: notch-1  
 A;Map position: 2  
 A;Note: proximal region of chromosome 2  
 C;Superfamily: Notch protein; ankyrin repeat homology; EGF homology  
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 F;144-175/Domain: EGF homology <EGF1>  
 F;222-254/Domain: EGF homology <EGF2>  
 F;261-292/Domain: EGF homology <EGF2>  
 F;339-370/Domain: EGF homology <EGF3>  
 F;416-449/Domain: EGF homology <EGF3>  
 F;456-487/Domain: EGF homology <EGF4>  
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Perfect score: 194

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1370721 seqs, 324215800 residues

Total number of hits satisfying chosen parameters: 1370721

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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# SUMMARIES

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7	69.5	35.8	77	14	US-10-072-602B-137
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9	69	35.6	39	9	US-09-894-882-497
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16	68	35.1	3501	14	US-10-158-790-37	Sequence 37, Appl
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18	68	35.1	3501	14	US-10-140-923-37	Sequence 37, Appl
19	68	35.1	3501	14	US-10-141-756-37	Sequence 37, Appl
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## ALIGNMENTS

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Patent No. US20020102607A1  
GENERAL INFORMATION:  
APPLICANT: University of Utah Research Foundation  
APPLICANT: Cognetix, Inc.  
APPLICANT: Walker, Craig S.  
APPLICANT: Shetty, Reshma  
APPLICANT: Jimenez, Elsie C.  
APPLICANT: McIntosh, J. Michael  
APPLICANT: Olivera, Baldomero M.  
APPLICANT: Watkins, Maren  
APPLICANT: Jones, Robert M.  
APPLICANT: Shen, Greg S.  
TITLE OF INVENTION: I-Superfamily Conotoxins  
FILE REFERENCE: 2314-238  
CURRENT APPLICATION NUMBER: US/09/894,882  
CURRENT FILING DATE: 2001-06-29  
PRIOR APPLICATION NUMBER: US 60/  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: US 60/243,410  
PRIOR FILING DATE: 2000-10-27  
PRIOR APPLICATION NUMBER: US 60/246,581  
PRIOR FILING DATE: 2000-11-08  
PRIOR APPLICATION NUMBER: US 60/247,714  
PRIOR FILING DATE: 2000-11-14  
PRIOR APPLICATION NUMBER: US 60/264,256  
PRIOR FILING DATE: 2001-01-29  
NUMBER OF SEQ ID NOS: 506  
SOFTWARE: Patent in version 3.0  
SEQ ID NO 3  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Hadronyche versuta  
US-09-894-882-3

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/ Patent No. US20020102607A1  
/ GENERAL INFORMATION:  
/ APPLICANT: University of Utah Research Foundation  
/ APPLICANT: Cognetix, Inc.  
/ APPLICANT: Walker, Craig S.  
/ APPLICANT: Shetty, Reshma  
/ APPLICANT: Jimenez, Elsie C.

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; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Hadronyche versuta
US-09-894-882-5

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Best Local Similarity 46.9%; Pred. No. 0.27;
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Db 2 ICTGADRPCAACCCPCPGTSCKAESNGSVYCR 33

RESULT 6
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; Sequence 570, Application US/10072602B
; Publication No. US20030109670A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Grilley, Michelle
; APPLICANT: Schoenfeld, Robert M.
; APPLICANT: Walker, Craig
; APPLICANT: Shetty, Reshma
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: Cone Snail Peptides
; FILE REFERENCE: 2314-249
; CURRENT APPLICATION NUMBER: US/10/072,602B
; CURRENT FILING DATE: 2002-02-11
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/267,408
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 570
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Conus lividus
US-10-072-602B-570

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RESULT 8
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; Sequence 461, Application US/09894882
; Patent No. US20020102607A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506

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; Sequence 137, Application US/10072602B
; Publication No. US20030109670A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Grilley, Michelle
; APPLICANT: Schoenfeld, Robert M.
; APPLICANT: Walker, Craig
; APPLICANT: Shetty, Reshma
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: Cone Snail Peptides
; FILE REFERENCE: 2314-249
; CURRENT APPLICATION NUMBER: US/10/072,602B
; CURRENT FILING DATE: 2002-02-11
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/267,408
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 137
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Conus lividus
US-10-072-602B-137

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Best Local Similarity 44.8%; Pred. No. 1.1;
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Db 49 CCHSGAGC-YTRPCPCPLGHLCSGGQAGGLC 76

RESULT 8
US-09-894-882-461
; Sequence 461, Application US/09894882
; Patent No. US20020102607A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
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; SOFTWARE: PatentIn version 3.0
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; ORGANISM: Conus emaciatus
US-09-894-882-461

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Best Local Similarity 44.8%; Pred. No. 0.57;
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; Patent No. US20020102607A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma C.
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 60/247,714
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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 497
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Conus emaciatus
US-09-894-882-497

Query Match      35.6%; Score 69; DB 9; Length 39;
Best Local Similarity 44.8%; Pred. No. 0.7;
Matches 13; Conservative 2; Mismatches 12; Indels 2; Gaps 1;

QY      4 CTPAGVKCPAALPCCPGRLRCIGGVNNKVC 32
Db      1 CFPFGIYCTPYLPCCWGICC--GTCRNVC 27

RESULT 10
US-09-894-882-247
; Sequence 247, Application US/09894882
; Patent No. US20020102607A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma C.
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 497
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Conus emaciatus
US-09-894-882-497

Query Match      35.6%; Score 69; DB 9; Length 39;
Best Local Similarity 44.8%; Pred. No. 0.7;
Matches 13; Conservative 2; Mismatches 12; Indels 2; Gaps 1;

QY      4 CTPAGVKCPAALPCCPGRLRCIGGVNNKVC 32
Db      1 CFPFGIYCTPYLPCCWGICC--GTCRNVC 27

RESULT 11
US-10-123-155-37
; Sequence 37, Application US/10123155
; Publication No. US20030068794A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330RIC30
; CURRENT APPLICATION NUMBER: US/10/123,155
; CURRENT FILING DATE: 2002-04-15
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 37
; LENGTH: 3501
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 2762, 2778
; OTHER INFORMATION: unknown base
US-10-123-155-37

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Query Match 35.1%; Score 68; DB 14; Length 3501;

Best Local Similarity 46.2%; Pred. No. 50;  
Matches 12; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 GKICTPAGVKCPAALPCCPGRLRCIGG 26  
DB 888 GACCAAGTACCAAGCCTGTGCTGG 913

RESULT 15  
US-10-142-885-37  
; Sequence 37, Application US/10142885  
; Publication No. US20030157604A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3330RIC248  
; CURRENT APPLICATION NUMBER: US/10/142,885  
; CURRENT FILING DATE: 2002-05-10  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 37  
; LENGTH: 3501  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: 2762..2778  
; OTHER INFORMATION: unknown base  
US-10-142-885-37

Query Match 35.1%; Score 68; DB 14; Length 3501;  
Best Local Similarity 46.2%; Pred. No. 50;  
Matches 12; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 GKICTPAGVKCPAALPCCPGRLRCIGG 26  
DB 888 GACCAAGTACCAAGCCTGTGCTGG 913

Search completed: October 28, 2004, 18:40:50  
Job time : 4.0145 secs





DR

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Q9UAA4
ID Q9UAA4 PRELIMINARY; PRT; 72 AA.
AC Q9UAA4
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Four-loop conotoxin LVVIA (Fragment).
OS Conus lividus.
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=89426;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99289555; PubMed=10359796;
RA Duda T.F. Jr., Palumbi S.R.;
RT "Molecular genetics of ecological diversification: duplication and
RL rapid evolution of toxin genes of the venomous gastropod Conus.";
DR EMBL; AF089955; AAD48210.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008200; F:ion channel inhibitor activity; IEA.
DR InterPro; IPR004214; Conotoxin.
DR Pfam; PF02950; Conotoxin; 1.
FT NON TER 1
SQ SEQUENCE 72 AA; 7998 MW; B4DE7DDC87533B8D CRC64;
Query Match 37.6%; Score 73; DB 2; Length 72;
Best Local Similarity 46.4%; Pred. No. 0.2;
Matches 13; Conservative 4; Mismatches 9; Indels 2; Gaps 1;
QY 2 KICTPAGVKCPAALPCCPGLRC--IGGV 27
Db :|||||:|||||:|||||:|||||:
42 RTCSPAGEVCTSKSPCCTGFLCSHIGM 69

RESULT 6
Q9UAA7
ID Q9UAA7 PRELIMINARY; PRT; 72 AA.
AC Q9UAA7
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Four-loop conotoxin LVVIA (Fragment).
OS Conus lividus.
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=89426;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99289555; PubMed=10359796;
RA Duda T.F. Jr., Palumbi S.R.;
RT "Molecular genetics of ecological diversification: duplication and
RL rapid evolution of toxin genes of the venomous gastropod Conus.";
DR EMBL; AF089912; AAD48167.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008200; F:ion channel inhibitor activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR004214; Conotoxin.
DR Pfam; PF02950; Conotoxin; 1.
FT NON TER 1
SQ SEQUENCE 72 AA; 7970 MW; B7A0DDDC87533B8D CRC64;
Query Match 37.6%; Score 73; DB 2; Length 72;
Best Local Similarity 46.4%; Pred. No. 0.2;
Matches 13; Conservative 4; Mismatches 9; Indels 2; Gaps 1;
QY 2 KICTPAGVKCPAALPCCPGLRC--IGGV 27
Db :|||||:|||||:|||||:|||||:
42 RTCSPAGEVCTSKSPCCTGFLCSHIGM 69

RESULT 7
Q9UAB0
ID Q9UAB0 PRELIMINARY; PRT; 72 AA.
AC Q9UAB0
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Four-loop conotoxin LVVIA (Fragment).
OS Conus lividus.
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=89426;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99289555; PubMed=10359796;
RA Duda T.F. Jr., Palumbi S.R.;
RT "Molecular genetics of ecological diversification: duplication and
RL rapid evolution of toxin genes of the venomous gastropod Conus.";
DR EMBL; AF089905; AAD48161.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008200; F:ion channel inhibitor activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR004214; Conotoxin.
DR Pfam; PF02950; Conotoxin; 1.
FT NON TER 1
SQ SEQUENCE 72 AA; 8028 MW; B5720DDC87503B8D CRC64;
Query Match 37.6%; Score 73; DB 2; Length 72;
Best Local Similarity 46.4%; Pred. No. 0.2;
Matches 13; Conservative 4; Mismatches 9; Indels 2; Gaps 1;
QY 2 KICTPAGVKCPAALPCCPGLRC--IGGV 27
Db :|||||:|||||:|||||:|||||:
42 RTCSPAGEVCTSKSPCCTGFLCSHIGM 69

RESULT 8
Q9UAB1
ID Q9UAB1 PRELIMINARY; PRT; 72 AA.
AC Q9UAB1
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Four-loop conotoxin LVVIA (Fragment).
OS Conus lividus.
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=89426;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99289555; PubMed=10359796;
RA Duda T.F. Jr., Palumbi S.R.;
RT "Molecular genetics of ecological diversification: duplication and
RL rapid evolution of toxin genes of the venomous gastropod Conus.";
DR EMBL; AF089904; AAD48160.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008200; F:ion channel inhibitor activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR004214; Conotoxin.
DR Pfam; PF02950; Conotoxin; 1.
FT NON TER 1
SQ SEQUENCE 72 AA; 7935 MW; 64C72DDC8755282F CRC64;
Query Match 37.6%; Score 73; DB 2; Length 72;
Best Local Similarity 46.4%; Pred. No. 0.2;
Matches 13; Conservative 4; Mismatches 9; Indels 2; Gaps 1;
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QY	2	KICTPAGVKCPAALPCCPGLRC--IGGV 27
DB	42	RTCSPAGEVCTSKSPCCTGFLGSHGGM 69
RESULT 9		
TXJC_HADVE		
ID	TXJC_HADVE	STANDARD; PRT; 37 AA.
AC	P82228;	
DT	30-MAY-2000	(Rel. 39, Created)
DT	30-MAY-2000	(Rel. 39, Last sequence update)
DT	01-OCT-2004	(Rel. 45, Last annotation update)
DE	Janus-atracotoxin-Hv1c (J-AcTx-Hv1c)	
OS	Hadronyche versuta (Blue mountains funnel-web spider) (Atrax versutus)	
OC	Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;	
OC	Mycgalomorphae; Hexathelidae; Hadronyche.	
NCBI_TaxID=6904;		
SEQUENCE, FUNCTION, X-RAY CRYSTALLOGRAPHY, AND STRUCTURE BY NMR.		
TISSUE=Venom;		
MEDLINE=20343014; PubMed=1081200;		
Wang X.-H., Connor M., Smith R., Maciejewski M.W., Howden M.E.H.		
Nicholson G.M., Christie M.J., King G.F.;		
"Discovery and characterization of a family of insecticidal		
neurotoxins with a rare vicinal disulfide bridge.";		
Nat. Struct. Biol. 7:505-513(2000).		
CC -1- FUNCTION: Insecticidal neurotoxin.		
CC -1- SUBCELLULAR LOCATION: Secreted.		
CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.		
PDB; 1D50; NMR; A=1-37.		
3D-structure; Direct protein sequencing; Neurotoxin; Toxin.		
FT DISULFID 3 17		
FT DISULFID 10 22		
FT DISULFID 13 14		
FT DISULFID 16 32		
FT TURN 6 7		
FT STRAND 9 9		
FT TURN 18 19		
FT STRAND 20 24		
FT TURN 26 27		
FT STRAND 30 34		
SEQUENCE 37 AA; 3768 MW; E4DDF046CC7507FC CRC64;		
Query Match	37.4%;	Score 72.5; DB 1; Length 37;
Best Local Similarity	46.9%;	Pred. No. 0.13;
Matches 15; Conservative 0; Mismatches 16; Indels 1;		
QY	3	ICTPAGVKCPAALPCCPGLRCIGGVNN-KVCR 33
DB	2	ICTGADRPCAACCCPGCTSKAESNGSVYCR 33
RESULT 10		
QJUA3		
ID	QJUA3	PRELIMINARY; PRT; 72 AA.
AC	Q9UAA3;	
DT	01-MAY-2000	(TREMBLrel. 13, Created)
DT	01-MAY-2000	(TREMBLrel. 13, Last sequence update)
DT	01-OCT-2003	(TREMBLrel. 25, Last annotation update)
DE	Four-loop conotoxin LVW1A (Fragment).	
OS	Conus lividus.	
OC	Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;	
OC	Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;	
OC	Neogastropoda; Conoidea; Conidae; Conus.	
NCBI_TaxID=89426;		
SEQUENCE FROM N.A.		
MEDLINE=99289555; PubMed=10359796;		
Duda T.F. Jr., Palumbi S.R.;		
"Molecular genetics of ecological diversification: duplication and		
rapid evolution of toxin genes of the venomous gastropod Conus."		
Proc. Natl. Acad. Sci. U.S.A. 96:6820-6823(1999).		

RA Abi-Rached L., Pontarotti P., Lardelli M.;  
 RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.  
 RN [2]

RP SEQUENCE FROM N.A.  
 RC TISSUE=Whole larvae;  
 RA Lardelli M.T.;

RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; Y12539; CAC19873.1; -;  
 DR HSP; P00740; IEDM.

DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0005509; F:calcium ion binding; IEA.  
 DR GO; GO:004872; F:receptor activity; IEA.

DR GO; GO:0030154; P:cell differentiation; IEA.  
 DR InterPro; IPR002110; ANK.  
 DR InterPro; IPR000152; Asx\_hydroxyl\_S.

DR InterPro; IPR008985; ConA\_like\_1ec\_g1.  
 DR InterPro; IPR000345; CytC\_heme\_BS.  
 DR InterPro; IPR000742; EGF\_2.

DR InterPro; IPR001891; EGF\_Ca.  
 DR InterPro; IPR001438; EGF\_II.  
 DR InterPro; IPR006209; EGF\_like.

DR InterPro; IPR010660; NOD\_Notch\_region.  
 DR InterPro; IPR000800; Notch\_region.  
 DR Pfam; PF00023; Ank; 6.

DR Pfam; PF00008; EGF; 34.  
 DR Pfam; PF07645; EGF\_CA; 2.  
 DR Pfam; PF06816; NOD; 1.

DR Pfam; PF00066; Notch; 3.  
 DR PRINTS; PR01415; ANKYRIN.  
 DR PRINTS; PR00010; EGFBLD.

DR PRINTS; PR01452; NOTCH.  
 DR SMART; SMC0248; ANK; 6.  
 DR SMART; SMC0179; EGF\_CA; 21.

DR SMART; SMC0004; NL; 3.  
 DR PROSITE; PS00088; ANK\_REPEAT; 4.  
 DR PROSITE; PS00297; ANK\_REPEAT\_REGION; 1.

DR PROSITE; PS00010; ASX\_HYDROXYL; 23.  
 DR PROSITE; PS00190; CYTOCHROME\_C; UNKNOWN\_1.  
 DR PROSITE; PS00022; EGF\_1; 34.

DR PROSITE; PS01186; EGF\_2; 28.  
 DR PROSITE; PS00026; EGF\_3; 36.  
 DR PROSITE; PS01187; EGF\_CA; 22.

DR ANK repeat; EGF-like domain; Receptor.  
 KW ANK repeat; EGF-like domain; Receptor.  
 SQ SEQUENCE 2524 AA; 270970 MW; C2CA57E306D23EC9 CRC64;

Query Match 37.1%; Score 72; DB 2; Length 2524;  
 Best Local Similarity 45.9%; Pred. No. 6.3;  
 Matches 17; Conservative 2; Mismatches 10; Indels 8; Gaps 2;

Qy 4 CTPA--GVKCP-----AALPCCPLRCIGGVNNKVC 32  
 Db 768 CLPGYGVNCDINTDECASNPQNGRCLDGVNNVC 804

RESULT 13  
 TXCS PHONI  
 ID TXCS PHONI \* STANDARD; PRT; 33 AA.

AC P84015;  
 DT 01-OCT-2004 (Rel. 45, Created)  
 DT 01-OCT-2004 (Rel. 45, Last sequence update)

DT 01-OCT-2004 (Rel. 45, Last annotation update)  
 DE Venom protein FN10C5.  
 OS Phoneutria nigriventer (Brazilian armed spider).

OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;  
 OC Araneomorphae; Entelegynae; Lycosoidea; Ctenidae; Phoneutria.  
 OX NCBI\_TaxID=6918;

FN [1]  
 RP SEQUENCE, FUNCTION, SUBCELLULAR LOCATION, TISSUE SPECIFICITY, AND MASS  
 RP SPECTROMETRY.

RC TISSUE=Venom;  
 RA Richardson M., Pimenta A.M.C., Benquerer M.P., Santoro M.M.,  
 RA Figueiredo S.G., Cordeliro M.N.; of Brazilian armed spider Phoneutria

RT "New peptide FN10C5 from venom of

nigriventer has sequence similarities with snake disintegrins,  
 RT vasetocin-neurophysins and other spider toxins.";  
 RL Submitted (JUN-2004) to Swiss-Prot.

CC -!- FUNCTION: Non-toxic to mice.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.

CC -!- MASS SPECTROMETRY: MW=3672.7; METHOD=Electrospray; RANGE=1-33;  
 CC NOTE=Ref.1.  
 KW Direct protein sequencing.

Qy 4 CTPAGVKCPAALPCCPLRCIGGVNNKVC 33  
 Db 3 CAQKGKIC-HDIHCCTNLKCYREGSNRVC 31

RESULT 14  
 Q7PMF9  
 ID Q7PMF9 PRELIMINARY; PRT; 3775 AA.

AC Q7PMF9;  
 DT 01-MAR-2004 (TRENBLrel. 26, Created)  
 DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)

DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)  
 DE ENSANGP00000011881 (Fragment).  
 GN Name=ENSANGG00000009392;

OS Anopheles gambiae str. PEST.  
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.

OC NCBI\_TaxID=180454;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC STRAIN=PEST;  
 RA Anopheles Genome Sequencing Consortium;  
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.

CC -!- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.

DR EMBL; AAB01008980; EAA13897.2;  
 DR GO; GO:0005509; F:calcium ion binding; IEA.  
 DR InterPro; IPR000152; Asx\_hydroxyl\_S.

DR InterPro; IPR000345; CytC\_heme\_BS.  
 DR InterPro; IPR000742; EGF\_2.  
 DR InterPro; IPR001891; EGF\_Ca.

DR InterPro; IPR006209; EGF\_like.  
 DR InterPro; IPR01304; Lectin\_C.  
 DR Pfam; PF00008; EGF; 3.

DR Pfam; PF07645; EGF\_CA; 16.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; 17.  
 DR PROSITE; PS00190; CYTOCHROME\_C; UNKNOWN\_1.

DR PROSITE; PS00615; C\_TYPE\_LECTIN\_1; UNKNOWN\_1.  
 DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
 DR PROSITE; PS01186; EGF\_2; 25.

DR PROSITE; PS00026; EGF\_3; 25.  
 DR PROSITE; PS01187; EGF\_CA; 16.  
 KW EGF-like domain.

FT NON\_TER 1  
 FT NON\_TER 3775  
 SQ SEQUENCE 3775 AA; 396198 MW; 51C4108F6E9908F4 CRC64;

Query Match 35.8%; Score 69.5; DB 2; Length 3775;  
 Best Local Similarity 41.9%; Pred. No. 18;  
 Matches 13; Conservative 5; Mismatches 12; Indels 1; Gaps 1;

Qy 3 ICT-PAGVKCPAALPCCPLRCIGGVNNKVC 32  
 Db 1353 VCTNPRQCCGANNQCPGCGVGVNNLC 1383

RESULT 15

```

CXK_CONV
ID  CXK_CONV  STANDARD;  PRT;  67 AA.
AC  Q7YZS9;
DT  29-MAR-2004 (Rel. 43, Created)
DT  29-MAR-2004 (Rel. 43, Last sequence update)
DT  05-JUL-2004 (Rel. 44, Last annotation update)
DE  Kappa-conotoxin ViTx precursor.
GN  Name=ViTx;
OS  Conus virgo (Virgin cone).
OC  Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC  Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC  Neogastropoda; Conoidea; Conidae; Conus.
OX  NCBI_TaxID=89427;
RN  [1]
RP  SEQUENCE FROM N.A., SEQUENCE OF 27-53, SYNTHESIS OF 27-60, AND MASS
RP  SPECTROMETRY.
RC  TISSUE=Venom, and Venom duct;
RX  PubMed=12893060;
RA  Kaufenstein S., Huys I., Lamthanh H., Stocklin R., Sotto F., Menez A.,
RA  Tytgat J., Mebs D.;
RT  "A novel conotoxin inhibiting vertebrate voltage-sensitive potassium
RL  channels.";
RL  Toxicon 42:43-52(2003).
RN  [2]
RP  SEQUENCE FROM N.A.
RC  TISSUE=Venom duct;
RA  Kaufenstein S.;
RL  Thesis (2001), University of Darmstadt, Germany.
CC  -!- FUNCTION: Kappa-conotoxins bind and inhibit voltage-sensitive
CC  potassium channels. This toxin inhibits the vertebrate potassium
CC  channels Kv1.1 and Kv1.3, but not Kv1.2. It has no effect on HERG-
CC  type channels, sodium hH1 channels and Kir-type channels (IRK1).
CC  -!- SUBCELLULAR LOCATION: Secreted.
CC  -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC  -!- FTW: Contains four disulfide bonds.
CC  -!- MASS SPECTROMETRY: MW=3933.3; METHOD=Electrospray; RANGE=27-60;
CC  NOTE=Ref.1.
CC  -!- SIMILARITY: Belongs to the conotoxin O-superfamily. Kappa-type
CC  family.
CC  -----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use by non-profit institutions as long as its content is in no way
CC  modified and this statement is not removed. Usage by and for commercial
CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; AJ560778; CAD90965.1; -.
KW  Direct protein sequencing; Signal; Toxin.
FT  SIGNAL 1 26
FT  CHAIN 27 60 Kappa-conotoxin ViTx.
FT  PROPEP 61 67
FT  CONFLICT 38 38 P -> S (in Ref. 1).
FT  CONFLICT 49 49 G -> S (in Ref. 1).
SQ  SEQUENCE 67 AA; 7599 MW; 4667D012446F62D CRC64;

Query Match 35.6%; Score 69; DB 1; Length 67;
Best Local Similarity 44.8%; Pred. No. 0.57;
Matches 13; Conservative 2; Mismatches 12; Indels 2; Gaps 1;

OY 4 CTPAGVCPALPCCPLRGCGVNNKVC 32
DB 29 CFPFGIYCTPLPCCGGCC--GTCRNV 55

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Search completed: October 28, 2004, 18:29:44  
Job time : 6.6608 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 28, 2004, 18:06:07 ; Search time 1.02508 Seconds  
(without alignments)  
2134.948 Million cell updates/sec

Title: US-10-019-823B-2  
Perfect score: 194  
Sequence: 1 GKICTAGVKCPAALPCCPLRCIGGVNKKVCR 33

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/ptodata/1/iaa/5A COMB.pcp.\*
- 2: /cgn2\_6/ptodata/1/iaa/5B COMB.pcp.\*
- 3: /cgn2\_6/ptodata/1/iaa/6A COMB.pcp.\*
- 4: /cgn2\_6/ptodata/1/iaa/6B COMB.pcp.\*
- 5: /cgn2\_6/ptodata/1/iaa/6C COMB.pcp.\*
- 6: /cgn2\_6/ptodata/1/iaa/6D COMB.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	82	42.3	36	4	US-09-894-882-3
2	79	40.7	36	4	US-09-894-882-4
3	75	38.7	36	1	US-08-882-485A-7
4	75	38.7	36	2	US-08-882-485A-7
5	75	38.7	37	1	US-08-882-485A-6
6	75	38.7	37	2	US-08-882-485A-6
7	72.5	37.4	37	4	US-09-894-882-5
8	69	35.6	31	4	US-09-894-882-461
9	69	35.6	29	4	US-09-894-882-497
10	69	35.6	67	4	US-09-894-882-247
11	67	34.5	32	4	US-09-894-882-470
12	67	34.5	40	4	US-09-894-882-498
13	67	34.5	68	4	US-09-894-882-274
14	59	30.4	155	4	US-09-252-991A-28474
15	59	30.4	2471	1	US-08-185-432-16
16	59	30.4	2471	1	US-08-883-590A-19
17	59	30.4	2471	3	US-08-532-584-19
18	59	30.4	2471	4	US-08-899-232-1
19	59	30.4	2471	4	US-09-121-457-1
20	58.5	30.2	34	1	US-08-117-080-5
21	58.5	30.2	34	1	US-08-471-329-5
22	58.5	30.2	34	2	US-08-915-142-5
23	58.5	30.2	908	4	US-08-714-741-44
24	58	29.9	39	4	US-09-894-882-248
25	57.5	29.6	180	4	US-09-510-238A-286
26	57.5	29.6	281	4	US-09-252-991A-23962
27	57.5	29.6	420	4	US-09-907-794A-109

Sequence 109, App  
Sequence 109, App  
Sequence 109, App  
Sequence 290, App  
Sequence 109, App  
Sequence 11, Appl  
Sequence 16925, A  
Sequence 474, App  
Sequence 296, App  
Sequence 502, App  
Sequence 295, App  
Sequence 10, Appl  
Sequence 30, Appl  
Sequence 1, Appl  
Sequence 1, Appl  
Sequence 471, App  
Sequence 475, App  
Sequence 278, App

ALIGNMENTS

RESULT 1  
US-09-894-882-3  
; Sequence 3, Application US/09894882  
; Patent No. 6767895  
; GENERAL INFORMATION:  
; APPLICANT: University of Utah Research Foundation  
; APPLICANT: Cognetix, Inc.  
; APPLICANT: Walker, Craig S.  
; APPLICANT: Shetty, Reshma  
; APPLICANT: Jimenez, Elsie C.  
; APPLICANT: McIntosh, J. Michael  
; APPLICANT: Olivera, Balcomero M.  
; APPLICANT: Watkins, Maren  
; APPLICANT: Jones, Robert M.  
; APPLICANT: Shen, Greg S.  
; TITLE OF INVENTION: I-Superfamily Conotoxins  
; FILE REFERENCE: 2314-238  
; CURRENT APPLICATION NUMBER: US/09/894,882  
; CURRENT FILING DATE: 2001-06-29  
; PRIOR APPLICATION NUMBER: US 60/  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 60/243,410  
; PRIOR FILING DATE: 2000-10-27  
; PRIOR APPLICATION NUMBER: US 60/246,581  
; PRIOR FILING DATE: 2000-11-08  
; PRIOR APPLICATION NUMBER: US 60/247,714  
; PRIOR FILING DATE: 2000-11-14  
; PRIOR APPLICATION NUMBER: US 60/264,256  
; PRIOR FILING DATE: 2001-01-29  
; NUMBER OF SEQ ID NOS: 506  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 3  
; LENGTH: 36  
; TYPE: PR  
; ORGANISM: Hadronyche versuta  
US-09-894-882-3

Query Match 42.3%; Score 82; DB 4; Length 36;  
Best Local Similarity 51.5%; Pred. No. 0.004;  
Matches 17; Conservative 1; Mismatches 13; Indels 2; Gaps 1;  
QY 3 ICTAGVKCPAALPCCPLRCIGGVNKKV--CR 33  
Db 2 ICTGADRCACCCCPGTSQQGPESNGVYCR 34  
RESULT 2  
US-09-894-882-4  
; Sequence 4, Application US/09894882  
; Patent No. 6767895

GENERAL INFORMATION:  
APPLICANT: University of Utah Research Foundation  
APPLICANT: Cognetix, Inc.  
APPLICANT: Walker, Craig S.  
APPLICANT: Shetty, Reshma  
APPLICANT: Jimenez, Elsie C.  
APPLICANT: McIntosh, J. Michael  
APPLICANT: Olivera, Balomero M.  
APPLICANT: Watkins, Maren  
APPLICANT: Jones, Robert M.  
APPLICANT: Shen, Greg S.  
TITLE OF INVENTION: I-Superfamily Conotoxins  
FILE REFERENCE: 2314-238  
CURRENT APPLICATION NUMBER: US/09/894,882  
CURRENT FILING DATE: 2001-06-29  
PRIOR APPLICATION NUMBER: US 60/  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: US 60/243,410  
PRIOR FILING DATE: 2000-10-27  
PRIOR APPLICATION NUMBER: US 60/246,581  
PRIOR FILING DATE: 2000-11-08  
PRIOR APPLICATION NUMBER: US 60/247,714  
PRIOR FILING DATE: 2000-11-14  
PRIOR APPLICATION NUMBER: US 60/264,256  
PRIOR FILING DATE: 2001-01-29  
NUMBER OF SEQ ID NOS: 506  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 4  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Hadronyche versuta  
US-09-894-882-4

Query Match 40.7%; Score 79; DB 4; Length 36;  
Best Local Similarity 51.5%; Pred. No. 0.009;  
Matches 17; Conservative 0; Mismatches 14; Indels 2; Gaps 1;

QY 3 ICTPAGVKCPAALPCPCGLRCIGGVNKKV--CR 33  
Db 2 ICTGADRPCAACCCPCPGTSCQGPENGVS YCR 34

RESULT 3  
US-08-682-485A-7  
Sequence 7, Application US/08682485A  
Patent No. 5763568  
GENERAL INFORMATION:  
APPLICANT: ATKINSON, RONALD K  
APPLICANT: HOWDEN, MERLIN E.H.  
APPLICANT: TYLER, MARGARET I  
APPLICANT: VONARX, EDWARD J  
TITLE OF INVENTION: Insecticidal Toxins Derived From  
Funnel Web (Atrax or Hadronyche Spiders)  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Zeneca, Inc.  
STREET: 1200 South 47th Street  
CITY: Richmond  
STATE: California  
COUNTRY: USA  
ZIP: 94804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/682,485A  
FILING DATE: 29-JAN-1993  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/682,485  
FILING DATE: 17-JULY-1996

APPLICATION NUMBER: US/08/256,933  
FILING DATE: 27-JULY-1994  
APPLICATION NUMBER: WO 93/15108  
FILING DATE: 29-JAN-1993  
APPLICATION NUMBER: AU PL0722  
FILING DATE: 31-JAN-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Shaw, Melissa A.  
REGISTRATION NUMBER: 38,301  
REFERENCE/DOCKET NUMBER: PPD 5099/D1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 510-231-1542  
TELEFAX: 510-231-1112  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Atrax formidabilis  
US-08-682-485A-7

Query Match 38.7%; Score 75; DB 1; Length 36;  
Best Local Similarity 50.0%; Pred. No. 0.026;  
Matches 16; Conservative 0; Mismatches 14; Indels 2; Gaps 1;

QY 4 CTPAGVKCPAALPCPCGLRCIGGVNKKV--CR 33  
Db 4 CTGADRPCAACCCPCPGTSCQGPENGVS YCR 35

RESULT 4  
US-08-933-314-7  
Sequence 7, Application US/08933314  
Patent No. 5959182  
GENERAL INFORMATION:  
APPLICANT: ATKINSON, RONALD K  
APPLICANT: HOWDEN, MERLIN E.H.  
APPLICANT: TYLER, MARGARET I  
APPLICANT: VONARX, EDWARD J  
TITLE OF INVENTION: Insecticidal Toxins Derived From  
Funnel Web (Atrax or Hadronyche Spiders)  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Zeneca, Inc.  
STREET: 1200 South 47th Street  
CITY: Richmond  
STATE: California  
COUNTRY: USA  
ZIP: 94804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/933,314  
FILING DATE: 27-JULY-1994  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/682,485  
FILING DATE: 17-JULY-1996  
APPLICATION NUMBER: US/08/256,933  
FILING DATE: 29-JAN-1993  
APPLICATION NUMBER: AU PL0722  
FILING DATE: 31-JAN-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Shaw, Melissa A.



CLASSIFICATION: 424  
PRIOR APPLICATION NUMBER: US/08/682,485  
FILING DATE: 17-JULY-1996  
APPLICATION NUMBER: US/08/256,933  
FILING DATE: 27-JULY-1994  
APPLICATION NUMBER: WO 93/15108  
FILING DATE: 29-JAN-1993  
APPLICATION NUMBER: AU PL0722  
FILING DATE: 31-JAN-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Shaw, Melissa A.  
REGISTRATION NUMBER: 38,301  
REFERENCE/DOCKET NUMBER: PFD 5099/D1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 510-231-1542  
TELEFAX: 510-231-1112  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 37 amino acids

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/933,314  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/682,485  
FILING DATE: 17-JULY-1996  
APPLICATION NUMBER: US/08/256,933  
FILING DATE: 27-JULY-1994  
APPLICATION NUMBER: WO 93/15108  
FILING DATE: 29-JAN-1993  
APPLICATION NUMBER: AU PL0722  
FILING DATE: 31-JAN-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Shaw, Melissa A.  
REGISTRATION NUMBER: 38,301  
REFERENCE/DOCKET NUMBER: PPD 5099/D1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 510-231-1542  
TELEFAX: 510-231-1112  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 37 amino acids  
TYPE: amino acid  
TOPOLOGY: linear

MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Atrax formidabilis  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 37  
; OTHER INFORMATION: /label=a  
; OTHER INFORMATION: /note="this site may be amidated without loss  
; OTHER INFORMATION: of biological activity"  
US-08-933-314-6  
Query Match 38.7%; Score 75; DB 2; Length 37;  
Best Local Similarity 50.0%; Pred. No. 0.027;  
Matches 16; Conservative 0; Mismatches 14; Indels 2; Gaps 1;  
QY 4 CTGAGVKKCPAALPCPGRLRCIGGVNKKV--CR 33  
DB 4 CTGADRPCAACCCPCPGTSCKGPPNGVSYCR 35  
RESULT 7  
US-09-894-882-5  
; Sequence 5, Application US/09894882  
; Patent No. 6767895  
; GENERAL INFORMATION:  
; APPLICANT: University of Utah Research Foundation  
; APPLICANT: Cognetix, Inc.  
; APPLICANT: Walker, Craig S.  
; APPLICANT: Shetty, Reshma  
; APPLICANT: Jimenez, Elsie C.  
; APPLICANT: McIntosh, J. Michael  
; APPLICANT: Olivera, Baldomero M.  
; APPLICANT: Watkins, Maren  
; APPLICANT: Jones, Robert M.  
; APPLICANT: Shen, Greg S.  
; TITLE OF INVENTION: I-Superfamily Conotoxins  
; FILE REFERENCE: 2314-238  
; CURRENT APPLICATION NUMBER: US 60/243,410  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 60/246,581  
; PRIOR FILING DATE: 2000-11-08  
; PRIOR APPLICATION NUMBER: US 60/247,714  
; PRIOR FILING DATE: 2000-11-14  
; PRIOR APPLICATION NUMBER: US 60/264,256  
; PRIOR FILING DATE: 2001-01-29  
; NUMBER OF SEQ ID NOS: 506  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 5  
; TYPE: PRT  
; ORGANISM: Hadronyche versuta  
US-09-894-882-5  
Query Match 37.4%; Score 72.5; DB 4; Length 37;  
Best Local Similarity 46.9%; Pred. No. 0.053;  
Matches 15; Conservative 0; Mismatches 16; Indels 1; Gaps 1;  
QY 3 ICTGAGVKKCPAALPCPGRLRCIGGVN--KVCR 33  
DB 2 ICTGADRPCAACCCPCPGTSCKAESNGVSYCR 33  
RESULT 8  
US-09-894-882-461  
; Sequence 461, Application US/09894882  
; Patent No. 6767895  
; GENERAL INFORMATION:  
; APPLICANT: University of Utah Research Foundation  
; APPLICANT: Cognetix, Inc.  
; APPLICANT: Walker, Craig S.  
; APPLICANT: Shetty, Reshma  
; APPLICANT: Jimenez, Elsie C.  
; APPLICANT: McIntosh, J. Michael  
; APPLICANT: Olivera, Baldomero M.  
; APPLICANT: Watkins, Maren  
; APPLICANT: Jones, Robert M.  
; APPLICANT: Shen, Greg S.  
; TITLE OF INVENTION: I-Superfamily Conotoxins  
; FILE REFERENCE: 2314-238  
; CURRENT APPLICATION NUMBER: US/09/894,882  
; PRIOR FILING DATE: 2001-06-29  
; PRIOR APPLICATION NUMBER: US 60/  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 60/243,410  
; PRIOR FILING DATE: 2000-11-08  
; PRIOR APPLICATION NUMBER: US 60/246,581  
; PRIOR FILING DATE: 2000-11-14  
; PRIOR APPLICATION NUMBER: US 60/247,714  
; PRIOR FILING DATE: 2000-11-14  
; PRIOR APPLICATION NUMBER: US 60/264,256  
; PRIOR FILING DATE: 2001-01-29  
; NUMBER OF SEQ ID NOS: 506  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 5  
; TYPE: PRT  
; ORGANISM: Hadronyche versuta  
US-09-894-882-5

APPLICANT: University of Utah Research Foundation  
; APPLICANT: Cognetix, Inc.  
; APPLICANT: Walker, Craig S.  
; APPLICANT: Shetty, Reshma  
; APPLICANT: Jimenez, Elsie C.  
; APPLICANT: McIntosh, J. Michael  
; APPLICANT: Olivera, Baldomero M.  
; APPLICANT: Watkins, Maren  
; APPLICANT: Jones, Robert M.  
; APPLICANT: Shen, Greg S.  
; TITLE OF INVENTION: I-Superfamily Conotoxins  
; FILE REFERENCE: 2314-238  
; CURRENT APPLICATION NUMBER: US/09/894,882  
; CURRENT FILING DATE: 2001-06-29  
; PRIOR APPLICATION NUMBER: US 60/  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 60/243,410  
; PRIOR FILING DATE: 2000-10-27  
; PRIOR APPLICATION NUMBER: US 60/246,581  
; PRIOR FILING DATE: 2000-11-08  
; PRIOR APPLICATION NUMBER: US 60/247,714  
; PRIOR FILING DATE: 2000-11-14  
; PRIOR APPLICATION NUMBER: US 60/264,256  
; PRIOR FILING DATE: 2001-01-29  
; NUMBER OF SEQ ID NOS: 506  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 461  
; LENGTH: 31  
; TYPE: PRT  
; ORGANISM: Conus emaciatus  
US-09-894-882-461  
Query Match 35.6%; Score 69; DB 4; Length 31;  
Best Local Similarity 44.8%; Pred. No. 0.12; Indels 2; Gaps 1;  
Matches 13; Conservative 2; Mismatches 12  
QY 4 CTGAGVKKCPAALPCPGRLRCIGGVNKKVC 32  
DB 1 CTGPGIYCTPYLPCCWGICC--GTCRNV 27  
RESULT 9  
US-09-894-882-497  
; Sequence 497, Application US/09894882  
; Patent No. 6767895  
; GENERAL INFORMATION:  
; APPLICANT: University of Utah Research Foundation  
; APPLICANT: Cognetix, Inc.  
; APPLICANT: Walker, Craig S.  
; APPLICANT: Shetty, Reshma  
; APPLICANT: Jimenez, Elsie C.  
; APPLICANT: McIntosh, J. Michael  
; APPLICANT: Olivera, Baldomero M.  
; APPLICANT: Watkins, Maren  
; APPLICANT: Jones, Robert M.  
; APPLICANT: Shen, Greg S.  
; TITLE OF INVENTION: I-Superfamily Conotoxins  
; FILE REFERENCE: 2314-238  
; CURRENT APPLICATION NUMBER: US/09/894,882  
; CURRENT FILING DATE: 2001-06-29  
; PRIOR APPLICATION NUMBER: US 60/  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 60/243,410  
; PRIOR FILING DATE: 2000-10-27  
; PRIOR APPLICATION NUMBER: US 60/246,581  
; PRIOR FILING DATE: 2000-11-08  
; PRIOR APPLICATION NUMBER: US 60/247,714  
; PRIOR FILING DATE: 2000-11-14  
; PRIOR APPLICATION NUMBER: US 60/264,256  
; PRIOR FILING DATE: 2001-01-29  
; NUMBER OF SEQ ID NOS: 506  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 497

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; LENGTH: 39
; TYPE: PRT
; ORGANISM: Conus emaciatus
US-09-894-882-497

Query Match      35.6%; Score 69; DB 4; Length 39;
Best Local Similarity 44.8%; Pred. No. 0.14;
Matches 13; Conservative 2; Mismatches 12; Indels 2; Gaps 1;

Qy 4 CTPAGVKCPAALPCCPLRGIGVNNKVC 32
  |||:|||||:|||||:
Db 1 CFPFGIYCTPLPCCWGICC--GTCRNVC 27

RESULT 10
US-09-894-882-247
; Sequence 247, Application US/09894882
; Patent No. 6767895
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT FILING DATE: 2001-06-29
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 247
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Conus emaciatus
US-09-894-882-247

Query Match      35.6%; Score 69; DB 4; Length 67;
Best Local Similarity 44.8%; Pred. No. 0.23;
Matches 13; Conservative 2; Mismatches 12; Indels 2; Gaps 1;

Qy 4 CTPAGVKCPAALPCCPLRGIGVNNKVC 32
  |||:|||||:|||||:
Db 29 CFPFGIYCTPLPCCWGICC--GTCRNVC 55

RESULT 11
US-09-894-882-470
; Sequence 470, Application US/09894882
; Patent No. 6767895
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
```

```
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT FILING DATE: 2001-06-29
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 470
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Conus virgo
US-09-894-882-470

Query Match      34.5%; Score 67; DB 4; Length 32;
Best Local Similarity 50.0%; Pred. No. 0.2;
Matches 11; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

Qy 4 CTPAGVKCPAALPCCPLRGICG 25
  |||:|||||:|||||:
Db 1 CFPGLTFCRSRYLPCSGMCCSG 22

RESULT 12
US-09-894-882-498
; Sequence 498, Application US/09894882
; Patent No. 6767895
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT FILING DATE: 2001-06-29
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 498
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Conus virgo
US-09-894-882-498

Query Match      34.5%; Score 67; DB 4; Length 40;
Best Local Similarity 50.0%; Pred. No. 0.25;
Matches 11; Conservative 1; Mismatches 10; Indels 0; Gaps 0;
```

QY 4 CTPAGVKCPAALPCCPGRLRCIG 25  
 DB 1 CFFLTGFCRSYLPCCSGMCCSG 22

RESULT 13  
 US-09-894-882-274  
 ; Sequence 274, Application US/09894882  
 ; Patent No. 6767895  
 ; GENERAL INFORMATION:  
 ; APPLICANT: University of Utah Research Foundation  
 ; APPLICANT: Cognetix, Inc.  
 ; APPLICANT: Walker, Craig S.  
 ; APPLICANT: Shetty, Reshma C.  
 ; APPLICANT: Jimenez, Elsie C.  
 ; APPLICANT: McIntosh, J. Michael  
 ; APPLICANT: Olivera, Baldomero M.  
 ; APPLICANT: Watkins, Warren  
 ; APPLICANT: Jones, Robert M.  
 ; APPLICANT: Shen, Greg S.  
 ; TITLE OF INVENTION: I-Superfamily Conotoxins  
 ; FILE REFERENCE: 2314-238  
 ; CURRENT APPLICATION NUMBER: US/09/894,882  
 ; CURRENT FILING DATE: 2001-06-29  
 ; PRIOR APPLICATION NUMBER: US 60/  
 ; PRIOR FILING DATE: 2000-06-30  
 ; PRIOR APPLICATION NUMBER: US 60/243,410  
 ; PRIOR FILING DATE: 2000-10-27  
 ; PRIOR APPLICATION NUMBER: US 60/246,581  
 ; PRIOR FILING DATE: 2000-11-08  
 ; PRIOR APPLICATION NUMBER: US 60/247,714  
 ; PRIOR FILING DATE: 2000-11-14  
 ; PRIOR APPLICATION NUMBER: US 60/264,256  
 ; PRIOR FILING DATE: 2001-01-29  
 ; NUMBER OF SEQ ID NOS: 506  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 274  
 ; LENGTH: 68  
 ; TYPE: PRT  
 ; ORGANISM: Conus virgo  
 US-09-894-882-274

Query Match 34.5%; Score 67; DB 4; Length 68;  
 Best Local Similarity 50.0%; Pred. No. 0.41;  
 Matches 11; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 4 CTPAGVKCPAALPCCPGRLRCIG 25  
 DB 29 CFFLTGFCRSYLPCCSGMCCSG 50

RESULT 14  
 US-09-252-991A-28474  
 ; Sequence 28474, Application US/09252991A  
 ; Patent No. 6651795  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Marc J. Rubenfield et al.  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
 ; FILE REFERENCE: 107196.136  
 ; CURRENT APPLICATION NUMBER: US/09/252,991A  
 ; CURRENT FILING DATE: 1999-02-18  
 ; PRIOR APPLICATION NUMBER: US 60/074,788  
 ; PRIOR FILING DATE: 1998-02-18  
 ; PRIOR APPLICATION NUMBER: US 60/094,190  
 ; PRIOR FILING DATE: 1998-07-27  
 ; NUMBER OF SEQ ID NOS: 33142  
 ; SEQ ID NO 28474  
 ; LENGTH: 155  
 ; TYPE: PRT  
 ; ORGANISM: Pseudomonas aeruginosa  
 US-09-252-991A-28474

Query Match 30.4%; Score 59; DB 4; Length 155;  
 Best Local Similarity 52.6%; Pred. No. 7.4;  
 Matches 10; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 5 TPAGVKCPAALPCCPGRLRC 23  
 DB 7 TPASPRPSTAMCCPGRR 25

RESULT 15  
 US-08-185-432-16  
 ; Sequence 16, Application US/08185432  
 ; Patent No. 5750652  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Attavanis-Tsakonas, Spyridon  
 ; APPLICANT: Bussseau, Isabelle  
 ; APPLICANT: Diederich, Robert J.  
 ; APPLICANT: Xu, Tian  
 ; APPLICANT: Matsuno, Kenji  
 ; TITLE OF INVENTION: DELTEX PROTEINS, NUCLEIC ACIDS, AND  
 ; TITLE OF INVENTION: ANTIBODIES, AND RELATED METHODS AND COMPOSITIONS  
 ; NUMBER OF SEQUENCES: 23  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: PENNIE & EDMONDS  
 ; STREET: 1155 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: U.S.A.  
 ; ZIP: 10036-2711  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/185,432  
 ; FILING DATE: 21-JAN-1994  
 ; CLASSIFICATION: 530  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Misrock, S. Lealie  
 ; REGISTRATION NUMBER: 18,872  
 ; REFERENCE/DOCKET NUMBER: 7326-006  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (212) 790-9090  
 ; TELEFAX: (212) 869-8864/9741  
 ; TELEX: 66141 PENNIE  
 ; INFORMATION FOR SEQ ID NO: 16:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 2471 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: unknown  
 ; MOLECULE TYPE: protein  
 ; US-08-185-432-16

Query Match 30.4%; Score 59; DB 1; Length 2471;  
 Best Local Similarity 36.8%; Pred. No. 94;  
 Matches 14; Conservative 4; Mismatches 12; Indels 9; Gaps 2;

QY 3 ICTTP-AGVKCP-----AALPCCPGLRCIGVNNKVC 32  
 DB 669 VCSPGTGORCNIDIDECASNFCRGATCINGVNGFR 706

Search completed: October 28, 2004, 18:34:07  
 Job time : 3.02508 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 28, 2004, 17:51:02 ; Search time 86.5697 Seconds  
(without alignments)  
2975.262 Million cell updates/sec

Title: US-10-019-823B-54

Perfect score: 3749  
Sequence: 1 MKLNQDQHQSFSNAKVDK.....KELFEIVKAYQLHIERNM 718

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A Genesep\_23Sep04:.\*  
1: Genesep1980s:.\*  
2: Genesep1990s:.\*  
3: Genesep2000s:.\*  
4: Genesep2001s:.\*  
5: Genesep2002s:.\*  
6: Genesep2003as:.\*  
7: Genesep2003bs:.\*  
8: Genesep2004s:.\*

Préd. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3747	99.9	718	4 AAB66907	Aab66907 Insectici
2	3747	99.9	718	6 AAE36271	Aae36271 B. thurin
3	3736.5	99.7	719	2 AAR08041	Aar08041 81 kD end
4	3732.5	99.6	719	4 AAU20095	Aau20095 Bacillus
5	3724.5	99.3	719	4 AAB66909	Aab66909 Insectici
6	3724.5	99.3	719	6 AAE36273	Aae36273 B. thurin
7	3722.5	99.3	719	6 AAB66908	Aab66908 Insectici
8	3722.5	99.3	719	6 AAE36272	Aae36272 B. thurin
9	3718.5	99.2	719	4 AAB66910	Aab66910 Insectici
10	3718.5	99.2	719	6 AAE36274	Aae36274 B. thurin
11	3711.5	99.0	719	4 AAB66911	Aab66911 Insectici
12	3711.5	99.0	719	6 AAE36275	Aae36275 B. thurin
13	3513.5	93.7	719	7 ADM74717	Adm74717 B. thurin
14	3482.5	92.9	719	4 AAB66912	Aab66912 Insectici
15	3482.5	92.9	719	6 AAE36276	Aae36276 B. thurin
16	3439	91.7	710	4 AAU02041	Aau02041 B. thurin
17	3359.5	89.6	719	3 ABB07073	Abb07073 Bacillus
18	3358.5	89.6	719	2 AAW49089	Aaw49089 Bacillus
19	3380.5	87.5	1217	4 AAU02032	Aau02032 Bacillus
20	2704.5	72.1	1208	4 AAU02093	Aau02093 Bacillus
21	2416.5	64.5	1230	8 ADK98484	Adk98484 B thuring
22	2416.5	64.5	1230	8 ADK98489	Adk98489 B thuring
23	2416.5	64.5	1230	8 ADK98481	Adk98481 B thuring
24	2416.5	64.5	1230	8 ADK98491	Adk98491 B thuring
25	2416.5	64.5	1230	8 ADK98487	Adk98487 B thuring

26	2415	64.4	1229	2 AAR54074	Aar54074 CryET5. 2
27	2415	64.4	1229	2 AAW35259	Aaw35259 Bacillus
28	2415	64.4	1229	2 AAW17699	Aaw17699 CryET5. 3
29	2415	64.4	1229	2 AAW87633	Aaw87633 CryET5. pr
30	2415	64.4	1229	2 AAY30923	Aay30923 B. thurin
31	2415	64.4	1229	8 ADK98479	Adk98479 B thuring
32	2319	61.9	488	2 AAW44322	Aaw44322 Bacillus
33	2319	61.9	488	4 AAB19947	Aab19947 Bacillus
34	2249	60.0	1228	2 AAR50955	Aar50955 Bacillus
35	2244	59.9	1209	4 AAU02094	Aau02094 Bacillus
36	2235	59.6	1227	2 AAY31990	Aay31990 Chimeric
37	2165	57.7	1227	2 AAW44321	Aaw44321 Bacillus
38	2165	57.7	1227	4 AAB19950	Aab19950 Bacillus
39	2156	57.5	1227	4 AAU02046	Aau02046 B. thurin
40	2141	57.1	1186	2 AAY16796	Aay16796 Amino aci
41	2121	56.6	1221	4 AAU00421	Aau00421 B. thurin
42	2107	56.2	1221	4 AAU00420	Aau00420 B. thurin
43	2085.5	55.6	1228	4 AAB84628	Aab84628 Amino aci
44	2085.5	55.6	1228	4 AAU02039	Aau02039 B. thurin
45	1902	50.7	643	2 AAY16797	Aay16797 Amino aci

ALIGNMENTS

RESULT 1  
AAB66907  
ID AAB66907 standard; protein; 718 AA.  
XX  
AC AAB66907;  
XX  
DT 12-APR-2001 (first entry)  
XX  
DE Insecticidal protein cryIIal.  
XX  
KW Insecticide; transgenic plant; insect-resistance.  
XX  
OS Paecilomyces sp.  
XX  
PN WO200100841-AL.  
XX  
PD 04-JAN-2001.  
XX  
PF 23-JUN-2000; 200CWO-GB002457.  
XX  
PR 29-JUN-1999; 99GB-00015215.  
PR 23-DEC-1999; 99GB-00030536.  
XX  
(ZENE ) ZENECA LTD.  
PA Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;  
PI Vincent JL, Lee MD;  
XX  
WPI; 2001-123015/13.  
XX  
Novel insecticidal protein obtained from species of Paecilomyces for controlling insects, and for insect-resistant transgenic plant production.  
XX  
PS Claim 14; Page 53-55; 72pp; English.  
XX  
The present invention relates to novel insecticidal proteins obtained from Paecilomyces sp. (see AAB6699 to AAB66901 and AAB66913). The insecticidal proteins can be used to produce transgenic plants, which are insect-resistant. Also, the insecticidal proteins are useful for controlling insects by providing them at a locus where insects feed

Query Match 99.93, Score 3747; DB 4; Length 718;  
Best Local Similarity 100.0%; Pred. No. 9e-296;  
Matches 718; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

My people

QY 1 MKLNQDKHQSFSSNAKVDKISTDSLNKNETDIELQININHEDECLKMSYENVEPFFVSASTI 60  
 DB 1 MKLNQDKHQSFSSNAKVDKISTDSLNKNETDIELQININHEDECLKMSYENVEPFFVSASTI 60  
 QY 61 QTGIGIAGKIILGTGVPFAGOVASLYSFIILGELWPKGNQWEIIPMEHVEEIIINQKISTYA 120  
 DB 61 QTGIGIAGKIILGTGVPFAGOVASLYSFIILGELWPKGNQWEIIPMEHVEEIIINQKISTYA 120  
 QY 121 RNKALTDLKGLGDALAVVHDSLEWVGNNRTRARSVVKSOYIALELMFVKQLPSPAVSG 180  
 DB 121 RNKALTDLKGLGDALAVVHDSLEWVGNNRTRARSVVKSOYIALELMFVKQLPSPAVSG 180  
 QY 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNRQVERAGDYSYHCVKWS 240  
 DB 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNRQVERAGDYSYHCVKWS 240  
 QY 241 TGLNNLRGTNAESWVRYNQFRDMTLMVLDLVALFPSPYDTQMPYPIKTAQTREVTYDAI 300  
 DB 241 TGLNNLRGTNAESWVRYNQFRDMTLMVLDLVALFPSPYDTQMPYPIKTAQTREVTYDAI 300  
 QY 301 GTVHPHPSTFTTWNNNAPSFSAIEAAVVRNPHLLDLEQVTIYSLLSRWSTQYNNMW 360  
 DB 301 GTVHPHPSTFTTWNNNAPSFSAIEAAVVRNPHLLDLEQVTIYSLLSRWSTQYNNMW 360  
 QY 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRVTSFAGLNLFLTPQVNVPRV 420  
 DB 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRVTSFAGLNLFLTPQVNVPRV 420  
 QY 421 DPHWKFTVTHPIASDNFYYPGAGICTQDSENELPPEATGQPNYESYSHRLSHIGLISA 480  
 DB 421 DPHWKFTVTHPIASDNFYYPGAGICTQDSENELPPEATGQPNYESYSHRLSHIGLISA 480  
 QY 481 SHVKALVSWTHRSADRNTTIEPNSITQIPLVKAFNLSGGAUVVRGPGFTGGDILRTNT 540  
 DB 481 SHVKALVSWTHRSADRNTTIEPNSITQIPLVKAFNLSGGAUVVRGPGFTGGDILRTNT 540  
 QY 541 GTFGDIRVNIINPPFAQRVRVIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYKT 600  
 DB 541 GTFGDIRVNIINPPFAQRVRVIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYKT 600  
 QY 601 FXTVGFTTFFSLLDVQSTFTTGANNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKVT 660  
 DB 601 FXTVGFTTFFSLLDVQSTFTTGANNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKVT 660  
 QY 661 ALFTSTNPRGLKTDVKDHIQOVSNLVSLSDEFLDEKRELFVYKAKQLHIERNM 718  
 DB 661 ALFTSTNPRGLKTDVKDHIQOVSNLVSLSDEFLDEKRELFVYKAKQLHIERNM 718

RESULT 2  
 ID AAE36271 standard; protein; 718 AA.  
 AC AAE36271;  
 DT 26-JUN-2003 (first entry)  
 DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa1.  
 KW Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.  
 OS Bacillus thuringiensis.  
 PN WC0200298911-A2.  
 PD 12-DEC-2002.  
 PF 30-MAY-2002; 2002WO-GB002666.  
 PR 07-JUN-2001; 2001GB-00013900.  
 PA (SYGN) SYNGENTA LTD.  
 XX

PI Vincent JL, Viner R;  
 XX WPI; 2003-175137/17.  
 XX  
 PT New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.  
 PT  
 XX  
 PS Claim 12; Page 42-44; 67pp; English.  
 XX  
 CC The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects.  
 CC Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is CC Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention  
 XX  
 SQ Sequence 718 AA;  
 Query Match 99.9%; Score 3747; DB 6; Length 718;  
 Best Local Similarity 99.9%; Pred. NO. 9e-296;  
 Matches 717; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MKLNQDKHQSFSSNAKVDKISTDSLNKNETDIELQININHEDECLKMSYENVEPFFVSASTI 60  
 DB 1 MKLNQDKHQSFSSNAKVDKISTDSLNKNETDIELQININHEDECLKMSYENVEPFFVSASTI 60  
 QY 61 QTGIGIAGKIILGTGVPFAGOVASLYSFIILGELWPKGNQWEIIPMEHVEEIIINQKISTYA 120  
 DB 61 QTGIGIAGKIILGTGVPFAGOVASLYSFIILGELWPKGNQWEIIPMEHVEEIIINQKISTYA 120  
 QY 121 RNKALTDLKGLGDALAVVHDSLEWVGNNRTRARSVVKSOYIALELMFVKQLPSPAVSG 180  
 DB 121 RNKALTDLKGLGDALAVVHDSLEWVGNNRTRARSVVKSOYIALELMFVKQLPSPAVSG 180  
 QY 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNRQVERAGDYSYHCVKWS 240  
 DB 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNRQVERAGDYSYHCVKWS 240  
 QY 241 TGLNNLRGTNAESWVRYNQFRDMTLMVLDLVALFPSPYDTQMPYPIKTAQTREVTYDAI 300  
 DB 241 TGLNNLRGTNAESWVRYNQFRDMTLMVLDLVALFPSPYDTQMPYPIKTAQTREVTYDAI 300  
 QY 301 GTVHPHPSTFTTWNNNAPSFSAIEAAVVRNPHLLDLEQVTIYSLLSRWSTQYNNMW 360  
 DB 301 GTVHPHPSTFTTWNNNAPSFSAIEAAVVRNPHLLDLEQVTIYSLLSRWSTQYNNMW 360  
 QY 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRVTSFAGLNLFLTPQVNVPRV 420  
 DB 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRVTSFAGLNLFLTPQVNVPRV 420  
 QY 421 DPHWKFTVTHPIASDNFYYPGAGICTQDSENELPPEATGQPNYESYSHRLSHIGLISA 480  
 DB 421 DPHWKFTVTHPIASDNFYYPGAGICTQDSENELPPEATGQPNYESYSHRLSHIGLISA 480  
 QY 481 SHVKALVSWTHRSADRNTTIEPNSITQIPLVKAFNLSGGAUVVRGPGFTGGDILRTNT 540  
 DB 481 SHVKALVSWTHRSADRNTTIEPNSITQIPLVKAFNLSGGAUVVRGPGFTGGDILRTNT 540  
 QY 541 GTFGDIRVNIINPPFAQRVRVIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYKT 600  
 DB 541 GTFGDIRVNIINPPFAQRVRVIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYKT 600  
 QY 601 FXTVGFTTFFSLLDVQSTFTTGANNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKVT 660  
 DB 601 FXTVGFTTFFSLLDVQSTFTTGANNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKVT 660  
 QY 661 ALFTSTNPRGLKTDVKDHIQOVSNLVSLSDEFLDEKRELFVYKAKQLHIERNM 718  
 DB 661 ALFTSTNPRGLKTDVKDHIQOVSNLVSLSDEFLDEKRELFVYKAKQLHIERNM 718

```

RESULT 3
AAR08041
ID AAR08041 standard; protein; 719 AA.
AC
XX
AC AAR08041;
XX
DT 24-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 27-FEB-1991 (first entry)
XX
XX 81 kD endotoxin deduced from DNA carried on pJH12.
XX
XX Crystal; insecticide; toxin; delta endotoxin.
XX
XX Bacillus thuringiensis; JHCC 4353 and 4835.
XX
XX WO9013651-A..
XX
XX PD 15-NOV-1990.
XX
XX PF 09-MAY-1989; 89GB-00010624.
XX
XX PR 09-MAY-1989; 89GB-00010624.
XX
XX PA (ICIL ) IMPERIAL CHEM IND PLC.
XX
XX PI Blank RG, Ely S, Tailor RH, Tippet JM;
XX
XX DR WPI; 1990-361486/48.
XX
XX DR N-PSDB; AAO05636.
XX
XX Bacillus thuringiensis strains - used for producing an endotoxin for
XX protecting plants against insects, partic. Lepidoptera and Coleoptera.
XX
XX Claim 5; Fig 5-10; 66pp; English.
XX
XX The sequence carried on pJH12 which was isolated from B. thurin- giensis
XX strains JHCC4835 and JHCC 4353 (NCIB 40091 and 40090 resp.). The DNA can
XX be used to produce transformants E.coli strain MCI2022/pJH12 (NCIB 40278,
XX or bacteriophage EMEL4 vector (NCIB 40279) or E.coli strain BL21/pJH11
XX (NCIB 40275). The delta-endo- toxin produced by the transformants can be
XX used in formulations for combating Lepidoptera and Coleoptera pests.
XX (Updated on 25-MAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to
XX standardise OS field)
XX
XX SQ Sequence 719 AA;
XX
XX Query Match 99.7%; Score 3736.5; DB 2; Length 719;
XX Best Local Similarity 99.9%; Pred. No. 6.4e-295;
XX Matches 718; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
XX
XX 1 MCLKNQDKHQSFSNAKVDKISTDSLKNETDIELQNHEDCLKMSEYENVEPFVSASTI 60
XX
XX 1 MCLKNQDKHQSFSNAKVDKISTDSLKNETDIELQNHEDCLKMSEYENVEPFVSASTI 60
XX
XX 61 QTGIGIAGKILGTILGVFPAGQASLYSFIILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
XX
XX 61 QTGIGIAGKILGTILGVFPAGQASLYSFIILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
XX
XX 121 RNKALTDLKLGDALAYVHDSLSWGNRNNTARSVVKSOYIALHMFVKLPSPAVSG 180
XX
XX 121 RNKALTDLKLGDALAYVHDSLSWGNRNNTARSVVKSOYIALHMFVKLPSPAVSG 180
XX
XX 181 EEVPLLPYQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVRAGDYSYHCVKWTYS 240
XX
XX 181 EEVPLLPYQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVRAGDYSYHCVKWTYS 240
XX
XX 241 TGLNLRGTAESWVRVYQRRDMLVLDLVALFSPYDTQMPYPIKTAQLTREYVTDAL 300
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XX 241 TGLNLRGTAESWVRVYQRRDMLVLDLVALFSPYDTQMPYPIKTAQLTREYVTDAL 300
XX
XX 301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW 360

```

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Db 301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW 360
Qy 361 GGHKLEFRITIGTILNISTOGSTNTSINPVTLPTGRDYYRTESLAGLNLFLTPQVN-VPR 419
Db 361 GGHKLEFRITIGTILNISTOGSTNTSINPVTLPTGRDYYRTESLAGLNLFLTPQVNGVPR 420
Qy 420 VDFHWKFVTHPIASDNFFYYPGYAGIGTQLQDSSENLPEPEATQOPNYESYSHLSHIGLIS 479
Db 421 VDFHWKFVTHPIASDNFFYYPGYAGIGTQLQDSSENLPEPEATQOPNYESYSHLSHIGLIS 480
Qy 480 ASHVXALVSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAYVRGPGFTGDDILRRTN 539
Db 481 ASHVXALVSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAYVRGPGFTGDDILRRTN 540
Qy 540 TGTFGDIRVNIINPPFAQRVVRVIRYASTTDLQFHTSINGKAINQGNFSAWNRGDDLDYK 599
Db 541 TGTFGDIRVNIINPPFAQRVVRVIRYASTTDLQFHTSINGKAINQGNFSAWNRGDDLDYK 600
Qy 600 TPTXVGFTTTPSLLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDPEKAQEKV 659
Db 601 TPTXVGFTTTPSLLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDPEKAQEKV 660
Qy 660 TALFTSTNPRGLKTDVKDHYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 718
Db 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719

```

```

RESULT 4
AAU02095
ID AAU02095 standard; protein; 719 AA.
XX
AC AAU02095;
XX
DT 07-SEP-2001 (first entry)
XX
DE Bacillus thuringiensis partial mutant CryIIa.
XX
KW Crystal protein; CryIIa; CryIIa; moth; butterfly; Colorado potato beetle;
KW mutant; mutein.
XX
OS Bacillus thuringiensis.
XX
FH Key Location/Qualifiers
FT Peptide 1..19 /label= Signal_peptide
FT Protein 20..719 /label= Mature_CryIIa
XX
XX EP1099760-Al.
XX
XX 16-MAY-2001.
XX
XX 09-NOV-1999; 99EP-00203723.
XX
XX 09-NOV-1999; 99EP-00203723.
XX
XX (CPRO-) CPRO-DLO CENT PLANTENVERDEDELINGS REPROD.
XX
XX De Maagd RA, Bosch HJ;
XX
XX WPI; 2001-337141/36.
XX
XX DR N-PSDB; AAS04855.
XX
XX New hybrid Bacillus thuringiensis hybrid toxins comprising structural
XX domains derived from at least 2 different crystal proteins, such as
XX CryIIa and CryIIb, and having insecticidal activity, useful for combating
XX insects.
XX
XX Example; Page 30-32; 43pp; English.
XX
XX The sequence is B. thuringiensis (Bt) crystal protein CryIIa, the DNA
XX encoding which was mutated to allow cloning of domain III or domains I
XX

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CC and II, to make the hybrid protoxins of the invention. The hybrid toxins  
 CC of the invention, having structural domains I, II and III in this order  
 CC starting from the N-terminal derived from at least 2 different crystal  
 CC proteins, are useful for protecting plants against pest insects, e.g.  
 CC moths, butterflies and Colorado potato beetle or for combating insects  
 XX  
 XX Sequence 719 AA;

Query Match 99.6%; Score 3732.5; DB 4; Length 719;  
 Best Local Similarity 99.6%; Pred. No. 1.4e-294;  
 Matches 716; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 MKLNQDKHQSFSSNAKVDKISTSLKNETDIELQNHEDCLKNSEYENVEPVSASTI 60  
 DB 1 MKLNQDKHQSFSSNAKVDKISTSLKNETDIELQNHEDCLKNSEYENVEPVSASTI 60

QY 61 QTGIGIAGKILGTGVPFAGQVASYLFGELMPKGNQWEIFMEHVEEIIINQKISTYA 120  
 DB 61 QTGIGIAGKILGTGVPFAGQVASYLFGELMPKGNQWEIFMEHVEEIIINQKISTYA 120

QY 121 RNKALTDLKGIDALAVYHDSLESVGNRNTRARSVVKSOYIALELMFVKLPSPAVSG 180  
 DB 121 RNKALTDLKGIDALAVYHDSLESVGNRNTRARSVVKSOYIALELMFVKLPSPAVSG 180

QY 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSHCVKWS 240  
 DB 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSHCVKWS 240

QY 241 TGLNLRGNTNABSWRYNQFRDMLVLDVALPSPDYDTQMYPIKTTAQLTRVYTDAL 300  
 DB 241 TGLNLRGNTNABSWRYNQFRDMLVLDVALPSPDYDTQMYPIKTTAQLTRVYTDAL 300

QY 301 GTVHPHPSTSTWYNNNAPSFAIEAAVVRNPHLLDLEQVTIYSLSRWSNTQYNNMW 360  
 DB 301 GTVHPHPSTSTWYNNNAPSFAIEAAVVRNPHLLDLEQVTIYSLSRWSNTQYNNMW 360

QY 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRVRESLAGLNLFLTQPNV 419  
 DB 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRVRESLAGLNLFLTQPNV 419

QY 420 VDFHWKFTVTHPIASDNFYYPGAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLIS 479  
 DB 420 VDFHWKFTVTHPIASDNFYYPGAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLIS 479

QY 480 ASHVKALVSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 539  
 DB 480 ASHVKALVSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540

QY 540 TGTFGDIRVNIINPPFAQRYVRIRVASTTDLPFTSINGKAINQGNFATNMRGEDLDYK 599  
 DB 540 TGTFGDIRVNIINPPFAQRYVRIRVASTTDLPFTSINGKAINQGNFATNMRGEDLDYK 599

QY 600 TERTVGTFTTPPSFLDVQSTFTIGAWNFSSGNEVIIDRIEFVPEVTEYAEYDFEKAQEKV 659  
 DB 600 TERTVGTFTTPPSFLDVQSTFTIGAWNFSSGNEVIIDRIEFVPEVTEYAEYDFEKAQEKV 660

QY 660 TALPSTNPRGKTQDKYHIDQVSNLVSISDEFLDEKELPEIVKAYAKQLHIERNM 718  
 DB 660 TALPSTNPRGKTQDKYHIDQVSNLVSISDEFLDEKELPEIVKAYAKQLHIERNM 719

RESULT 5  
 ID AAB66909 standard; protein; 719 AA.  
 AC AAB66909;  
 XX  
 XX  
 DT 12-APR-2001 (first entry)  
 XX Insecticidal protein cryIIa3.  
 DE  
 XX Insecticide; transgenic plant; insect-resistance.  
 XX

OS Paecilomyces sp.  
 XX WO200100841-A1.  
 XX 04-JAN-2001.  
 XX 23-JUN-2000; 2000WO-GB002457.  
 XX 29-JUN-1999; 99GB-00015215.  
 XX 23-DEC-1999; 99GB-00030536.  
 XX (ZENE ) ZENECA LTD.  
 XX Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;  
 XX Vincent JL, Lee MD;  
 XX WPI; 2001-123015/13.  
 XX Novel insecticidal protein obtained from species of Paecilomyces for  
 PT controlling insects, and for insect-resistant transgenic plant  
 PT production.  
 XX Claim 14; Page 57-59; 72pp; English.  
 XX The present invention relates to novel insecticidal proteins obtained  
 CC from Paecilomyces sp. (see AAB6699 to AAB6901 and AAB6913). The  
 CC insecticidal proteins can be used to produce transgenic plants, which are  
 CC insect-resistant. Also, the insecticidal proteins are useful for  
 CC controlling insects by providing them at a locus where insects feed  
 XX  
 XX Sequence 719 AA;

Query Match 99.3%; Score 3724.5; DB 4; Length 719;  
 Best Local Similarity 99.3%; Pred. No. 6.1e-294;  
 Matches 714; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 1 MKLNQDKHQSFSSNAKVDKISTSLKNETDIELQNHEDCLKNSEYENVEPVSASTI 60  
 DB 1 MKLNQDKHQSFSSNAKVDKISTSLKNETDIELQNHEDCLKNSEYENVEPVSASTI 60

QY 61 QTGIGIAGKILGTGVPFAGQVASYLFGELMPKGNQWEIFMEHVEEIIINQKISTYA 120  
 DB 61 QTGIGIAGKILGTGVPFAGQVASYLFGELMPKGNQWEIFMEHVEEIIINQKISTYA 120

QY 121 RNKALTDLKGIDALAVYHDSLESVGNRNTRARSVVKSOYIALELMFVKLPSPAVSG 180  
 DB 121 RNKALTDLKGIDALAVYHDSLESVGNRNTRARSVVKSOYIALELMFVKLPSPAVSG 180

QY 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSHCVKWS 240  
 DB 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSHCVKWS 240

QY 241 TGLNLRGNTNABSWRYNQFRDMLVLDVALPSPDYDTQMYPIKTTAQLTRVYTDAL 300  
 DB 241 TGLNLRGNTNABSWRYNQFRDMLVLDVALPSPDYDTQMYPIKTTAQLTRVYTDAL 300

QY 301 GTVHPHPSTSTWYNNNAPSFAIEAAVVRNPHLLDLEQVTIYSLSRWSNTQYNNMW 360  
 DB 301 GTVHPHPSTSTWYNNNAPSFAIEAAVVRNPHLLDLEQVTIYSLSRWSNTQYNNMW 360

QY 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRVRESLAGLNLFLTQPNV 419  
 DB 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRVRESLAGLNLFLTQPNV 420

QY 420 VDFHWKFTVTHPIASDNFYYPGAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLIS 479  
 DB 420 VDFHWKFTVTHPIASDNFYYPGAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLIS 480

QY 480 ASHVKALVSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 539  
 DB 480 ASHVKALVSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540

QY 540 TGTFGDIRVNIINPPFAQRYVRIRVASTTDLPFTSINGKAINQGNFATNMRGEDLDYK 599



Db	541	TGTFGDIRVNPFPFAQRYRIRYASTTDLQFHTSINGKAINQNFSAATMRGEDLDYK	600	QY	181	EEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSYHCVKWS	240
Qy	600	TFXTVGTTPPSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDEKAQEKV	659	Db	181	EEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSYHCVKWS	240
Db	601	TFRVGTTPPSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDEKAQEKV	660	Qy	241	TGLNLRGNTNAESWRYNQFRDMLMVLDLVALFPSTYDTQMPYIKTTAQLTREVYTDI	300
Qy	660	TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFPEIKVAKQKHIERNM	718	Db	241	TGLNLRGNTNAESWRYNQFRDMLMVLDLVALFPSTYDTQMPYIKTTAQLTREVYTDI	300
Db	661	TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFPEIKVAKQKHIERNM	719	Qy	301	GTVHPHPSFTSTWYNNNAPSFAEAAVVRNPHLLDLEQVTIYSLLSRWSTQYMMNM	360
RESULT 6				Db	301	GTVHPHPSFTSTWYNNNAPSFAEAAVVRNPHLLDLEQVTIYSLLSRWSTQYMMNM	360
AAE36273				Qy	361	GGHLEFRITIGTLMISTQSTNTSINPVTLTPTSRDVRVTESLAGLNLFTQPVN-VR	419
ID	AAE36273	standard; protein; 719 AA.		Db	361	GGHLEFRITIGTLMISTQSTNTSINPVTLTPTSRDVRVTESLAGLNLFTQPVN-VR	420
XX	AAE36273;			Qy	420	VDFHKKFVTHPIASDNFYPGYAGIGTOLDSNENLPPPEATGQPNYESYSHRLSHIGLIS	479
XX	26-JUN-2003	(first entry)		Db	421	VDFHKKFVTHPIASDNFYPGYAGIGTOLDSNENLPPPEATGQPNYESYSHRLSHIGLIS	480
DE	B. thuringiensis	insecticidal crystal endotoxin (CRY) protein, cryIIa3.		Qy	480	ASHVKALVYSWTHRSADRNTNTEPNSITQIPLVKAFNLSSGAAVVRGFGFTGGDILRRTN	539
XX	Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.			Db	481	ASHVKALVYSWTHRSADRNTNTEPNSITQIPLVKAFNLSSGAAVVRGFGFTGGDILRRTN	540
OS	Bacillus thuringiensis.			Qy	540	TCTFGDIRVNPFPFAQRYRIRYASTTDLQFHTSINGKAINQNFSAATMRGEDLDYK	599
XX	WO200298911-A2.			Db	541	TCTFGDIRVNPFPFAQRYRIRYASTTDLQFHTSINGKAINQNFSAATMRGEDLDYK	600
PD	12-DEC-2002.			Qy	600	TEXTVGTTPPSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDEKAQEKV	659
XX	30-MAY-2002; 2002WO-GB002666.			Db	601	TEXTVGTTPPSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDEKAQEKV	660
PR	07-JUN-2001; 2001GB-00013900.			Qy	660	TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFPEIKVAKQKHIERNM	718
XX	(SYGN ) SYNGENTA LTD.			Db	661	TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFPEIKVAKQKHIERNM	719
PA	Vincent JL, Viner R;			RESULT 7			
PI	WPI; 2003-175137/17.			AAE66908			
DR				ID	AAE66908	standard; protein; 719 AA.	
XX				XX	AAE66908;		
PT	New insecticidal protein comprising an X-glycine motif at the amino-			XX	12-APR-2001	(first entry)	
PT	terminus, useful as an active ingredient of a pesticide.			DT	Insecticidal protein cryIIa2.		
XX	Claim 12; Page 47-50; 67pp; English.			XX	Insecticide; transgenic plant; insect-resistance.		
XX				XX	Paecilomyces sp.		
CC	The invention relates to insecticidal protein comprising an X-glycine			XX	WO200100841-A1.		
CC	motif at the amino-terminus. Polynucleotide or DNA constructs of the			XX	04-JAN-2001.		
CC	invention are useful for producing plants or plant parts that are			XX	23-JUN-2000; 2000WO-GB002457.		
CC	resistant to insects. The protein or synergistic combination is useful as			XX	29-JUN-1999; 99GB-00015215.		
CC	an active ingredient of a pesticide or for controlling insects.			PR	23-DEC-1999; 99GB-00030536.		
CC	Antibodies raised to the insecticidal proteins can be used to identify			XX	(ZENE ) ZENECA LTD.		
CC	other proteins with insecticidal activity. The present sequence is			XX	Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;		
CC	Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This			PI	Vincent JL, Lee MD;		
CC	sequence is used in the invention			XX	WPI; 2001-123015/13.		
XX				DR			
SQ	Sequence 719 AA;			XX			
	Query Match	99.3%; Score 3724.5; DB 6; Length 719;		XX			
	Best Local Similarity	99.3%; Pred No. 6.1e-294;		PR			
	Matches 714; Conservative	1; Mismatches 3; Indels 1; Gaps 1;		XX			
Qy	1	MKLKQDKHQSFSNAKVKISTDSLKNETDIELQINNHEDCLKMSEYENVEPVSASTI	60	PA			
Db	1	MKLKQDKHQSFSNAKVKISTDSLKNETDIELQINNHEDCLKMSEYENVEPVSASTI	60	PI			
Qy	61	QTGIGAKILGTGVFPAGVASLYFILGELMPKKNQWEIFMEHVEEIIINQISTYA	120	XX			
Db	61	QTGIGAKILGTGVFPAGVASLYFILGELMPKKNQWEIFMEHVEEIIINQISTYA	120	XX			
Qy	121	RNKALTDKLGGLDALVYHDSLSRWGNRNNTARSVVKSQYIALELMFVKLPSPAVSG	180	PT			
Db	121	RNKALTDKLGGLDALVYHDSLSRWGNRNNTARSVVKSQYIALELMFVKLPSPAVSG	180	XX			

CC The present invention relates to novel insecticidal proteins obtained from *Paecilomyces* sp. (see AAB6699 to AAB6901 and AAB6913). The insecticidal proteins can be used to produce transgenic plants, which are insect-resistant. Also, the insecticidal proteins are useful for controlling insects by providing them at a locus where insects feed

XX Sequence 719 AA;

Query Match 99.3%; Score 3722.5; DB 4; Length 719;  
 Best Local Similarity 99.4%; Pred. No. 8.9e-294;  
 Matches 715; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 MKLKNQDKHQSFSSNAKVDKISTSLKNETDIELQNHEDCLKSEYENVEPVSASTI 60  
 DB 1 MKLKNQDKHQSFSSNAKVDKISTSLKNETDIELQNHEDCLKSEYENVEPVSASTI 60

QY 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELMPKGNQWEIFMEHVEEIIINQKISTYA 120  
 DB 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELMPKGNQWEIFMEHVEEIIINQKISTYA 120

QY 121 RNKALTDLKGDLALAVYHDSLESWGNNRNRTRSVVKSQYIALELMFVKLPSPFVSG 180  
 DB 121 RNKALTDLKGDLALAVYHDSLESWGNNRNRTRSVVKSQYIALELMFVKLPSPFVSG 180

QY 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSHCVKWS 240  
 DB 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSHCVKWS 240

QY 241 TGLNLRGTNAESWRYNQFRDRTLMLVDLVALPSPYDTQMPYIKTTAQLTRVYTDAL 300  
 DB 241 TGLNLRGTNAESWRYNQFRDRTLMLVDLVALPSPYDTQMPYIKTTAQLTRVYTDAL 300

QY 301 GTVHPHPSFTSTWYNNAPSAEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYNNMW 360  
 DB 301 GTVHPHPSFTSTWYNNAPSAEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYNNMW 360

QY 361 GGHKLEFRITIGTLNISTQGSTNTSINPVTLPFTSRDVRYESLAGNLFITQPNV-VP 419  
 DB 361 GGHKLEFRITIGTLNISTQGSTNTSINPVTLPFTSRDVRYESLAGNLFITQPNV-VP 420

QY 420 VDFHWKFVTHPIASDNFFYPGAGIGTQLODSENELPEATGQPNYESYHSLSHIGLIS 479  
 DB 420 VDFHWKFVTHPIASDNFFYPGAGIGTQLODSENELPEATGQPNYESYHSLSHIGLIS 480

QY 480 ASHVKALVSWTHRSADRNTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 539  
 DB 480 ASHVKALVSWTHRSADRNTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 540

QY 540 TGTFGDIRVNPPFAQRYRVRIRYASTDLOFHTSINGKAINOGNFSATNRCGEDLDYK 599  
 DB 540 TGTFGDIRVNPPFAQRYRVRIRYASTDLOFHTSINGKAINOGNFSATNRCGEDLDYK 600

QY 600 TETVTGFTTPSLLDVQSTFTIGAMNPFSSGNEVIDRIEFVPVEVTEAEYDFEKAQEKV 659  
 DB 600 TETVTGFTTPSLLDVQSTFTIGAMNPFSSGNEVIDRIEFVPVEVTEAEYDFEKAQEKV 660

QY 660 TALFTSTNPRGLTKVDKDYHIDQVSNLVESLDEFYLDKRELFEIVKYAKQLHIERNM 718  
 DB 660 TALFTSTNPRGLTKVDKDYHIDQVSNLVESLDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 8  
 AAE36272  
 ID AAE36272 standard; protein; 719 AA.  
 XX  
 AC AAE36272;  
 XX  
 DT 26-JUN-2003 (first entry)  
 XX  
 DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa2.  
 XX  
 KW Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.  
 XX

OS *Bacillus thuringiensis*.  
 XX WO200299911-A2.  
 XX 12-DEC-2002.  
 XX 30-MAY-2002; 2002WO-GB002666.  
 XX 07-JUN-2001; 2001GB-00013900.  
 XX (SYGN) SYNGENTA LTD.  
 XX Vincent JL, Viner R;  
 XX WPI; 2003-175137/17.  
 XX New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.  
 XX Claim 12; Page 44-47; 67pp; English.  
 XX The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects.  
 CC Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is *Bacillus thuringiensis* insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention

XX Sequence 719 AA;

Query Match 99.3%; Score 3722.5; DB 6; Length 719;  
 Best Local Similarity 99.4%; Pred. No. 8.9e-294;  
 Matches 715; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 MKLKNQDKHQSFSSNAKVDKISTSLKNETDIELQNHEDCLKSEYENVEPVSASTI 60  
 DB 1 MKLKNQDKHQSFSSNAKVDKISTSLKNETDIELQNHEDCLKSEYENVEPVSASTI 60

QY 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELMPKGNQWEIFMEHVEEIIINQKISTYA 120  
 DB 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELMPKGNQWEIFMEHVEEIIINQKISTYA 120

QY 121 RNKALTDLKGDLALAVYHDSLESWGNNRNRTRSVVKSQYIALELMFVKLPSPFVSG 180  
 DB 121 RNKALTDLKGDLALAVYHDSLESWGNNRNRTRSVVKSQYIALELMFVKLPSPFVSG 180

QY 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSHCVKWS 240  
 DB 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSHCVKWS 240

QY 241 TGLNLRGTNAESWRYNQFRDRTLMLVDLVALPSPYDTQMPYIKTTAQLTRVYTDAL 300  
 DB 241 TGLNLRGTNAESWRYNQFRDRTLMLVDLVALPSPYDTQMPYIKTTAQLTRVYTDAL 300

QY 301 GTVHPHPSFTSTWYNNAPSAEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYNNMW 360  
 DB 301 GTVHPHPSFTSTWYNNAPSAEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYNNMW 360

QY 361 GGHKLEFRITIGTLNISTQGSTNTSINPVTLPFTSRDVRYESLAGNLFITQPNV-VP 419  
 DB 361 GGHKLEFRITIGTLNISTQGSTNTSINPVTLPFTSRDVRYESLAGNLFITQPNV-VP 420

QY 420 VDFHWKFVTHPIASDNFFYPGAGIGTQLODSENELPEATGQPNYESYHSLSHIGLIS 479  
 DB 420 VDFHWKFVTHPIASDNFFYPGAGIGTQLODSENELPEATGQPNYESYHSLSHIGLIS 480

QY 480 ASHVKALVSWTHRSADRNTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 539  
 DB 480 ASHVKALVSWTHRSADRNTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 540

QY 540 TGTGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLDYK 599  
 DB 541 TGTGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLDYK 600  
 QY 600 TFXTVGFTTTPSFLDVQSTFTIGAWNFSSGNEVYDRIEFVPEVVEVYEAAYDEFEKAQEKV 659  
 DB 601 TFRIVGFTTTPSFLDVQSTFTIGAWNFSSGNEVYDRIEFVPEVVEVYEAAYDEFEKAQEKV 660  
 QY 660 TALFTSTNPRGLKTDVQYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 718  
 DB 661 TALFTSTNPRGLKTDVQYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 9  
 AAB66910  
 ID AAB66910 standard; protein; 719 AA.  
 XX AC AAB66910;  
 XX DT 12-APR-2001 (first entry)  
 XX Insecticidal protein cryIIa4.  
 XX Insecticide; transgenic plant; insect-resistance.  
 XX Paecilomyces sp.  
 XX WO200100841-A1.  
 XX PD 04-JAN-2001.  
 XX PF 23-JUN-2000; 2000WO-GB002457.  
 XX PR 29-JUN-1999; 99GB-00015215.  
 XX PR 23-DEC-1999; 99GB-00030536.  
 XX PA (ZENE ) ZENECA LTD.  
 XX Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;  
 XX Vincent JL, Lee MD;  
 XX WPI; 2001-123015/13.  
 XX Novel insecticidal protein obtained from species of Paecilomyces for  
 PT controlling insects, and for insect-resistant transgenic plant  
 PT production.  
 XX Claim 14; Page 60-62; 72pp; English.  
 XX The present invention relates to novel insecticidal proteins obtained  
 CC from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The  
 CC insecticidal proteins can be used to produce transgenic plants, which are  
 CC insect-resistant. Also, the insecticidal proteins are useful for  
 CC controlling insects by providing them at a locus where insects feed  
 XX Sequence 719 AA;  
 SQ

Query Match 99.2%; Score 3718.5; DB 4; Length 719;  
 Best Local Similarity 99.3%; Pred. No. 1.9e-293;  
 Matches 714; Conservative 0; Mismatches 4; Indels 1; Gaps 1;  
 QY 1 MCLKNQKHQSFSSNAKVKIDSTSLKNETDIELQNHEDCLKMSEYENVEPFVASTI 60  
 DB 1 MCLKNQKHQSFSSNAKVKIDSTSLKNETDIELQNHEDCLKMSEYENVEPFVASTI 60  
 QY 61 QTGIGIAGKIILGTGVFAGQVSLYFIIGELWPKGNQWEIFMEHVEEIIINQKISTVA 120  
 DB 61 QTGIGIAGKIILGTGVFAGQVSLYFIIGELWPKGNQWEIFMEHVEEIIINQKISTVA 120  
 QY 121 RNKALTDLKGLDALAVYHDSLSWGVRNNTARSVVKSOYIALHMFVKLPSPAVSG 180  
 DB 121 RNKALTDLKGLDALAVYHDSLSWGVRNNTARSVVKSOYIALHMFVKLPSPAVSG 180

QY 181 BEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISITFYNRQVERAGDYSYHCWKYS 240  
 DB 181 BEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISITFYNRQVERAGDYSYHCWKYS 240  
 QY 241 TGLNLRGTNABSWRYNQFRDMLMVLDLVALPSPYDTOMYPIKTTAQLTREVYTDAL 300  
 DB 241 TGLNLRGTNABSWRYNQFRDMLMVLDLVALPSPYDTOMYPIKTTAQLTREVYTDAL 300  
 QY 301 GTVHPHPTSTTWNNNAPSPAIEAAVVRNPHLLDLEQVTIYSLSRWSNTQYMMNMW 360  
 DB 301 GTVHPHPTSTTWNNNAPSPAIEAAVVRNPHLLDLEQVTIYSLSRWSNTQYMMNMW 360  
 QY 361 GGHKLEFRTIGTLNISTQGSTNTSINPVTLPFTSRDVVRTESLAGLNLFTQPVN-VPR 419  
 DB 361 GGHKLEFRTIGTLNISTQGSTNTSINPVTLPFTSRDVVRTESLAGLNLFTQPVN-VPR 420  
 QY 420 VDFHMKFVTHPIASDNFYYPGYAGIGTQDSSENELPEEATGQPNYESYSHLSHIGLIS 479  
 DB 421 VDFHMKFVTHPIASDNFYYPGYAGIGTQDSSENELPEEATGQPNYESYSHLSHIGLIS 480  
 QY 480 ASHKVYKALVSWTHRSADRNTNIEPNSITQIPLVKAFNLSSGAUVRGSGFTGGDILRRTN 539  
 DB 481 ASHKVYKALVSWTHRSADRNTNIEPNSITQIPLVKAFNLSSGAUVRGSGFTGGDILRRTN 540  
 QY 540 TGTGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLDYK 599  
 DB 541 TGTGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLDYK 600  
 QY 600 TFXTVGFTTTPSFLDVQSTFTIGAWNFSSGNEVYDRIEFVPEVVEVYEAAYDEFEKAQEKV 659  
 DB 601 TFRIVGFTTTPSFLDVQSTFTIGAWNFSSGNEVYDRIEFVPEVVEVYEAAYDEFEKAQEKV 660  
 QY 660 TALFTSTNPRGLKTDVQYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 718  
 DB 661 TALFTSTNPRGLKTDVQYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 10  
 AAB66910  
 ID AAB66910 standard; protein; 719 AA.  
 XX AC AAB66910;  
 XX DT 26-JUN-2003 (first entry)  
 XX DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa4.  
 XX Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.  
 XX Bacillus thuringiensis.  
 XX WO200298911-A2.  
 XX PD 12-DEC-2002.  
 XX PF 30-MAY-2002; 2002WO-GB002666.  
 XX PR 07-JUN-2001; 2001GB-00013900.  
 XX PA (SYGN ) SYNGENTA LTD.  
 XX Vincent JL, Viner R;  
 XX WPI; 2003-175137/17.  
 XX New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.  
 PT Claim 12; Page 50-53; 67pp; English.  
 CC The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are

CC resistant to insects. The protein or synergistic combination is useful as  
 CC an active ingredient of a pesticide or for controlling insects.  
 CC Antibodies raised to the insecticidal proteins can be used to identify  
 CC other proteins with insecticidal activity. The present sequence is  
 CC Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This  
 CC sequence is used in the invention  
 XX  
 SQ Sequence 719 AA;

Query Match 99.2%; Score 3718.5; DB 6; Length 719;  
 Best Local Similarity 99.3%; Pred. No. 1.9e-293;  
 Matches 714; Conservative 0; Mismatches 4; Indels 1; Gaps 1;  
 QY 1 MKLNQDKHQSSNAKVDKISTDSLNKNETDIELQNHEDCLKSEYENVEPVSASTI 60  
 DB 1 MKLNQDKHQSSNAKVDKISTDSLNKNETDIELQNHEDCLKSEYENVEPVSASTI 60  
 QY 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINOKISTYA 120  
 DB 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINOKISTYA 120  
 QY 121 RNKALTDLKGDLAVYHDSLESWGVRNNTTRASVVKSOYIAELMFVOKLPSFAVSG 180  
 DB 121 RNKALTDLKGDLAVYHDSLESWGVRNNTTRASVVKSOYIAELMFVOKLPSFAVSG 180  
 QY 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNRQVERAGDYSYHCVKWS 240  
 DB 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNRQVERAGDYSYHCVKWS 240  
 QY 241 TGLNLRGTNABSWRVYNOFRDMLVLDLVALPSPDYDTOMYPIKTTAQLTRVYTDAL 300  
 DB 241 TGLNLRGTNABSWRVYNOFRDMLVLDLVALPSPDYDTOMYPIKTTAQLTRVYTDAL 300  
 QY 301 GTVHPHPSFTTWNNAAPSFAEAAVVRNPHLLDLEQVTIYSLLSRWNTQYNNMW 360  
 DB 301 GTVHPHPSFTTWNNAAPSFAEAAVVRNPHLLDLEQVTIYSLLSRWNTQYNNMW 360  
 QY 361 GGHKLEFRITIGTGLNISTQGSTNTSINPVTLPFTSRDYRTESLAGNLFITQPNV 419  
 DB 361 GGHKLEFRITIGTGLNISTQGSTNTSINPVTLPFTSRDYRTESLAGNLFITQPNV 419  
 QY 420 VDFHWKFTVHTPTASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHLSHIGLIS 479  
 DB 420 VDFHWKFTVHTPTASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHLSHIGLIS 479  
 QY 480 ASHVKALVYSWTHRSADRTNITIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 539  
 DB 480 ASHVKALVYSWTHRSADRTNITIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 539  
 QY 540 TGTGDIRVNPPPAQRYRVRIRYASTDIOFTSINGKAINQGNFSATNWRGEDLDYK 599  
 DB 540 TGTGDIRVNPPPAQRYRVRIRYASTDIOFTSINGKAINQGNFSATNWRGEDLDYK 599  
 QY 600 TGTGDIRVNPPPAQRYRVRIRYASTDIOFTSINGKAINQGNFSATNWRGEDLDYK 659  
 DB 600 TGTGDIRVNPPPAQRYRVRIRYASTDIOFTSINGKAINQGNFSATNWRGEDLDYK 659  
 QY 660 TALFTSTNPRGLTKVDKYHDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 718  
 DB 660 TALFTSTNPRGLTKVDKYHDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 718

RESULT 11  
 AAB66911 standard; protein; 719 AA.  
 XX  
 AC AAB66911;  
 XX  
 DT 12-APR-2001 (first entry)  
 XX  
 DE Insecticidal protein cryIIas.  
 XX  
 KW Insecticide; transgenic plant; insect-resistance.

XX Paecilomyces sp.  
 OS WO200100841-A1.  
 PN 04-JAN-2001.  
 PD 23-JUN-2000; 2000WO-CB002457.  
 PF 29-JUN-1999; 99GB-00015215.  
 PR 23-DEC-1999; 99GB-00030536.  
 XX  
 PA (ZENE ) ZENECA LTD.  
 XX Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;  
 PI Vincent JL, Lee MD;  
 XX MPI; 2001-123015/13.  
 DR Novel insecticidal protein obtained from species of Paecilomyces for  
 XX controlling insects, and for insect-resistant transgenic plant  
 PT production.  
 PT  
 XX Claim 14; Page 62-64; 72pp; English.  
 PS  
 CC The present invention relates to novel insecticidal proteins obtained  
 CC from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The  
 CC insecticidal proteins can be used to produce transgenic plants, which are  
 CC insect-resistant. Also, the insecticidal proteins are useful for  
 CC controlling insects by providing them at a locus where insects feed  
 XX  
 SQ Sequence 719 AA;  
 Query Match 99.0%; Score 3711.5; DB 4; Length 719;  
 Best Local Similarity 99.0%; Pred. No. 7e-293;  
 Matches 712; Conservative 2; Mismatches 4; Indels 1; Gaps 1;  
 QY 1 MKLNQDKHQSSNAKVDKISTDSLNKNETDIELQNHEDCLKSEYENVEPVSASTI 60  
 DB 1 MKLNQDKHQSSNAKVDKISTDSLNKNETDIELQNHEDCLKSEYENVEPVSASTI 60  
 QY 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINOKISTYA 120  
 DB 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINOKISTYA 120  
 QY 121 RNKALTDLKGDLAVYHDSLESWGVRNNTTRASVVKSOYIAELMFVOKLPSFAVSG 180  
 DB 121 RNKALTDLKGDLAVYHDSLESWGVRNNTTRASVVKSOYIAELMFVOKLPSFAVSG 180  
 QY 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNRQVERAGDYSYHCVKWS 240  
 DB 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNRQVERAGDYSYHCVKWS 240  
 QY 241 TGLNLRGTNABSWRVYNOFRDMLVLDLVALPSPDYDTOMYPIKTTAQLTRVYTDAL 300  
 DB 241 TGLNLRGTNABSWRVYNOFRDMLVLDLVALPSPDYDTOMYPIKTTAQLTRVYTDAL 300  
 QY 301 GTVHPHPSFTTWNNAAPSFAEAAVVRNPHLLDLEQVTIYSLLSRWNTQYNNMW 360  
 DB 301 GTVHPHPSFTTWNNAAPSFAEAAVVRNPHLLDLEQVTIYSLLSRWNTQYNNMW 360  
 QY 361 GGHKLEFRITIGTGLNISTQGSTNTSINPVTLPFTSRDYRTESLAGNLFITQPNV 419  
 DB 361 GGHKLEFRITIGTGLNISTQGSTNTSINPVTLPFTSRDYRTESLAGNLFITQPNV 419  
 QY 420 VDFHWKFTVHTPTASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHLSHIGLIS 479  
 DB 420 VDFHWKFTVHTPTASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHLSHIGLIS 479  
 QY 480 ASHVKALVYSWTHRSADRTNITIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 539  
 DB 480 ASHVKALVYSWTHRSADRTNITIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 539



XX CC The invention relates to a novel Bacillus thuringiensis cryI gene, gene  
 CC combination, expression vector, nucleotide sequence of the B  
 CC thuringiensis cryI gene with high-toxicity to lepidoptera pests and the  
 CC amino acid sequence of the protein encoded by it, cooperative use of the  
 CC cryI gene with the expression product of cryIaB or cryIaA, primer  
 CC sequences for expressing the genes, and the constructed shuttle vector  
 CC PSXY422b. The gene in combination with the cryIaB or cryIaA genes  
 CC displays high toxicity to the lepidoptera, coleoptera and diptera pests.  
 CC The present sequence represents the cryIIel protein.  
 XX CC Sequence 719 AA;  
 SQ  
 Query Match 93.7%; Score 3513.5; DB 7; Length 719;  
 Best Local Similarity 93.0%; Pred. No. 9.2e-277;  
 Matches 669; Conservative 26; Mismatches 23; Indels 1; Gaps 1;  
 QY 1 M K L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E V N V P F V S A S T I 60  
 D b 1 M K L K N P D K H Q S L S S N A K V D K I A T S L K N E T D I E L K N I N H E D F L R M S E H S I D F V S A S T I 60  
 QY 61 Q T G I G I A G K I L G T L G V P P A G V A S L Y S F I L G E L M P K G K N Q W E I F M E H V E E I I N Q I S T Y A 120  
 D b 61 Q T G I G I A G K I L G T L G V P P A G Q I A S L Y S F I L G E L M P K G S Q W E I F M E H V E E I I D Q I S T Y A 120  
 QY 121 R N K A L T D L K G L G D A L A V Y H S L E S W G N R N T R A S V V K S Q I A L E L M F V Q K L P S F A V S G 180  
 D b 121 R N I A L A D L K G L G D A L A V Y H S L E S W I K N R N A R A T S V V K S Q I A L E L L F V Q K L P S F A V S G 180  
 QY 181 B E V P L L P I Y A Q A A N L H L L L L D A S I F G K E W G L S S E I S T F Y N R O V E R A G D Y S Y H C V K W Y S 240  
 D b 181 B E V P L L P I Y A Q A A N L H L L L L D A S V F G K E W L S N S Q I S T F Y N R Q V E R T S Y S D H C V K W Y S 240  
 QY 241 T G L N L R G T N A E S W R Y N Q F R D M T L M V L D I V A L P P S Y D T Q M Y P I K T T A Q L T R E V Y T D A I 300  
 D b 241 T G L N L R G T N A E S W R Y N Q F R K D M T L M V L D I A L F P S Y D T L V P I K T S Q L T R E V Y T D A I 300  
 QY 301 G T V H P H P F T T T W Y N N N A P S F A I E A A V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y N M W 360  
 D b 301 G T V H P N A S F A S T T W Y N N N A P S F A I E A V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y N M W 360  
 QY 361 G G H K L E P R T I G G T L N I S T Q G S T N T S I N P V T L P F T S R D V Y R T E S L A G N L F L T Q P V N - V P R 419  
 D b 361 G G H R L E S P I G G A L N T S T Q G S T N T S I N P V T L Q F T S R D V Y R T E S L A G N L F L T Q P V N G V P R 420  
 QY 420 V D F H W K F V T H P I A S D N F Y P G Y A G I G T Q L O D S E N E L P E A T G Q N Y E S Y S H R L S H I G L I S 479  
 D b 420 V D F H W K F A T L P I A S D N F Y L G Y A G V G T Q L O D S E N E L P E T T G Q D N Y E S Y S H R L S H I G L I S 480  
 QY 480 A S H V K A L Y S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V R P G P T G D I L R R T N 539  
 D b 481 A S H V K A L Y S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V R P G P T G D I L R R T N 540  
 QY 540 T G T G D I R V N I N P P A G R Y R I R Y A S T D L Q F T S I N G R A I N Q G N F S A T M N G E D L D Y K 599  
 D b 541 T G T G D I R V N I N P P A G R Y R I R Y A S T D L Q F T S I N G R A I N Q G N F S A T M N G E D L D Y K 600  
 QY 600 T F T V G F T T P F S L L D V Q S T F T I G A W N F S S G N E V Y I D R I E F V P V E V T Y E A E Y D F E K A Q E V 659  
 D b 601 T F R T V G F T T P F S D V Q S T F T I G A W N F S S G N E V Y I D R I E F V P V E V T Y E A E Y D F E K A Q E V 660  
 QY 660 T A L T S T N P R G L K T D V K D Y H I D Q V S N L V E S I S D E F Y L D E K R E L F E I V K Y A K Q I H I E R N M 718  
 D b 661 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S I S D E F Y L D E K R E L F E I V K Y A K Q I H I E R N M 719

RESULT 14  
 ID AAB66912 standard; protein: 719 AA.  
 XX AAB66912;  
 AC AAB66912;  
 DT 12-APR-2001 (first entry)

XX Insecticidal protein cryIIb1.  
 DE Insecticide; transgenic plant; insect-resistance.  
 KW Paecilomyces sp.  
 OS WO200100841-A1.  
 PN 04-JAN-2001.  
 PD 23-JUN-2000; 2000WO-CB002457.  
 PE 29-JUN-1999; 99GB-00015215.  
 PR 23-DEC-1999; 99GB-00030536.  
 XX (ZENE ) ZENECA LTD.  
 PA Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;  
 PI Vincent JL, Lee MD;  
 PI WPI; 2001-123015/13.  
 DR Novel insecticidal protein obtained from species of Paecilomyces for  
 XX controlling insects, and for insect-resistant transgenic plant  
 PT production.  
 PT Claim 14; Page 64-66; 72pp; English.  
 PS The present invention relates to novel insecticidal proteins obtained  
 CC from Paecilomyces sp. (see AAB66912 to AAB66913). The  
 CC insecticidal proteins can be used to produce transgenic plants, which are  
 CC insect-resistant. Also, the insecticidal proteins are useful for  
 CC controlling insects by providing them at a locus where insects feed  
 XX Sequence 719 AA;  
 SQ

Query Match 92.9%; Score 3482.5; DB 4; Length 719;  
 Best Local Similarity 92.4%; Pred. No. 3.1e-274;  
 Matches 664; Conservative 31; Mismatches 23; Indels 1; Gaps 1;  
 QY 1 M K L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E V N V P F V S A S T I 60  
 D b 1 M K L K N P D K H Q S L S S N A K V D K I A T S L K N E T D I E L K N M N E D Y L R M S E H S I D P F V S A S T I 60  
 QY 61 Q T G I G I A G K I L G T L G V P P A G V A S L Y S F I L G E L M P K G K N Q W E I F M E H V E E I I N Q I S T Y A 120  
 D b 61 Q T G I G I A G K I L G T L G V P P A G Q I A S L Y S F I L G E L M P K G S Q W E I F M E H V E E I I N Q I L T Y A 120  
 QY 121 R N K A L T D L K G L G D A L A V Y H S L E S W G N R N T R A S V V K S Q I A L E L M F V Q K L P S F A V S G 180  
 D b 121 R N K A L S D L R G L G D A L A V Y H S L E S W E N R N T R A S V V K N Q Y I A L E L M F V Q K L P S F A V S G 180  
 QY 181 B E V P L L P I Y A Q A A N L H L L L L D A S I F G K E W G L S S E I S T F Y N R O V E R A G D Y S Y H C V K W Y S 240  
 D b 181 B E V P L L P I Y A Q A A N L H L L L L D A S I F G K E W L S S E I S T F Y N R Q V E R T R D S D H C I K W Y N 240  
 QY 241 T G L N L R G T N A E S W R Y N Q F R D M T L M V L D I V A L P P S Y D T Q M Y P I K T T A Q L T R E V Y T D A I 300  
 D b 241 T G L N L R G T N A E S W R Y N Q F R K D M T L M V L D I A L F P S Y D T L V P I K T S Q L T R E V Y T D A I 300  
 QY 301 G T V H P H P F T T T W Y N N N A P S F A I E A A V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y N M W 360  
 D b 301 G T V H P N Q A P A S T T W Y N N N A P S F A I E A A V I R S P H L L D F L E K V T I Y S L L S R W S N T Q Y N M W 360  
 QY 361 G G H K L E P R T I G G T L N I S T Q G S T N T S I N P V T L P F T S R D V Y R T E S L A G N L F L T Q P V N - V P R 419  
 D b 361 G G H R L E S P I G G A L N T S T Q G S T N T S I N P V T L Q F T S R D V Y R T E S L A G N L F L T Q P V N G V P R 420  
 QY 420 V D F H W K F V T H P I A S D N F Y P G Y A G I G T Q L O D S E N E L P E A T G Q N Y E S Y S H R L S H I G L I S 479  
 D b 421 V D F H W K F P T L P I A S D N F Y L G Y A G V G T Q L O D S E N E L P E T T G Q D N Y E S Y S H R L S H I G L I S 480

QY 480 ASHKALVSWTHRSADRTNTEIPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 539  
 DB 481 ASHKALVSWTHRSADRTNTEIPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 540  
 QY 540 TGTGDIRVNIWPPFAQRVVRIRYASTTDLQPHTSINGKAINQGNFSAATMARGEDLDYK 599  
 DB 541 TGTGDIRVNIWPPFAQRVVRIRYASTTDLQPHTSINGKAINQGNFSAATMARGEDLDYK 600  
 QY 600 TFXTVGFTTTPFSLDDVQSTFTIGAWNFSSNGNEVYIDRIEFVPEVTEAEYDPEKAQEKV 659  
 DB 601 TFXTVGFTTTPFSDVQSTFTIGAWNFSSNGNEVYIDRIEFVPEVTEAEYDPEKAQEKV 660  
 QY 660 TALFTSTNPRGLTKTDVKDYHIDQVSNLVESLSDEFYLDKRELFELVVKYAKQIHIERNM 718  
 DB 661 TALFTSTNPRGLTKTDVKDYHIDQVSNLVESLSDEFYLDKRELFELVVKYAKQIHIERNM 719

RESULT 15  
 AAE36276  
 ID AAE36276 standard; protein; 719 AA.  
 XX AAE36276;  
 AC  
 XX 26-JUN-2003 (first entry)  
 DT  
 XX B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cry1Ib1.  
 DE Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.  
 XX Bacillus thuringiensis.  
 OS  
 XX Bacillus thuringiensis.  
 XX WO200298911-A2.  
 PN  
 XX 12-DEC-2002.  
 PD  
 XX 30-MAY-2002; 2002WO-GB002666.  
 PF  
 XX 07-JUN-2001; 2001GB-00013900.  
 PR  
 XX (SYGN ) SYNGENTA LTD.  
 PA Vincent JL, Viner R;  
 XX WPI; 2003-175137/17.  
 XX  
 PT New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.  
 PS  
 XX Claim 12; Page 56-58; 67pp; English.

XX The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects. Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention  
 XX  
 SQ Sequence 719 AA;

Query Match 92.9%; Score 3482.5; DB 6; Length 719;  
 Best Local Similarity 92.4%; Pred. No. 3.1e-274;  
 Matches 664; Conservative 31; Mismatches 23; Indels 1; Gaps 1;  
 QY 1 MCLKNQKHQSFSSNAKVDKISTDLKNETDIELONINHEDECLKMSEYENVEPVSASTI 60  
 DB 1 MCLKNPDKHQSLSNAKVDKIATDSLNETDIELKNNNEDYLRMSHESIDPVSASTI 60  
 QY 61 QTGIGIAGKILGTGVFPAGQVAGLSYFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
 DB 61 QTGIGIAGKILGTGVFPAGQVAGLSYFILGELWPKGNQWEIFMEHVEEIIINQKILTYA 120

QY 121 RNKALTDLKGLGDALAVVHDSLESWGNRNNTNRARSVVKSOYIALELMFVQKLSFAVSG 180  
 DB 121 RNKALSDLRGLGDALAVVHDSLESWGNRNNTNRARSVVKQYIALELMFVQKLSFAVSG 180  
 QY 181 BEVPLLPITYAQAANLHLLLRDASIFGKEWGLSSSEISTFNROVERAGDYSYCVKWS 240  
 DB 181 BEVPLLPITYAQAANLHLLLRDASIFGKEWGLSSSEISTFNROVERTRDYSDCIKWYN 240  
 QY 241 TGLNNLRGTNAESVRYNQFRDRLMTLMLDLVALFPSPYDTOMYPIKTTAQULTRVYTDAL 300  
 DB 241 TGLNNLRGTNAESVRYNQFRDRLMTLMLDLVALFPSPYDTLVPYPIKTTQSQTREYTDAL 300  
 QY 301 GTVHPHPSFTTWTNNNAPSFAIEAAVVRNPHLLDFLEOVTTYSLLSRWSNTQYMNW 360  
 DB 301 GTVHPNQAFSTTWTNNNAPSFAIEAAVIRSPHLLDFLEKVTTYSLLSRWSNTQYMNW 360  
 QY 361 GGHKLEFETIGGTNLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFLTQPVN-VPR 419  
 DB 361 GGHRLSESPIGALNTSTQGSTNTSINPVTLOFTSRDVRTESLAGLNLFLTQPVNGVPR 420  
 QY 420 VDFHWKFVTHPIASDNFYYPQYAGIGTLODSENELPEATGQPNYESYSHRLSHIGLIS 479  
 DB 421 VDFHWKFPTLPIASDNFYYPQYAGVGTLODSENELPETTGQPNYESYSHRLSHIGLIS 480  
 QY 480 ASHKALVSWTHRSADRTNTEIPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 539  
 DB 481 ASHKALVSWTHRSADRTNTEIPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 540  
 QY 540 TGTGDIRVNIWPPFAQRVVRIRYASTTDLQPHTSINGKAINQGNFSAATMARGEDLDYK 599  
 DB 541 TGTGDIRVNIWPPFAQRVVRIRYASTTDLQPHTSINGKAINQGNFSAATMARGEDLDYK 600  
 QY 600 TFXTVGFTTTPFSLDDVQSTFTIGAWNFSSNGNEVYIDRIEFVPEVTEAEYDPEKAQEKV 659  
 DB 601 TFXTVGFTTTPFSDVQSTFTIGAWNFSSNGNEVYIDRIEFVPEVTEAEYDPEKAQEKV 660  
 QY 660 TALFTSTNPRGLTKTDVKDYHIDQVSNLVESLSDEFYLDKRELFELVVKYAKQIHIERNM 718  
 DB 661 TALFTSTNPRGLTKTDVKDYHIDQVSNLVESLSDEFYLDKRELFELVVKYAKQIHIERNM 719

Search completed: October 28, 2004, 18:19:45  
 Job time : 91.5697 secs





GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 28, 2004, 18:05:43 ; Search time 19.1643 Seconds  
(without alignments)  
3604.811 Million cell updates/sec

Title: US-10-019-823B-54  
Perfect score: 3749  
Sequence: 1 MKLNQDKHQSFSSNAKVDK.....KRELFEIVKAKOLHIERNM 718

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_791\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	3732.5	99.6	719 2 S25383	parasporal crystal
2	3724.5	99.3	719 2 I39814	insecticidal prote
3	3722.5	99.3	719 2 I39815	insecticidal prote
4	3482.5	92.9	719 2 I40580	crvV465 protein -
5	2248	60.0	1228 2 S00873	parasporal crystal
6	1891	50.4	380 2 B42459	hypothetical prote
7	1480.5	39.5	1157 1 S49247	parasporal crystal
8	1462	39.0	1166 2 S32645	parasporal crystal
9	1455.5	38.8	1174 2 S32649	parasporal crystal
10	1448.5	38.6	1155 2 A26513	parasporal crystal
11	1441.5	38.5	1155 2 JD0002	parasporal crystal
12	1441.5	38.5	1156 2 A29185	parasporal crystal
13	1433	38.2	934 2 A22798	parasporal crystal
14	1432	38.2	1176 2 JT0241	parasporal crystal
15	1426	38.0	1176 2 JC2219	parasporal crystal
16	1424.5	38.0	1155 2 S02134	parasporal crystal
17	1424	38.0	1181 2 A41052	parasporal crystal
18	1422	37.9	1176 2 A22671	parasporal crystal
19	1422	37.9	1176 2 S02215	parasporal crystal
20	1420.5	37.9	1155 2 I39838	parasporal crystal
21	1354.5	36.1	1174 2 A42459	parasporal crystal
22	1340.5	35.8	1138 2 A48944	parasporal crystal
23	1319	35.2	1156 2 A29838	parasporal crystal
24	1310	34.9	823 2 S04181	parasporal crystal
25	1298	34.6	1189 2 S00944	parasporal crystal
26	1288.5	34.4	1154 2 S39536	parasporal crystal
27	1257.5	33.5	1171 2 I40572	parasporal crystal
28	1257.5	33.5	1171 2 A37839	parasporal crystal
29	1248.5	33.3	1176 2 A48970	parasporal crystal

30	1205.5	32.2	1160 2 S32647	parasporal crystal
31	1197	31.9	1165 2 S11446	parasporal crystal
32	1185	31.6	655 2 UC7140	protoxin - Bacillu
33	1184.5	31.6	1172 2 S32689	parasporal crystal
34	1179.5	31.5	1160 2 I40589	parasporal crystal
35	1149.5	30.7	1177 2 A49785	parasporal crystal
36	1146	30.6	1178 1 USBSXH	parasporal crystal
37	1136.5	30.3	652 2 A27323	parasporal crystal
38	1114.5	29.7	659 2 S0228	parasporal crystal
39	1082	28.9	652 2 I39811	parasporal crystal
40	977.5	26.1	649 1 JH0261	parasporal crystal
41	921.5	24.6	618 2 S11445	parasporal crystal
42	875.5	23.4	1156 2 S19306	parasporal crystal
43	818.5	21.8	1136 1 USBS81	parasporal crystal
44	686	18.3	934 2 B39838	parasporal crystal
45	658.5	17.6	1180 2 I39870	parasporal crystal

## ALIGNMENTS

## RESULT 1

S25383  
parasporal crystal protein cryIIal - Bacillus thuringiensis  
N:Alternate names: delta-endotoxin; parasporal crystal protein cryV  
C:Species: Bacillus thuringiensis  
C:Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 09-Jul-2004  
C:Accession: S25383  
R:Tailor, R.; Tippett, J.; Gibb, G.; Pells, S.; Pike, D.; Jordan, L.; Ely, S.  
Mol. Microbiol. 6, 1211-1217, 1992  
A:Title: Identification and characterization of a novel Bacillus thuringiensis delta-end  
A:Reference number: S25383; MUID:92269582; PMID:1588820  
A:Accession: S25383  
A:Molecule type: DNA  
A:Residues: 1-719 <TAI>  
A:Cross-references: UNIPROT:Q45752; EMBL:X62821; NID:940289; PIDN:CAA44633.1; PID:940290  
C:Genetics:  
C:Superfamily: parasporal crystal protein  
C:Keywords: delta-endotoxin

Query Match		99.6%;	Score 3732.5;	DB 2;	Length 719;
Best Local Similarity		99.6%;	Pred. No. 2.2e-250;		
Matches: 716;		Conservative	0;	Mismatches	2;
				Indels	1;
				Gaps	1;
QY	1	MKLNQDKHQSFSSNAKVDKISTSLKNETDIELQNIHEDCLKMSYEYENVEPFSASTI	60		
DB	1	MKLNQDKHQSFSSNAKVDKISTSLKNETDIELQNIHEDCLKMSYEYENVEPFSASTI	60		
QY	61	QTGIGIAGKILGTGVPPAGQVASLYSILGELWPKGNQWEIFMEHVEEIIINQKISTYA	120		
DB	61	QTGIGIAGKILGTGVPPAGQVASLYSILGELWPKGNQWEIFMEHVEEIIINQKISTYA	120		
QY	121	RNKALTDLKGDLAVVHDSLESWGNRNNTRARSVKSOVIALELMFVKLPSPFVSG	180		
DB	121	RNKALTDLKGDLAVVHDSLESWGNRNNTRARSVKSOVIALELMFVKLPSPFVSG	180		
QY	181	BEVPLPIYAQAANLHLLLRDASIFGKMWGLSSSEISTFYNNRQVERAGDYSYHCWKYS	240		
DB	181	BEVPLPIYAQAANLHLLLRDASIFGKMWGLSSSEISTFYNNRQVERAGDYSYHCWKYS	240		
QY	241	TGNNLRGNABSWRYNQFRDMLVLDLVALPSPYDTOMYPIKTTAQLTREYVTTAI	300		
DB	241	TGNNLRGNABSWRYNQFRDMLVLDLVALPSPYDTOMYPIKTTAQLTREYVTTAI	300		
QY	301	GTVHPHPSFTSTTWNNAFSAIEAAVARNPHLLDLEQVITYISLLSRMSNTQYMNW	360		
DB	301	GTVHPHPSFTSTTWNNAFSAIEAAVARNPHLLDLEQVITYISLLSRMSNTQYMNW	360		
QY	361	GGHKLFEFRITGTLNISTQGSTNTSINPTLPFTSRDVRRTESLACLNFLTQPNV-VPR	419		
DB	361	GGHKLFEFRITGTLNISTQGSTNTSINPTLPFTSRDVRRTESLACLNFLTQPNV-VPR	420		

QY 420 VDFHKKFVTHPIASDNFYYPGVAGIGTQLODSENELPPEATGQPNYSYSHRLSHIGLIS 479  
 DB 421 VDFHKKFVTHPIASDNFYYPGVAGIGTQLODSENELPPEATGQPNYSYSHRLSHIGLIS 480  
 QY 480 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 539  
 DB 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 540  
 QY 540 TGTGDIRWNNPPPAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATNWRGDDLYK 599  
 DB 541 TGTGDIRWNNPPPAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATNWRGDDLYK 600  
 QY 600 TFXTVGFTTTPFSLDVQSTFTIGAMNFGSGNEVYIDRIEFVPEVVTYEAEDYDFAKQEKV 659  
 DB 601 TFXTVGFTTTPFSLDVQSTFTIGAMNFGSGNEVYIDRIEFVPEVVTYEAEDYDFAKQEKV 660  
 QY 660 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEPYLDEKRELFEIVKYAKQLHIERNM 718  
 DB 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEPYLDEKRELFEIVKYAKQLHIERNM 719

RESULT 2  
 I39814  
 Insecticidal protein cryI - Bacillus thuringiensis  
 C:Species: Bacillus thuringiensis  
 C:Date: 19-Jul-1996 #sequence\_revision 19-Jul-1996 #text\_change 26-Aug-1999  
 C:Accession: I39814  
 R:Shin, B.S.; Park, S.H.; Choi, S.K.; Koo, B.T.; Lee, S.T.; Kim, J.I.  
 Appl. Environ. Microbiol. 61: 2402-2407, 1995  
 A:Title: Distribution of cryI-type insecticidal protein genes in Bacillus thuringiensis  
 tomocodus.  
 A:Reference number: I39814; MUID:95314293; PMID:7793960  
 A:Accession: I39814  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-719 <RES>  
 A:Cross-references: GB:L36338; NID:9540281; PIDN:AAC36999.1; PID:9540282  
 C:Genetics:  
 A:Gene: cryI  
 C:Superfamily: parasporal crystal protein

Query Match 99.3%; Score 3724.5; DB 2; Length 719;  
 Best Local Similarity 99.3%; Pred. No. 7.8e-250;  
 Matches 714; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMSYENVEPVSASTI 60  
 DB 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMSYENVEPVSASTI 60  
 QY 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEIFMEHVVEEIIINQKISTYA 120  
 DB 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEIFMEHVVEEIIINQKISTYA 120  
 QY 121 RNKALTDLKGLDALAVYHDSLESWGNRNNTARSVVKVQYIALELMFVQKLPSPFVSG 180  
 DB 121 RNKALTDLKGLDALAVYHDSLESWGNRNNTARSVVKVQYIALELMFVQKLPSPFVSG 180  
 QY 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFFNROVERAGDYSYHCVKWYS 240  
 DB 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFFNROVERAGDYSYHCVKWYS 240  
 QY 241 TGLNLRGTNAESWRYNQFRDMLVLDLVALFPSTQYPIKTAQLTREVVYTDI 300  
 DB 241 TGLNLRGTNAESWRYNQFRDMLVLDLVALFPSTQYPIKTAQLTREVVYTDI 300  
 QY 301 GTVHPHPSFTSTWNNNAPSFAIEAAVVRNPHLLDLEQVTIYSLSRWSNTQYNNMW 360  
 DB 301 GTVHPHPSFTSTWNNNAPSFAIEAAVVRNPHLLDLEQVTIYSLSRWSNTQYNNMW 360  
 QY 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRVRESLAGLNLFTQPVN-VPR 419  
 DB 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRVRESLAGLNLFTQPVNGVPR 420

QY 420 VDFHKKFVTHPIASDNFYYPGVAGIGTQLODSENELPPEATGQPNYSYSHRLSHIGLIS 479  
 DB 421 VDFHKKFVTHPIASDNFYYPGVAGIGTQLODSENELPPEATGQPNYSYSHRLSHIGLIS 480  
 QY 480 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 539  
 DB 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 540  
 QY 540 TGTGDIRWNNPPPAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATNWRGDDLYK 599  
 DB 541 TGTGDIRWNNPPPAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATNWRGDDLYK 600  
 QY 600 TFXTVGFTTTPFSLDVQSTFTIGAMNFGSGNEVYIDRIEFVPEVVTYEAEDYDFAKQEKV 659  
 DB 601 TFXTVGFTTTPFSLDVQSTFTIGAMNFGSGNEVYIDRIEFVPEVVTYEAEDYDFAKQEKV 660  
 QY 660 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEPYLDEKRELFEIVKYAKQLHIERNM 718  
 DB 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEPYLDEKRELFEIVKYAKQLHIERNM 719

RESULT 3  
 I39815  
 Insecticidal protein cryV - Bacillus thuringiensis  
 C:Species: Bacillus thuringiensis  
 C:Date: 19-Jul-1996 #sequence\_revision 19-Jul-1996 #text\_change 09-Jul-2004  
 C:Accession: I39815  
 R:Gleave, A.P.; Williams, R.; Hedges, R.J.  
 Appl. Environ. Microbiol. 59: 1683-1687, 1993  
 A:Title: Screening by polymerase chain reaction of Bacillus thuringiensis serotypes for t  
 leusis subsp. kurstaki.  
 A:Reference number: I39815; MUID:93298009; PMID:8517758  
 A:Accession: I39815  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-719 <RES>  
 A:Cross-references: UNIPROT:Q45752; GB:M98544; NID:9142767; PIDN:AAA22354.1; PID:9142768  
 C:Genetics:  
 A:Gene: cryV  
 C:Superfamily: parasporal crystal protein

Query Match 99.3%; Score 3722.5; DB 2; Length 719;  
 Best Local Similarity 99.4%; Pred. No. 1.1e-249;  
 Matches 715; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMSYENVEPVSASTI 60  
 DB 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMSYENVEPVSASTI 60  
 QY 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEIFMEHVVEEIIINQKISTYA 120  
 DB 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEIFMEHVVEEIIINQKISTYA 120  
 QY 121 RNKALTDLKGLDALAVYHDSLESWGNRNNTARSVVKVQYIALELMFVQKLPSPFVSG 180  
 DB 121 RNKALTDLKGLDALAVYHDSLESWGNRNNTARSVVKVQYIALELMFVQKLPSPFVSG 180  
 QY 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFFNROVERAGDYSYHCVKWYS 240  
 DB 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFFNROVERAGDYSYHCVKWYS 240  
 QY 241 TGLNLRGTNAESWRYNQFRDMLVLDLVALFPSTQYPIKTAQLTREVVYTDI 300  
 DB 241 TGLNLRGTNAESWRYNQFRDMLVLDLVALFPSTQYPIKTAQLTREVVYTDI 300  
 QY 301 GTVHPHPSFTSTWNNNAPSFAIEAAVVRNPHLLDLEQVTIYSLSRWSNTQYNNMW 360  
 DB 301 GTVHPHPSFTSTWNNNAPSFAIEAAVVRNPHLLDLEQVTIYSLSRWSNTQYNNMW 360  
 QY 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRVRESLAGLNLFTQPVN-VPR 419  
 DB 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRVRESLAGLNLFTQPVNGVPR 420

QY 420 VDFHMKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 479  
DB 421 VDFHMKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
QY 480 ASHVKALVYSWTHRSADRTNTHIEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRTN 539  
DB 481 ASHVKALVYSWTHRSADRTNTHIEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRTN 540  
QY 540 TGFPGDIRVNIPTPPAQRVRYRIRYASTTDLQPHTSINGKAINQGNFSAATMNRGEBLDYK 599  
DB 541 TGFPGDIRVNIPTPPAQRVRYRIRYASTTDLQPHTSINGKAINQGNFSAATMNRGEBLDYK 600  
QY 600 TFXTVGTTTPPSLLDVOSTTTIGAMNPFSSGNEVYIDRIEFPVPEVYEAEDFEKAQEKV 659  
DB 601 TERTVGTTPPSFLDVOSTTTIGAMNPFSSGNEVYIDRIEFPVPEVYEAEDFEKAQEKV 660  
QY 660 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFELVYAKQLHIERNM 718  
DB 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFELVYAKQLHIERNM 719

RESULT 4  
I40590  
cryV465 protein - Bacillus thuringiensis  
C:Species: Bacillus thuringiensis  
C:Date: 12-Aug-1996 #sequence\_revision 12-Aug-1996 #text\_change 09-Jul-2004  
C:Accession: I40590  
R:Shin, B.S.; Park, S.H.; Choi, S.K.; Koo, B.T.; Lee, S.T.; Kim, J.I.  
Appl. Environ. Microbiol. 61, 2402-2407, 1995  
A:Title: Distribution of cryV-type insecticidal protein genes in Bacillus thuringiensis  
tomocidus  
A:Reference number: I39814; MUID:95314293; PMID:7793960  
A:Accession: I40590  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-719 <RES>  
A:Cross-references: UNIPROT:Q45709; EMBL:U07642; NID:9467234; PIDN:AAA82114.1; PID:94672  
C:Genetics:  
A:Gene: cryV465  
C:Superfamily: parasporal crystal protein

Query Match 92.9%; Score 3482.5; DB 2; Length 719;  
Best Local Similarity 92.4%; Pred. No. 4.5e-233;  
Matches 664; Conservative 31; Mismatches 23; Indels 1; Gaps 1;  
QY 1 MKLKNQKHQSFSSNAKVDKISTDSLNKQETDIELONINHEDCIKMSEYENVEPVSASTI 60  
DB 1 MKLKNPDKHQSLSNAKVDKIATDSLNKQETDIELKNNNEDYLRMSHESIDPFVSASTI 60  
QY 61 QTGIGIAGKILGTGVPFAGQVASYFLGELWPKGNQWEIFMEHVEEIIINOKISTYA 120  
DB 61 QTGIGIAGKILGTGVPFAGQIASLYFLGELWPKGKQWEIFMEHVEEIIINOKILTYA 120  
QY 121 RNKALTDLKGDLALAVYHDSLESWGNRNNTARSVVKSQYIALELMFVKQLPSPFVSG 180  
DB 121 RNKALSRLGLGDLALAVYHDSLESWGNRNNTARSVVKQYIALELMFVKQLPSPFVSG 180  
QY 181 BEVPLLPYIAQAANLHLLLRDASIFGKENGSLSSSETTFYNNQVERAGDYSYHCVKWKYS 240  
DB 181 BEVPLLPYIAQAANLHLLLRDASIFGKENGSLSSSETTFYNNQVERAGDYSYHCVKWKYS 240  
QY 241 TGLNLRGTNAESWVRYNQFRDMTLMVLVALFPSSYDTQMYPIKTTAQLTREYVTDI 300  
DB 241 TGLNLRGTNAESWVRYNQFRDMTLMVLVALFPSSYDTQMYPIKTTAQLTREYVTDI 300  
QY 301 GTVHPHPSFTTWNANAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYNNMW 360  
DB 301 GTVHPHPSFTTWNANAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYNNMW 360  
QY 361 GGHLKLEFRTIGGTLNISTQGSTNTSINPVTLPFTSRDVRYESLAGLNLF--LTQPVN-VPRVDFHMKFV 427  
DB 361 GGHLKLEFRTIGGTLNISTQGSTNTSINPVTLPFTSRDVRYESLAGLNLF--LTQPVN-VPRVDFHMKFV 427

QY 420 VDFHMKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 479  
DB 421 VDFHMKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
QY 480 ASHVKALVYSWTHRSADRTNTHIEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRTN 539  
DB 481 ASHVKALVYSWTHRSADRTNTHIEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRTN 540  
QY 540 TGFPGDIRVNIPTPPAQRVRYRIRYASTTDLQPHTSINGKAINQGNFSAATMNRGEBLDYK 599  
DB 541 TGFPGDIRVNIPTPPAQRVRYRIRYASTTDLQPHTSINGKAINQGNFSAATMNRGEBLDYK 600  
QY 600 TFXTVGTTTPPSLLDVOSTTTIGAMNPFSSGNEVYIDRIEFPVPEVYEAEDFEKAQEKV 659  
DB 601 TERTVGTTPPSFLDVOSTTTIGAMNPFSSGNEVYIDRIEFPVPEVYEAEDFEKAQEKV 660  
QY 660 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFELVYAKQLHIERNM 718  
DB 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFELVYAKQLHIERNM 719

RESULT 5  
S00873  
parasporal crystal protein cryBa1 - Bacillus thuringiensis subsp. thuringiensis  
N:Alternate names: Parasporal crystal protein cryA4  
C:Species: Bacillus thuringiensis subsp. thuringiensis  
C:Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 09-Jul-2004  
C:Accession: S00873  
R:Brizzard, B.L.; Whiteley, H.R.  
Nucleic Acids Res. 16, 2723-2724, 1988  
A:Title: Nucleotide sequence of an additional crystal protein gene cloned from Bacillus t  
A:Reference number: S00873; MUID:88203216; PMID:3362680  
A:Accession: S00873  
A:Molecule type: DNA  
A:Residues: 1-1228 <BRI>  
A:Cross-references: UNIPROT:P05517; EMBL:X06711; NID:940264; PIDN:CAA29898.1; PID:958094;  
C:Genetics:  
A:Gene: cryA4  
A:Start codon: TTG  
A:Superfamily: parasporal crystal protein  
C:Keywords: delta-endotoxin

Query Match 60.0%; Score 2248; DB 2; Length 1228;  
Best Local Similarity 62.3%; Pred. No. 3.2e-147;  
Matches 446; Conservative 80; Mismatches 164; Indels 26; Gaps 7;  
QY 23 TDSLKNQETDIELONINH-----EDCLKMSEYENVEPVSASTIQTGIGIAGKI 70  
DB 2 TSNRKNEEIIINAVSNHSAQMDLLDPARIEDPSLCIAEGNNIDPFVSASTVQTGIIAGRI 61  
QY 71 LGTLGVPPAGQVASYFLGELWPKGNQWEIFMEHVEEIIINOKISTYARNKALTDLKG 130  
DB 62 LGVLGVPPAGQVASYFLGELWPKGRDQWEIFLEHVEQLINQOITENARNALARLQG 121  
QY 131 LGDALAVYHDSLESWGNRNNTARSVVKSQYIALELMFVKQLPSPFVSGBEVPLPIYA 190  
DB 122 LGDSFRAYQQSLEDLENRDARTSRVLYTQYIALELDFLNAMPFLAIRNQEVPLLMVYA 181  
QY 191 QAANLHLLLRDASIFGKENGSLSSSETTFYNNQVERAGDYSYHCVKWKYSTGLNLRGTN 250  
DB 182 QAANLHLLLRDASIFGSEFGLTSQEIORYERQVERTRDSDYCVENWYGLNSLRGTN 241  
QY 251 AESWRYNQFRDMTLMVLVALFPSSYDTQMYPIKTTAQLTREYVTDIAGTVHPHPSFT 310  
DB 242 AASWRYNQFRDMLTLGVLDLVALFPSSYDTQMYPIKTTAQLTREYVTDIAGT--GVNMA 299  
QY 311 STTWNANAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYNNMWGKLEFRTI 370  
DB 300 SMWYNNANAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYNNMWGKLEFRTI 359  
QY 371 GGHLKLEFRTIGGTLNISTQGSTNTSINPVTLPFTSRDVRYESLAGLNLF--LTQPVN-VPRVDFHMKFV 427  
DB 360 GGGLTSTHGATNTSINPVTLPFTSRDVRYESLAGLNLF--LTQPVN-VPRVDFHMKFV 416



Db 722 AAKLSRERNL 732

## RESULT 8

S32645  
parasporal crystal protein cry1Gal - *Bacillus thuringiensis*  
C;Species: *Bacillus thuringiensis*  
C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
C;Accession: S32645  
R;Lambert, B.  
submitted to the EMBL Data Library, April 1993  
A;Reference number: S32645  
A;Accession: S32645  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-1166 <LAMB>  
A;Cross-references: UNIPROT:Q45746; EMBL:Z22510; NID:G295861; PIDN:CAA80233  
C;Superfamily: parasporal crystal protein  
C;Keywords: delta-endotoxin

Query Match 39.0%; Score 1462; DB 2; Length 1166;  
Best Local Similarity 45.7%; Pred. NO. 7.9e-93;  
Matches 322; Conservative 101; Mismatches 207; Indels 74; Gaps 17;

QY	41	DCLKMSYB----	NVEPVSASTTQTGTIGAKILGILVFPACQVASLVSFILGELWPK	96	
DB	13	NCLNPNSEI	FNARNSFGIVSQVSSGL---TRFLEAAVPEAGFALGDFDIIWGAL---	66	
QY	97	GKQWEI	FMEHVEBI	INOKISTYARNKALTDKLGDALAVYHDSLESWGVRNNTARS	156
DB	67	GVDQWS	FLFQIEQIL	IQEITELEBRNATAILTGLSSYNLYVEALREWENDPNNPASQE	125
QY	157	VKVSQY	IALELMFVOKLPSFAVSGEEVPLPIPIYAQANLHLLLLRDASI	FKKEWGLSSSE	216
DB	127	RVRTRE	FLTDDAI	VTGLPTLAIRNLVVNLSVYTAQANLHLSLLRDVAVYFGERMGLTQAN	186
QY	217	ISIPYARQ	VERAGDYSHCVKWKVYSTGLNNLRGTNAESVVRVNOFRDDMTLWLDLVALFP	276	
DB	187	IEDLYT	LTENIQISYDHCARVNOQNEIGGISR---	RKDFQDRLTISVLDIVALFP	242
QY	277	SYTQMYP	IKTTAQLTREVTDAI--	GTVHPHPSFTSTWYNNNAPSFAIEAAVWRNPH	334
DB	243	NYDIRTYPI	TQSQLTREIVTSPVAGNI-----	NFGLSIANVLGRAPH	285
QY	335	LLDFLEQV	TYISLLSRNSNTQYMNWGGHKLFPRTIG--GTJN-----	ISTOGSNTS	385
DB	286	LMDFID	RIVITYNSVR--STPY--	WAGHEVISRRTGGQNEIRFFLYGVYAAANAEPPVT	340
QY	386	INPVTLE	FTSRDVRYES-----	LAGNLFLTPQVNVNPRVDFHWKVTHTPIASDNFYYP	439
DB	341	IRPTGF	DEQEQWYPARSRVVSFRSSQDPSLVDVG-----	PLT-IFSAVSIYRN	390
QY	440	GYAGIG	TQLODSENELPEATQGPNYESYSHRLSHIGLISAS-----	HVKALVYSWTHRS	494

## RESULT 9

S32649  
 parasporeal crystal protein crylPa3 - *Bacillus thuringiensis*  
 C/Species: *Bacillus thuringiensis*  
 C/Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 0  
 C/Accession: S32649  
 R/Lambert, B.  
 submitted to the EMBL Data Library, April 1993  
 A/Reference number: S32645  
 A/Accession: S32649  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-1174 xLAM-  
 A/Cross-references: UNIPROT:Q45749; EMBL:Z22512; NID:G295861  
 C/Superfamily: parasporal crystal protein  
 C/Keywords: delta-endotoxin

Query Match 38.8%; Score 1455.5; DB 2; Length 1174;  
Best Local Similarity 44.7%; Pred. No. 2.3e-92;

Qy	36	NINHE-----DCLUKMEYENBPFFVASTIQIGGICIA-GKILGTGLVPFPAGQVASLYSFYL 90
Dy	:	: : : :
Dy	4	NIQCVCVFNCLSNPEVEILSEERSTGRPLDISLSLTRPILLSFEFVGPGVAFGLPDLLW 63
Qy	91	GELWPCKGNOWEIMFHVHBEELIINOKEISTYARNKALTDLKGDLALAVYHDSLESWSYGNEN 150
Dy	64	GTITP----SEWSLFLOLEQIEORIETLBERNRAITTLRGLADSYEVYLEAREWEENEN 120
Qy	151	NTRARSVVKSOXIALELMFVKLPFSFAVSSEEPLPIYAQAANLHLLLRLDASIFEGKW 210
Dy	121	NAQLREDVRIRPANTDDALIITAINNFILTSPFILLSVYQAAHLHSULLRADAVSFGQM 180
Qy	211	GLUSSEISTFYNRQVERAGDYSHCVKWKYSTGLNLRGTVNAESWRYNOFRRDNTLMULD 270
Dy	181	GLDIATVNHNVLNLINHRYTECHLDTYNQGLENGTNTROWSRFNQFRRELTITVLVD 240
Qy	271	LVALPSYDTQWPKTTAQLTREWDIDAICTVHPHSPSTTWYNKNAPS-FSALEAAV 329
Dy	241	IVALPENXDARAPIQTSSQUTRSIIYSVV--IEDSP-----VSANTPNGNRAEPG- 290
Qy	330	VRNPHLLDFLEQVIYTISLLSRWSTQTMNMWGGHKLEFRTIGTGLNISQGSTNTSINPV 389
Dy	291	VRPPLMLDMFN-----SLFVTAETVRSQTVGGHLV-----SSRNTAGNFI 331
Qy	390	TUPF-----TSRDVYRTESLAGLNLFITQPVNVPVRVDFHWKFVTHPIADSD 434
Dy	332	NFTPYGFENPGCAIWAIEDPRPYRT-----LSDPFVF-RGGF-----GN 371
Qy	435	NYYYPCYAGIGTOLQ-----DSENELPEATGPQNYSESYSHRLSHI----- 475
Dy	372	PHYVJGLRGVAPQQGTNHTTFRNSGTIOSLDEIPQDNSGAPMNDYSHVLNHVTFTVRW 431
Qy	476	-GLISASHV-KALVYSWTHRSGADRNTIEPNSTIQPLVKAPFLNSSGAAVRGPGFTGSD 533
Dy	432	PGEIAGSDSWRAPMSWTHRSGADRNTIINPNIITQIPAKAHNLHSGSTVVRGPGFTGSD 491
Qy	534	IILRNTGTGFDIRVINNPFAQRVYRIRYASTDLOHTSINGKALINQGNFASATMNRG 593
Dy	492	LLRNTGTGFADIRVNTIGPLSQSRVYRIRYASTDLOFFTIRNGTSVAQNQFQRTMNRG 551
Qy	594	EIDLKYTKTXGVFTTPSSLDOVQSFTFTIGAWNFSNGNEVIDIERFVPEVVEYAEYDFE 653
Dy	552	GNLESGNFTTAGFPSPFSNAQSTFTILGTQAFSN-QEVYIDIERFVPAEVTFEABSDLE 610
Qy	654	KAQEKVATLFTSTNPRGLKTVDKDYHDIOVSNLVESLSDDEFYLDKREKLEFIVKYAKQLH 713
Dy	611	RAQKAVNALFTSTSGLQKTNVTGYHDIOVSNLVACLSDEFCLDKREKSELSEKYVCHAKRLS 670
Qy	714	IERNM 718
Dy	671	KRENL 675

## RESULT 10

A26513  
 parasporal crystal protein - Bacillus thuringiensis (strain aizawai)  
 C:Species: Bacillus thuringiensis  
 C>Date: 11-Mar-1988 #sequence\_revision 11-Mar-1988 #text\_change 09-Jul-2004  
 C:Accession: A26513  
 R:Oeda, K.; Oshie, K.; Shimizu, M.; Nakamura, K.; Yamamoto, H.; Nakayama, H.; Gene 53, 113-119, 1987  
 A:Title: Nucleotide sequence of the insecticidal protein gene of Bacillus thuringiensis  
 A:Reference number: A26513; MUID:87248103; PMID:3297927  
 A:Accession: A26513  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-1155 <DB>  
 A:Cross-references: UNIPROT:P06578; GB:M16463; NID:g143098; PIDN:AAA22551.1; PID:g143098  
 C:Superfamily: parasporal crystal protein  
 C:Keywords: delta-endotoxin

Query Match 38.6%; Score 1448.5; DB 2; Length 1155;  
 Best Local Similarity 44.1%; Pred. No. 6.7e-92;  
 Matches 313; Conservative 112; Mismatches 229; Indels 55; Gaps 13;

QY 36 NINHEDCIKMEYENVE-PFVSASTIQG-----IGIAGKILGTGLVPPAGQVSLYS 87  
 DB 4 NPTNIECPYNCLSNPEVEVLGGERIEGTPTDLSLTQFILSEF-VPGAGFVLGLVD 62  
 QY 88 FILGELWPKGNQWEIFMEHVEIINQKISTYARKALTDLKGGLDALAVYHDSLSWVG 147  
 DB 63 IIWGIF---GPSQWDAFLVQIEQLINQRIEFAFNQAIISRLGLSLNLYQIYAESFREWEA 119  
 QY 148 NNNTRARSVVKSQVIALELMFVQKLPSPFVSGSEVPLPIYAAANLHLLLDASIFG 207  
 DB 120 DPTNPALEEMRIQDNWSALTITAPLFAVQNTQVPLLSVYQAANLHLSVLKDSVFG 179  
 QY 208 KEWGLSSSEISTFYNRQVERAGDYSYHCWKYSTGLANLGTNAESWVRYNQFRDNTLM 267  
 DB 180 QRWGFDAATINSRYNDLRILGNVTDHAVRYNTGLERVWGDSDRDIRYNQPRELTLT 239  
 QY 268 VLDLVALPSTQYTPKTKTAQLTREVYTDATGTVHPHPSFTTWNWNNAPSIAEA 327  
 DB 240 VLDIVSLFPNDSRTYPIRTVSQLTREIYNPV-----LENPDGSRALAQ 285  
 QY 328 AV---VRNPHLLDFEQVITYSLLSR---WSNTQYMMN---WGCHKLEFRTIGTLNIS 377  
 DB 286 GIEGSIKSPHLMILNSITTYDAHGEYKSGHQIYASPVGSGPEFTPLYGTMGNA 345  
 QY 378 TQGSTNTSINPVTLPTFGSDRVYRTESLAGLFLTPQVNV-PRVDFHKKFVTHFIADNF 436  
 DB 346 PQORIVAGLGGVYRTLSLTYRFPNIGIN---NQQLSLVDGTEFAYG-----TSN 396  
 QY 437 YYPGAGIGTQLQDSENLPEATQPNYVESYHRLSHGLI-----SASHVKALVYS 489  
 DB 397 PSAVTRKSGT--VDBLDIIPQNNVPPROQFSRLSHSVSMFRSGFNSVSIIRAPMFS 454  
 QY 490 WTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTNTGTGDIRVN 549  
 DB 455 WTHRSAEFNNIIPSSQITQIPLTRSTNLGSGTSVVGKPGFTGGDILRTSPGQISTLRVN 514  
 QY 550 INPPEAQRVYRIRVASTDQLQFHTSINGKAINQNFSAATNMGEDLDLYKFTXVGTTP 609  
 DB 515 ITAPUSQRYRIRVASTNTQFHTSIDGRPINQNFSAATNMGSSNLSQSGFRVVGTTTP 574  
 QY 610 FSLLDVQSTFTIGAWNFSSGNEVYIDRIEFYFVEVTEAEYDFEKAQKVTALTSTNPR 669  
 DB 575 FNFSGSVFTLSAHVFNSSGNEVYIDRIEFYFPAEYVTEAEYDLERAKQAVNELFTSSNQI 634  
 QY 670 GLKTDVQYHIDQVNSVYESJSDPEYLDKSELPEIVKYAKOLHERNM 718  
 DB 635 GLKTDVTDYHIDQVNSLVECLSDDEFCLDEKKELSEKVKHAKRLSDERNL 683

## RESULT 11

## JD0002

parasporal crystal protein cryIIAb3 - Bacillus thuringiensis  
 N:Alternate names: delta-endotoxin-2; entomocidal protoxin; entomopathogenic crystal prot  
 C:Species: Bacillus thuringiensis  
 C>Date: 28-Dec-1987 #sequence\_revision 28-Dec-1987 #text\_change 09-Jul-2004  
 C:Accession: A90025; A91560; A90955; S14555; A26461; A24172; A29043; JD0002  
 R:Kondo, S.; Tamura, N.; Kunitake, A.; Hattori, M.; Akashi, A.; Ohmori, I.  
 Agric. Biol. Chem. 51, 458-463, 1987  
 A:Title: Cloning and nucleotide sequencing of two insecticidal delta-endotoxin genes from  
 A:Reference number: A90025  
 A:Accession: A90025  
 A:Molecule type: mRNA  
 A:Residues: 1-1155 <KON>  
 A:Cross-references: UNIPROT:P06578  
 A:Experimental source: subsp. kurstaki  
 R:Geiser, M.; Schweitzer, S.; Grimm, C.  
 Gene 48, 109-118, 1986  
 A:Title: The hypervariable region in the genes coding for entomopathogenic crystal protei  
 A:Reference number: A91560; MUID:87163505; PMID:3557124  
 A:Accession: A91560  
 A:Molecule type: DNA  
 A:Residues: 1-1155 <GEI>  
 A:Cross-references: GB:M15271; NID:g143123; PIDN:AAA22561.1; PID:g143124  
 A:Experimental source: subsp. kurstaki  
 R:Wabiko, H.; Raymond, K.C.; Bulla Jr., L.A.  
 DNA 5, 305-314, 1986  
 A:Title: Bacillus thuringiensis entomocidal protoxin gene sequence and gene product anal  
 A:Reference number: A90955; MUID:86300092; PMID:3743328  
 A:Accession: A90955  
 A:Molecule type: DNA  
 A:Residues: 1-1155 <WAB>  
 A:Cross-references: GB:M13898; NID:g142719; PIDN:AAA22330.1; PID:g142720  
 A:Experimental source: subsp. berliner  
 R:Chak, K.P.; Jen, J.C.  
 submitted to the EMBL Data Library, October 1990  
 A:Description: Complete nucleotide sequence and expression in Escherichia coli of a cry S  
 A:Reference number: S14555  
 A:Accession: S14555  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-1155 <CHA>  
 A:Cross-references: EMBL:X54939; NID:g40272; PIDN:CAA38701.1; PID:g40273  
 R:Hofte, H.; de Greve, H.; Seurinck, J.; Janssens, S.; Mahillon, J.; Amps, C.; Vandekerck  
 Eur. J. Biochem. 161, 273-280, 1986  
 A:Title: Structural and functional analysis of a cloned delta endotoxin of Bacillus thuri  
 A:Reference number: A26461; MUID:87054026; PMID:3023091  
 A:Accession: A26461  
 A:Molecule type: DNA  
 A:Residues: 1-730, 'L', 732-784, 'R', 786-1155 <HOF>  
 A:Cross-references: GB:X04698; NID:g40254; PIDN:CAA28405.1; PID:g40255  
 A:Experimental source: strain berliner 1715  
 C:Comment: This toxin is lethal to the larvae of lepidopterans and dipterans.  
 C:Genetics:  
 A:Gene: cry-1-2; bt2  
 A:Superfamily: parasporal crystal protein  
 C:Keywords: delta-endotoxin  
 F:82-586/Product: toxic peptide #status predicted <TYP>  
 F:82-300/Region: toxic #status predicted  
 F:300-586/Region: insecticidal #status predicted

Query Match 38.5%; Score 1441.5; DB 2; Length 1155;  
 Best Local Similarity 44.2%; Pred. No. 2e-91;  
 Matches 314; Conservative 111; Mismatches 228; Indels 57; Gaps 14;

QY 36 NINHEDCIKMEYENVE-PFVSASTIQG-----IGIAGKILGTGLVPPAGQVSLYS 87  
 DB 4 NPTNIECPYNCLSNPEVEVLGGERIEGTPTDLSLTQFILSEF-VPGAGFVLGLVD 62  
 QY 88 FILGELWPKGNQWEIFMEHVEIINQKISTYARKALTDLKGGLDALAVYHDSLSWVG 147  
 DB 63 IIWGIF---GPSQWDAFLVQIEQLINQRIEFAFNQAIISRLGLSLNLYQIYAESFREWEA 119  
 QY 148 NNNTRARSVVKSQVIALELMFVQKLPSPFVSGSEVPLPIYAAANLHLLLDASIFG 207

Db 120 DPTNPALEEMRIQFNDMNSALTTAIPFLFAVQVQVPLLSVYVQAANLHLVLSDRVSVFG 179  
QY 208 KEWGLSSSEISTFYNRQVERAGDYSYHCWKVYSTGLNLRGTNAESWRYNQFRDRTML 267  
Db 180 QRMGDAATINSRYNDLRLIGNYTDHARVWYNTGLERWGPDSRDWIRYNQFRRELTLT 239  
QY 268 VLDLVALPPSYDQVPIKTTAQLTREYVTDAGTVHPHPSFTSTWYNNAPSF-----S 323  
Db 240 VLDIVSLFPNDSDRYPIRTVSQLTREIYTNPV-----LENDGSPRGSQAQ 285  
QY 324 AIEAAVVRNPHLLDFEQVITYSLLSR-----WSNTQYMM--WGGHKLERTIGTGLNI 376  
Db 286 GIEGS-IRSPHMDILNSITITDAHRGEYVWSGHQIMASPVGSGPPEFTPLVGTMGNA 344  
QY 377 STQSTNTSINPVTLPFTSRDVTRESLAGNLFLTPQVNV-PRVDPHKKFVTHPIASDN 435  
Db 345 APQQRIVAGLGGVYRTLSSTLRYRPNIGIN---NQOLSVLDGTBFAYG-----TSN 395  
QY 436 FYYPGAGITQLOQDSNELPPZATGQPNYESYSHLSHIGLI-----SASHVKALVY 488  
Db 396 LPSAVYRKSGT--VDSLDEIPQNNVPPRQGFHSHLSHVMSFRSGFSNVSIIIRPMF 453  
QY 489 SWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVRGPFGTGGDILRRTNTGTFDIRV 548  
Db 454 SWIHSABFNIIIPSSQITQIPLTSTNLGSGTSVVKPGFTGGDILRRTSPQISTLRV 513  
QY 549 NINPPFAQRYVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDELDYKTXTVGFTT 608  
Db 514 NITAPLSQRYVRIRYASTTNLQFHTSIDGRPIQGNFSATMSSGSLQSGSFRIVGFTT 573  
QY 609 PFSLLDVQSTFTIGAMFNSSGNEVYIDRIEFVPEVYEAEDYFKAQEKVYALFTSTNP 668  
Db 574 PFNFGSGSVFTLSAHVFNSSGNEVYIDRIEFVPAEVTFEAYEDLERAQKAVNELFTSSNQ 633  
QY 669 RGLKTDVYKHIDQVSNLVESLDEFLDKRELFEIVKYAKOLHIERNM 718  
Db 634 IGLKTDVTDYHIDQVSNLVESLDEFLDKRELSEKVKHAKLSDERNL 683

## RESULT 12

A29125  
Parasporal crystal protein Bt2 - *Bacillus thuringiensis* subsp. *kurstaki* (strain HD-1)  
C:Species: *Bacillus thuringiensis* subsp. *kurstaki*  
C:Date: 15-Dec-1988 #sequence\_revision 15-Dec-1988 #text\_change 09-Jul-2004  
C:Accession: A29125  
R:Fishhoff, D.A.; Bowdish, K.S.; Perlak, F.J.; Marrone, P.G.; McCormick, S.M.; Niederme  
Bio/Technology 5, 807-813, 1987  
A:Title: Insect tolerant transgenic tomato plants.  
A:Reference number: A29125  
A:Accession: A29125  
A>Status: not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-1156 <PIS>  
A:Cross-references: UNIPROT:Q9P296; UNIPROT:Q93T21  
C:Superfamily: parasporal crystal protein  
C:Keywords: delta-endotoxin

Query Match 38.5%; Score 1441.5; DB 2; Length 1156;  
Best Local Similarity 44.2%; Pred. No. 2.1e-91;  
Matches 314; Conservative 111; Mismatches 228; Indels 57; Gaps 14;

QY 36 NINHEDCLKMSEYENVE-PFVSASTIQG-----IGIAGKILGTLCVPPAGQVASLYS 87  
Db 4 NPINIECIPYCNLSNPEVEVLGGERIETGYTPIDISLSTQFLLSBF-VPGAGFVLGLVD 62  
QY 88 FILGLMWPKNQKWEIEMHVEEIIINQKISTYARNKALTDLKGDLAVYHDSLESWVG 147  
Db 63 IIWGIF---GPSQWDAFLVQIEQLINQRIEFPARNQAISLEGLSNLYQIYAESFREWEA 119  
QY 148 NRNNTARSVVKQYIALEMLFVQKLPFAVSGEVEPPLPIYAOAANLHLLLDRASIFG 207  
Db 120 DPTNPALEEMRIQFNDMNSALTTAIPFLFAVQVQVPLLSVYVQAANLHLVLSDRVSVFG 179

QY 208 KEWGLSSSEISTFYNRQVERAGDYSYHCWKVYSTGLNLRGTNAESWRYNQFRDRTML 267  
Db 180 QRMGDAATINSRYNDLRLIGNYTDHARVWYNTGLERWGPDSRDWIRYNQFRRELTLT 239  
QY 268 VLDLVALPPSYDQVPIKTTAQLTREYVTDAGTVHPHPSFTSTWYNNAPSF-----S 323  
Db 240 VLDIVSLFPNDSDRYPIRTVSQLTREIYTNPV-----LENDGSPRGSQAQ 285  
QY 324 AIEAAVVRNPHLLDFEQVITYSLLSR-----WSNTQYMM--WGGHKLERTIGTGLNI 376  
Db 286 GIEGS-IRSPHMDILNSITITDAHRGEYVWSGHQIMASPVGSGPPEFTPLVGTMGNA 344  
QY 377 STQSTNTSINPVTLPFTSRDVTRESLAGNLFLTPQVNV-PRVDPHKKFVTHPIASDN 435  
Db 345 APQQRIVAGLGGVYRTLSSTLRYRPNIGIN---NQOLSVLDGTBFAYG-----TSN 395  
QY 436 FYYPGAGITQLOQDSNELPPZATGQPNYESYSHLSHIGLI-----SASHVKALVY 488  
Db 396 LPSAVYRKSGT--VDSLDEIPQNNVPPRQGFHSHLSHVMSFRSGFSNVSIIIRPMF 453  
QY 489 SWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVRGPFGTGGDILRRTNTGTFDIRV 548  
Db 454 SWIHSABFNIIIPSSQITQIPLTSTNLGSGTSVVKPGFTGGDILRRTSPQISTLRV 513  
QY 549 NINPPFAQRYVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDELDYKTXTVGFTT 608  
Db 514 NITAPLSQRYVRIRYASTTNLQFHTSIDGRPIQGNFSATMSSGSLQSGSFRIVGFTT 573  
QY 609 PFSLLDVQSTFTIGAMFNSSGNEVYIDRIEFVPEVYEAEDYFKAQEKVYALFTSTNP 668  
Db 574 PFNFGSGSVFTLSAHVFNSSGNEVYIDRIEFVPAEVTFEAYEDLERAQKAVNELFTSSNQ 633  
QY 669 RGLKTDVYKHIDQVSNLVESLDEFLDKRELFEIVKYAKOLHIERNM 718  
Db 634 IGLKTDVTDYHIDQVSNLVESLDEFLDKRELSEKVKHAKLSDERNL 683

## RESULT 13

A22798  
Parasporal crystal protein - *Bacillus thuringiensis*  
C:Species: *Bacillus thuringiensis*  
C:Date: 23-Aug-1987 #sequence\_revision 23-Aug-1987 #text\_change 09-Jul-2004  
C:Accession: A22798  
R:Shibano, Y.; Yamagata, A.; Nakamura, N.; Iizuka, T.; Sugisaki, H.; Takanami, M.  
Gene 34, 243-251, 1985  
A:Title: Nucleotide sequence coding for the insecticidal fragment of the *Bacillus thuring*  
A:Reference number: A22798; PMID:2989108  
A:Accession: A22798  
A:Molecule type: DNA  
A:Residues: 1-934 <SHI>  
A:Cross-references: UNIPROT:Q9SSV8; GB:M10917; NID:G143100; PIDN:AAA22552.1; PID:9551713  
C:Comment: The authors translated the codon ACA for residue 264 as Ser.  
C:Superfamily: parasporal crystal protein  
C:Keywords: delta-endotoxin

Query Match 38.2%; Score 1433; DB 2; Length 934;  
Best Local Similarity 43.1%; Pred. No. 5.7e-91;  
Matches 308; Conservative 119; Mismatches 221; Indels 66; Gaps 13;

QY 36 NINHEDCLKMSEYENVE-PFVSASTIQG-----IGIAGKILGTLCVPPAGQVASLYS 87  
Db 4 NPINIECIPYCNLSNPEVEVLGGERIETGYTPIDISLSTQFLLSBF-VPGAGFVLGLVD 62  
QY 88 FILGLMWPKNQKWEIEMHVEEIIINQKISTYARNKALTDLKGDLAVYHDSLESWVG 147  
Db 63 IIWGIF---GPSQWDAFLVQIEQLINQRIEFPARNQAISLEGLSNLYQIYAESFREWEA 119  
QY 148 NRNNTARSVVKQYIALEMLFVQKLPFAVSGEVEPPLPIYAOAANLHLLLDRASIFG 207  
Db 120 DPTNPALEEMRIQFNDMNSALTTAIPFLFAVQVQVPLLSVYVQAANLHLVLSDRVSVFG 179  
QY 208 KEWGLSSSEISTFYNRQVERAGDYSYHCWKVYSTGLNLRGTNAESWRYNQFRDRTML 267

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Db 180 QRWGDAATINSRYNDLTRLGNITDYAVRWYNTGLRWGPDSDRWVRYNQFRELTLT 239
QY 268 VLDLVALFPSPDYDTOMYPIKTTAQLTREYVYDAIGTVHPHPSFTSTWYNNAPSFSAIEA 327
Db 240 VLDLVALFNSYDSRRYPRTVSQLTRITYNPV-----LENFDGSRFGMAQ 285
QY 328 AV---VRNPHLLDFLEQVYIYLLSRWNTQYMMWGGHKLFEFTIGCT---LNISTQGS 381
Db 286 RIEQNIROPHLMDILNRIITYTDVHRG-----FNWSGHQITASPVGSGPEFAFPLFGN 340
QY 382 TMTSINPVTLPTSRDVTYTESL-----AGLN---LFLTQPVNVPRVDHMKFVTH 429
Db 341 AGNAPPVVLVSLTGLGIFRTLSSPLRYRIILGSGPNNQELFV-----LDGTEFSASLT 395
QY 430 PIASNFYYPGAGTGLQDSENELPPEATGQPNYESYSHRLSHIGLISAS-----HVK 484
Db 396 NLPSTIYRQGTV-----DSLVIIPQDNSVPFRAGFSHRLSHVMTLSQAAGAVYTLR 448
QY 485 ALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVRGPGFTGCDILRRTNTGTFG 544
Db 449 APTFSWQHRSAEFNNIIPSSQITQIPLTKSTNLGSGTSVVKGPGFTGCDILRRTSPQIS 508
QY 545 DIRVNINPPAQRVRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGSDLDYKFTXV 604
Db 509 TLRVNITAPLSQRYRVIRYASTTNLQFHTSIDGRPINQGNFSATMSSGSLQSGSPRTV 568
QY 605 GFTTFPSLLDVQSTTIGAMNFSNGNEVYIDRIEFPVVEVYEAEDFEKAQKVTAFLT 664
Db 569 GFTTFPNSGSSVFTLSAHVFNSEVYIDRIEFPVPAEVTFEAYDIERAQKAVNELFT 628
QY 665 STNPRGLKTDVKYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKOLHIERNM 718
Db 629 SSNQIGLKTVDYHIDQVSNLVESLSDEFYLDKRELSEKVKHAKRLSDERNL 682

RESULT 14
JT0241
parasporal crystal protein - Bacillus thuringiensis (strain aizawai IPL7)
N:Alternate names: 135k insecticidal protein
C:Species: Bacillus thuringiensis
C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C:Accession: JT0241
R:Shimizu, M.; Oshie, K.; Nakamura, K.; Takada, Y.; Oeda, K.; Ohkawa, H.
A:Agri. Biol. Chem. 52, 1565-1573, 1988
A>Title: Cloning and expression in Escherichia coli of the 135-kDa insecticidal protein
A:Reference number: JT0241
A:Accession: JT0241
A:Molecule type: DNA
A:Residues: 1-1176 <SHI>
A:Cross-references: UNIPROT:P02965
A>Note: b. thuringiensis aizawai IPL7 produces similar 130K and 135k insecticidal protein
C:Comment: The 135k protein has insecticidal activity against Plutella xylostella larvae
C:Superfamily: parasporal crystal protein
C:Keywords: delta-endotoxin

Query Match 38.2%; Score 1432; DB 2; Length 1176;
Best Local Similarity 43.1%; Pred. No. 9.6e-91;
Matches 308; Conservative 118; Mismatches 222; Indels 66; Gaps 13;

QY 36 NINHEDCLKMEYENVE-PFVSASTIQG-----IGIAGKILGTGVPPAGQVASLYS 87
Db 4 NPNINECIYPNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLSEF-VPAGFVLGLVD 62
QY 88 FILGELMPKGNQWEIFMEHVEEIIINOKISTYARKALTDLKGGLDALAVTHDSLESWVG 147
Db 63 IIWGIF---GPSQWDAFLVQIEQLINQRIEIEFARQALSRLEGSLNYQIYAEFREWEA 119
QY 148 NNNTRASVVKVQSVIALELMFVKLPSPFVSGEVPLPIYAAQANLHLLLRDASIFG 207
Db 120 DPTPALREEMRIQENDMNSALTITAIPLFAVQNYQVPLLSVYVQAANLHLSVLDRDVSFVG 179
QY 208 KEWGLSSEISTFTYNNQVERAGDYSYHCVKWYSTGLNLRGTNAESWVRYNQFREDMTLM 267

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Db 180 QRWGDAATINSRYNDLTRLGNITDYAVRWYNTGLRWGPDSDRWVRYNQFRELTLT 239
QY 268 VLDLVALFPSPDYDTOMYPIKTTAQLTREYVYDAIGTVHPHPSFTSTWYNNAPSFSAIEA 327
Db 240 VLDLVALFNSYDSRRYPRTVSQLTRITYNPV-----LENFDGSRFGMAQ 285
QY 328 AV---VRNPHLLDFLEQVYIYLLSRWNTQYMMWGGHKLFEFTIGCT---LNISTQGS 381
Db 286 RIEQNIROPHLMDILNRIITYTDVHRG-----FNWSGHQITASPVGSGPEFAFPLFGN 340
QY 382 TMTSINPVTLPTSRDVTYTESL-----AGLN---LFLTQPVNVPRVDHMKFVTH 429
Db 341 AGNAPPVVLVSLTGLGIFRTLSSPLRYRIILGSGPNNQELFV-----LDGTEFSASLT 395
QY 430 PIASNFYYPGAGTGLQDSENELPPEATGQPNYESYSHRLSHIGLISAS-----HVK 484
Db 396 NLPSTIYRQGTV-----DSLVIIPQDNSVPFRAGFSHRLSHVMTLSQAAGAVYTLR 448
QY 485 ALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVRGPGFTGCDILRRTNTGTFG 544
Db 449 APTFSWQHRSAEFNNIIPSSQITQIPLTKSTNLGSGTSVVKGPGFTGCDILRRTSPQIS 508
QY 545 DIRVNINPPAQRVRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGSDLDYKFTXV 604
Db 509 TLRVNITAPLSQRYRVIRYASTTNLQFHTSIDGRPINQGNFSATMSSGSLQSGSPRTV 568
QY 605 GFTTFPSLLDVQSTTIGAMNFSNGNEVYIDRIEFPVVEVYEAEDFEKAQKVTAFLT 664
Db 569 GFTTFPNSGSSVFTLSAHVFNSEVYIDRIEFPVPAEVTFEAYDIERAQKAVNELFT 628
QY 665 STNPRGLKTDVKYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKOLHIERNM 718
Db 629 SSNQIGLKTVDYHIDQVSNLVESLSDEFYLDKRELSEKVKHAKRLSDERNL 682

RESULT 15
JC2219
parasporal crystal protein cryIIa - Bacillus thuringiensis
C:Species: Bacillus thuringiensis
C>Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
C:Accession: JC2219
R:Udayasuriyan, V.; Nakamura, A.; Mori, H.; Masaki, H.; Uozumi, T.
A:Biocli. Biotechnol. Biochem. 58, 830-835, 1994
A>Title: Cloning of a new cryIIa(a) gene from Bacillus thuringiensis strain FU-2-7 and ana
A:Reference number: JC2219; MUID:94289859; PMID:7764972
A:Accession: JC2219
A:Molecule type: DNA
A:Residues: 1-1176 <UDA>
A:Cross-references: UNIPROT:Q45736; DDBJ:D17518; NID:G506190; PIDN:BAA04468.1; PID:G53578
C:Genetics:
C:Superfamily: parasporal crystal protein
C:Keywords: delta-endotoxin

Query Match 38.0%; Score 1426; DB 2; Length 1176;
Best Local Similarity 43.0%; Pred. No. 2.5e-90;
Matches 307; Conservative 118; Mismatches 223; Indels 66; Gaps 13;

QY 36 NINHEDCLKMEYENVE-PFVSASTIQG-----IGIAGKILGTGVPPAGQVASLYS 87
Db 4 NPNINECIYPNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLSEF-VPAGFVLGLVD 62
QY 88 FILGELMPKGNQWEIFMEHVEEIIINOKISTYARKALTDLKGGLDALAVTHDSLESWVG 147
Db 63 IIWGIF---GPSQWDAFLVQIEQLINQRIEIEFARQALSRLEGSLNYQIYAEFREWEA 119
QY 148 NNNTRASVVKVQSVIALELMFVKLPSPFVSGEVPLPIYAAQANLHLLLRDASIFG 207
Db 120 DPTPALREEMRIQENDMNSALTITAIPLFAVQNYQVPLLSVYVQAANLHLSVLDRDVSFVG 179
QY 208 KEWGLSSEISTFTYNNQVERAGDYSYHCVKWYSTGLNLRGTNAESWVRYNQFREDMTLM 267

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Db 180 QRWGFAATINSRYNDLRLIGNYTDYAVRWYNTGLERWVGPSDRDMVRYNQFRRELTLT 239  
QY 268 VLDELVALFPSTQMPKTKTAQLTREVYTDAGTGVHPHPSFTSTWYNNAPSPSAIEA 327  
Db 240 VLDIVALFSNYDSRRYPPIRVSQLTREIYNPV-----LENFDGSPRMAQ 285  
QY 328 AV---VRNPHLLDFLEQVITYLSLSRWSNTQYNNMGCHKLEPRTIGGT---LNISTQGS 381  
Db 286 RISCNIRQPHLMDILNSITTYDVHRG-----FNYWSGHQITASPVGSGPFAFELFCN 340  
QY 382 TMTSINPVTLPFTSRDVRPESL-----AGLN---LFLTQPVNVPRVDFHMKFVTH 429  
Db 341 AGNAAPVLVSLGLGIFRTLSPLYRRILGSGPNNQELFV-----LDGTFSPASLT 395  
QY 430 PIASDNFYPGYAGIGTQLODSNELPPREATGPNYESYSHRLSHIGLISAS-----HVK 484  
Db 396 NLFSTIYRQGTV-----DSLVDIPPQDNSVPPRAGFSHRLSHVMTLSQAAGAVYTLR 448  
QY 485 ALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRNTGTGTFG 544  
Db 449 APTFSWQHRSABFNIIIPSSQITQIPLTKSTNLGSGTSVVGPGFTGGDILRRTSFGQIS 508  
QY 545 DIRVNIAPPQAQRYRIRYASTDLQFHTSINGKAINQGNFSATMNRGEDLDYKTFXTV 604  
Db 509 TLRVNITAPLSQRYRVRIRYASTNLQFHTSIDGRPINQGNFSATMSSGSLQSGSFRV 568  
QY 605 GFTTPESLDDVQSTFTIGAWNFSNGNEVXIDRIEFVPEVVEYEAEDFEKAQCKYALFT 664  
Db 569 GFTTPFNFSNGSVFTLSAHVFNNGNEVYIDRIEFVPAEVTPEAYDLERAKAVNELFT 628  
QY 665 STNPRGLKTDVDKDYHIDQVSNLVESLSDEFYLDKSELFEIVKYAKQLHIERNM 718  
Db 629 SSNQIGLKTVDVTDYHIDQVSNLVESLSDEFCLDEKQELSEKVKHAKRLSDERNL 682

Search completed: October 28, 2004, 18:31:47  
Job time : 21.1643 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 28, 2004, 18:10:58 ; Search time 65.5881 Seconds  
(without alignments)  
3549.224 Million cell updates/sec

Title: US-10-019-823B-54  
Perfect score: 3749  
Sequence: 1 MKLNQDKHQSFSSNAKVDK.....KRLFEIVYAKQLHIERNM 718

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1370721 seqs, 324215800 residues

Total number of hits satisfying chosen parameters: 1370721

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:  
1: /cgn2\_6/prodata/2/pubpaa/US07\_PUBCOMB.pep:  
2: /cgn2\_6/prodata/2/pubpaa/PCT\_NEW\_PUB.pep:  
3: /cgn2\_6/prodata/2/pubpaa/US06\_NEW\_PUB.pep:  
4: /cgn2\_6/prodata/2/pubpaa/US06\_PUBCOMB.pep:  
5: /cgn2\_6/prodata/2/pubpaa/US07\_NEW\_PUB.pep:  
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8: /cgn2\_6/prodata/2/pubpaa/US08\_PUBCOMB.pep:  
9: /cgn2\_6/prodata/2/pubpaa/US09A\_PUBCOMB.pep:  
10: /cgn2\_6/prodata/2/pubpaa/US09B\_PUBCOMB.pep:  
11: /cgn2\_6/prodata/2/pubpaa/US09C\_PUBCOMB.pep:  
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13: /cgn2\_6/prodata/2/pubpaa/US10A\_PUBCOMB.pep:  
14: /cgn2\_6/prodata/2/pubpaa/US10B\_PUBCOMB.pep:  
15: /cgn2\_6/prodata/2/pubpaa/US10C\_PUBCOMB.pep:  
16: /cgn2\_6/prodata/2/pubpaa/US10D\_PUBCOMB.pep:  
17: /cgn2\_6/prodata/2/pubpaa/US10\_NEW\_PUB.pep:  
18: /cgn2\_6/prodata/2/pubpaa/US11\_NEW\_PUB.pep:  
19: /cgn2\_6/prodata/2/pubpaa/US60\_NEW\_PUB.pep:  
20: /cgn2\_6/prodata/2/pubpaa/US60\_PUBCOMB.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3722.5	99.3	719	17	US-10-782-020-10
2	3722.5	99.3	719	17	US-10-782-141-8
3	3722.5	99.3	719	17	US-10-782-096-10
4	3722.5	99.3	719	17	US-10-782-570-7
5	3439	91.7	710	14	US-10-428-961-42
6	2249	60.0	1228	16	US-10-809-953-10
7	2236	59.6	1207	10	US-09-988-462-7
8	2156	57.5	1227	14	US-10-428-961-63
9	2141	57.1	1186	9	US-09-826-660-23
10	2085.5	55.6	1228	14	US-10-428-961-38
11	2085.5	55.6	1228	15	US-10-614-524-2
12	1902	50.7	643	9	US-09-826-660-25
13	1708	45.6	1167	14	US-10-089-678-1

14	1658	44.2	653	14	US-10-428-961-6	Sequence 6, Appli
15	1652	44.1	1157	17	US-10-782-141-16	Sequence 16, Appli
16	1652	44.1	1157	17	US-10-782-096-17	Sequence 17, Appli
17	1652	44.1	1157	17	US-10-782-570-13	Sequence 13, Appli
18	1500.5	40.0	1206	13	US-10-032-717-2	Sequence 2, Appli
19	1500.5	40.0	1206	14	US-10-414-637-2	Sequence 2, Appli
20	1500.5	40.0	1206	15	US-10-606-320-2	Sequence 2, Appli
21	1477.5	39.4	1210	13	US-10-032-717-4	Sequence 4, Appli
22	1477.5	39.4	1210	14	US-10-414-637-4	Sequence 4, Appli
23	1477.5	39.4	1210	15	US-10-606-320-4	Sequence 4, Appli
24	1477.5	39.4	1210	17	US-10-746-914-4	Sequence 4, Appli
25	1474	39.3	1156	14	US-10-032-855-72	Sequence 72, Appli
26	1474	39.3	1156	14	US-10-428-961-28	Sequence 28, Appli
27	1441.5	38.5	1155	9	US-09-756-643-2	Sequence 2, Appli
28	1441.5	38.5	1155	10	US-09-988-462-9	Sequence 9, Appli
29	1441.5	38.5	1155	14	US-10-136-998A-2	Sequence 2, Appli
30	1441.5	38.5	1177	14	US-10-035-060-6	Sequence 6, Appli
31	1441.5	38.5	1181	10	US-09-988-462-11	Sequence 11, Appli
32	1441.5	38.5	1181	10	US-09-988-462-13	Sequence 13, Appli
33	1441.5	38.5	1181	10	US-09-988-462-15	Sequence 15, Appli
34	1441.5	38.5	1181	10	US-09-988-462-17	Sequence 17, Appli
35	1441.5	38.5	1181	10	US-09-988-462-28	Sequence 28, Appli
36	1441.5	38.5	1181	14	US-10-136-998A-4	Sequence 4, Appli
37	1441.5	38.5	1181	14	US-10-136-998A-8	Sequence 8, Appli
38	1441.5	38.5	1181	14	US-10-136-998A-10	Sequence 10, Appli
39	1441.5	38.5	1181	14	US-10-136-998A-12	Sequence 12, Appli
40	1436.5	38.3	1177	14	US-10-035-060-8	Sequence 8, Appli
41	1436.5	38.3	1177	14	US-10-102-469-24	Sequence 24, Appli
42	1433.5	37.9	1176	17	US-10-782-141-6	Sequence 6, Appli
43	1422	37.9	1176	17	US-10-782-096-7	Sequence 7, Appli
44	1422	37.9	1176	17	US-10-782-096-7	Sequence 7, Appli
45	1422	37.9	1176	17	US-10-782-096-7	Sequence 7, Appli

## ALIGNMENTS

RESULT 1  
US-10-782-020-10  
; Sequence 10, Application US/10782020  
; Publication No: US20040197916A1  
; GENERAL INFORMATION:  
; APPLICANT: Carozzi, Nadine  
; APPLICANT: Hargiss, Tracy  
; APPLICANT: Koziel, Michael G.  
; APPLICANT: Duck, Nicholas B.  
; APPLICANT: Carr, Brian  
; TITLE OF INVENTION: AXMI-004, A Delta-Endotoxin Gene and  
; FILE OF INVENTION: Methods for its use  
; FILE REFERENCE: 045600/274139  
; CURRENT APPLICATION NUMBER: US/10782.020  
; CURRENT FILING DATE: 2004-02-19  
; PRIOR APPLICATION NUMBER: 60/448,810  
; PRIOR FILING DATE: 2003-02-20  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 719  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
US-10-782-020-10

Query Match 99.3%; Score 3722.5; DB 17; Length 719;  
Best Local Similarity 99.4%; Pred. No. 1.7e-302;  
Matches 715; Conservative 0; Mismatches 3; Indels 1; Gaps 1;  
QY 1 MKLNQDKHQSFSSNAKVDKISTDLSKNETDIQLQNHEDCLKMSYENVEPVSASTI 60  
DB 1 MKLNQDKHQSFSSNAKVDKISTDLSKNETDIQLQNHEDCLKMSYENVEPVSASTI 60  
QY 61 QTGIGIAGKILGTGVFPFAGQVASYLSFILGELWPXKQKQWEIFMEHVEIINOKISTYA 120  
DB 61 QTGIGIAGKILGTGVFPFAGQVASYLSFILGELWPXKQKQWEIFMEHVEIINOKISTYA 120

QY	121	RNKALTDLKGGLDALAVYHDSLESWGVRNTRRSVVKSYIALELMFVQKLPFAVSG	180
DB	121	RNKALTDLKGGLDALAVYHDSLESWGVRNTRRSVVKSYIALELMFVQKLPFAVSG	180
QY	181	BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSYHCVKWS	240
DB	181	BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSYHCVKWS	240
QY	241	TGLNNLRGTNAESWVRYNQFRDMTLMVLDLVALFPSTYDQMPYIKTTAQLTREVTDAI	300
DB	241	TGLNNLRGTNAESWVRYNQFRDMTLMVLDLVALFPSTYDQMPYIKTTAQLTREVTDAI	300
QY	301	GTVHPHPSFTSTTWNNAAPSAIEAAVVRNPHLLDFLEQVITYSLSSWSNTQYNNMW	360
DB	301	GTVHPHPSFTSTTWNNAAPSAIEAAVVRNPHLLDFLEQVITYSLSSWSNTQYNNMW	360
QY	361	GGHKLFPRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRRTESLAGLNLFLTQPVN-VPR	419
DB	361	GGHKLFPRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRRTESLAGLNLFLTQPVN-VPR	419
QY	420	VDHFWKFTVTHPIASDNFYPGYAGIGTQLODSENELPEATGQPNYESYSHRLSHIGLIS	479
DB	420	VDHFWKFTVTHPIASDNFYPGYAGIGTQLODSENELPEATGQPNYESYSHRLSHIGLIS	479
QY	480	ASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN	539
DB	480	ASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN	539
QY	540	TGTFGDIRVNINPPPAQRYRIRYASTTDLOFTSINGKAINQGNFSATNMRGEDLDYK	599
DB	540	TGTFGDIRVNINPPPAQRYRIRYASTTDLOFTSINGKAINQGNFSATNMRGEDLDYK	599
QY	600	TFXTVGFPTPSFLDVQSTFTIGAWNFSNGNEVVDRIEFVPEVVEYAEYDFEKAQEKV	659
DB	600	TFXTVGFPTPSFLDVQSTFTIGAWNFSNGNEVVDRIEFVPEVVEYAEYDFEKAQEKV	659
QY	660	TALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM	718
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RESULT 2			
US-10-782-141-8			
; Sequence 8, Application US/10782141			
; Publication No. US20040197917A1			
; GENERAL INFORMATION:			
; APPLICANT: Carozzi, Nadine			
; APPLICANT: Hargiss, Tracy			
; APPLICANT: Kozziel, Michael G.			
; APPLICANT: Duck, Nicholas B.			
; APPLICANT: Carr, Brian			
; TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and			
; TITLE OF INVENTION: Methods for Its Use			
; FILE REFERENCE: 045600/274143			
; CURRENT APPLICATION NUMBER: US/10/782,141			
; CURRENT FILING DATE: 2004-02-20			
; PRIOR APPLICATION NUMBER: 60/448,632			
; PRIOR FILING DATE: 2003-02-20			
; NUMBER OF SEQ ID NOS: 23			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 8			
; LENGTH: 719			
; TYPE: PRT			
; ORGANISM: Bacillus thuringiensis			
US-10-782-141-8			
Query Match 99.3%; Score 3722.5; DB 17; Length 719;			
Best Local Similarity 99.4%; Pred. No. 1.7e-302;			
Matches 715; Conservative 0; Mismatches 3; Indels 1; Gaps 1;			
QY	1	MKLKNQDKHQSFSSNAKVDKISTDSLKNETHEDCLKMSYENVEPVSASTI	60

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Best Local Similarity 99.4%; Pred. No. 1.7e-302;
Matches 715; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy 1 MKLNQDQKHSFSSNAKVDSKISTDSLNKNETDIELOQINHEDECLKMEYENVEPFFVASTI 60
Db 1 MKLNQDQKHSFSSNAKVDSKISTDSLNKNETDIELOQINHEDECLKMEYENVEPFFVASTI 60
Qy 61 QTGIGIAGKILGTGVPFAGQVAVSLYFSGILGELWPKGKNQWEIFMEHVEEIIQNKISTYA 120
Db 61 QTGIGIAGKILGTGVPFAGQVAVSLYFSGILGELWPKGKNQWEIFMEHVEEIIQNKISTYA 120
Qy 121 RNKALTDLKGDLAVYHDSLSWGNNRNTARSVVKSYQYIALELMFVQKLPSPAVSG 180
Db 121 RNKALTDLKGDLAVYHDSLSWGNNRNTARSVVKSYQYIALELMFVQKLPSPAVSG 180
Qy 181 BEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSVHCWKYS 240
Db 181 BEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSVHCWKYS 240
Qy 241 TGLNLRGTNAESWVRYNQFRDMLMVLDLVALFPSTQMYPIKTTAQLTREYTDI 300
Db 241 TGLNLRGTNAESWVRYNQFRDMLMVLDLVALFPSTQMYPIKTTAQLTREYTDI 300
Qy 301 GTVHPHPSFTSTWYNNAPSAIEAAVVRNPHLLDLEQVTTIYSLSRWSNTQYMMW 360
Db 301 GTVHPHPSFTSTWYNNAPSAIEAAVVRNPHLLDLEQVTTIYSLSRWSNTQYMMW 360
Qy 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRATESLAGLNLFITQPVN-VPR 419
Db 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRATESLAGLNLFITQPVN-VPR 420
Qy 420 VDFHWKFTPIASDNFYPGYAGIGTQLODSENEPPEATGQPNYESYSHLSHIGLIS 479
Db 420 VDFHWKFTPIASDNFYPGYAGIGTQLODSENEPPEATGQPNYESYSHLSHIGLIS 480
Qy 480 ASHVKALVYSWTHRSADRTNTEPNSTQIPLVKAFLNLSGAAVVRGPGFTGGDIILRTN 539
Db 480 ASHVKALVYSWTHRSADRTNTEPNSTQIPLVKAFLNLSGAAVVRGPGFTGGDIILRTN 540
Qy 540 TGTFGDIRVNINPPFAQRYRIRYASTTDLQPHTSINGKAINQGNFSATMNRGEDLDYK 599
Db 540 TGTFGDIRVNINPPFAQRYRIRYASTTDLQPHTSINGKAINQGNFSATMNRGEDLDYK 600
Qy 600 TFXTVGFTTTPFSLDVQSTFTIGAWNFSSGNEVVIDRIEFVPEVVEYAEYDPEKAQEKV 659
Db 600 TFXTVGFTTTPFSLDVQSTFTIGAWNFSSGNEVVIDRIEFVPEVVEYAEYDPEKAQEKV 660
Qy 660 TALFTSTNPRGLKTDVKDHYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 718
Db 660 TALFTSTNPRGLKTDVKDHYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 4
US-10-782-570-7
; Sequence 7, Application US/10782570
; Publication No. US20040210965A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Kozziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-007, A Delta-Endotoxin Gene and
; FILE REFERENCE: 045600/274144
; CURRENT APPLICATION NUMBER: US/10/782,570
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: 60/448,812
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 719

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; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-782-570-7

Query Match 99.3%; Score 3722.5; DB 17; Length 719;
Best Local Similarity 99.4%; Pred. No. 1.7e-302;
Matches 715; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy 1 MKLNQDQKHSFSSNAKVDSKISTDSLNKNETDIELOQINHEDECLKMEYENVEPFFVASTI 60
Db 1 MKLNQDQKHSFSSNAKVDSKISTDSLNKNETDIELOQINHEDECLKMEYENVEPFFVASTI 60
Qy 61 QTGIGIAGKILGTGVPFAGQVAVSLYFSGILGELWPKGKNQWEIFMEHVEEIIQNKISTYA 120
Db 61 QTGIGIAGKILGTGVPFAGQVAVSLYFSGILGELWPKGKNQWEIFMEHVEEIIQNKISTYA 120
Qy 121 RNKALTDLKGDLAVYHDSLSWGNNRNTARSVVKSYQYIALELMFVQKLPSPAVSG 180
Db 121 RNKALTDLKGDLAVYHDSLSWGNNRNTARSVVKSYQYIALELMFVQKLPSPAVSG 180
Qy 181 BEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSVHCWKYS 240
Db 181 BEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSVHCWKYS 240
Qy 241 TGLNLRGTNAESWVRYNQFRDMLMVLDLVALFPSTQMYPIKTTAQLTREYTDI 300
Db 241 TGLNLRGTNAESWVRYNQFRDMLMVLDLVALFPSTQMYPIKTTAQLTREYTDI 300
Qy 301 GTVHPHPSFTSTWYNNAPSAIEAAVVRNPHLLDLEQVTTIYSLSRWSNTQYMMW 360
Db 301 GTVHPHPSFTSTWYNNAPSAIEAAVVRNPHLLDLEQVTTIYSLSRWSNTQYMMW 360
Qy 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRATESLAGLNLFITQPVN-VPR 419
Db 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRATESLAGLNLFITQPVN-VPR 420
Qy 420 VDFHWKFTPIASDNFYPGYAGIGTQLODSENEPPEATGQPNYESYSHLSHIGLIS 479
Db 420 VDFHWKFTPIASDNFYPGYAGIGTQLODSENEPPEATGQPNYESYSHLSHIGLIS 480
Qy 480 ASHVKALVYSWTHRSADRTNTEPNSTQIPLVKAFLNLSGAAVVRGPGFTGGDIILRTN 539
Db 480 ASHVKALVYSWTHRSADRTNTEPNSTQIPLVKAFLNLSGAAVVRGPGFTGGDIILRTN 540
Qy 540 TGTFGDIRVNINPPFAQRYRIRYASTTDLQPHTSINGKAINQGNFSATMNRGEDLDYK 599
Db 540 TGTFGDIRVNINPPFAQRYRIRYASTTDLQPHTSINGKAINQGNFSATMNRGEDLDYK 600
Qy 600 TFXTVGFTTTPFSLDVQSTFTIGAWNFSSGNEVVIDRIEFVPEVVEYAEYDPEKAQEKV 659
Db 600 TFXTVGFTTTPFSLDVQSTFTIGAWNFSSGNEVVIDRIEFVPEVVEYAEYDPEKAQEKV 660
Qy 660 TALFTSTNPRGLKTDVKDHYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 718
Db 660 TALFTSTNPRGLKTDVKDHYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 5
US-10-428-961-42
; Sequence 42, Application US/10428961
; Publication No. US2003023711A1
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Chu, Chih-Rei
; APPLICANT: Donovan, William P.
; APPLICANT: Gilmer, Amy J.
; APPLICANT: Ruper, Mark J.
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin
; FILE REFERENCE: MECO201--1
; CURRENT APPLICATION NUMBER: US/10/428,961
; CURRENT FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: 09/661,322

```

; PRIOR FILING DATE: 2000-09-13		; APPLICANT: Van Mellaert, Herman	
; PRIOR APPLICATION NUMBER: 60/153,995		; APPLICANT: Botterman, Johan	
; PRIOR FILING DATE: 1999-09-15		; APPLICANT: Van Rie, Jeroen	
; NUMBER OF SEQ ID NOS: 63		; APPLICANT: Joos, Henk	
; SOFTWARE: Patent in version 3.2		; TITLE OF INVENTION: RECOMBINANT PLANT EXPRESSING NON-COMPETITIVELY BINDING Bt INSECTIC	
; SEQ ID NO 42		; TITLE OF INVENTION: CRYSTAL PROTEINS	
; LENGTH: 710		; FILE REFERENCE: 021565-078	
; TYPE: PRT		; CURRENT APPLICATION NUMBER: US/10/809,953	
; ORGANISM: Bacillus thuringiensis		; CURRENT FILING DATE: 2004-03-26	
; NAME/KEY: misc feature		; PRIOR APPLICATION NUMBER: US/09/661,016	
; LOCATION: (2001..(200)		; PRIOR FILING DATE: 2000-09-13	
; OTHER INFORMATION: The 'Xaa' at location 200 stands for any naturally occurring amin		; PRIOR APPLICATION NUMBER: PCT/EP90/00905	
US-10-428-961-42		; PRIOR FILING DATE: 1990-05-30	
		; PRIOR APPLICATION NUMBER: GB 89401499.2	
		; PRIOR FILING DATE: 1989-05-31	
		; NUMBER OF SEQ ID NOS: 10	
		; SOFTWARE: Patent in Ver. 2.0	
		; SEQ ID NO 10	
		; LENGTH: 1228	
		; TYPE: PRT	
		; ORGANISM: Bacillus thuringiensis	
		US-10-809-953-10	
		Query Match 60.0%; Score 2249; DB 16; Length 1228;	
		Best Local Similarity 62.3%; Pred. No. 9,9e-179;	
		Matches 446; Conservative 80; Mismatches 164; Indels 26; Gaps 7;	
QY	23	TDLSKNETDIELQNH-----EDCLKSEYENVEPVSASTIGTIGIAGKI	70
DB	2	TENRKNENEIINAVNSHGAQMDLLPDAIEDSLCAEGNNIDPFVSASTVGTGINIAGRI	61
QY	71	LCTGLVPAGOVASLYSFIILGELMPKGNQWEIFMEHVEEIIINQKISTYARKALTDLKG	130
DB	62	LVGLVGPAGQLASYSFLVGLMPPRGDQWEIFLVEHQIINQOITENARTALARIQG	121
QY	131	LGDAVALYHDSLESWGNRNTRARSVVKVSYQYIALELMFVKLPFSVAGSBEVLLPIYA	190
DB	122	LGDSFRAYQOQSLDLEWLNRRDARTSVLHTQVIALELDFLNAFLFAIRNCEVPLMVA	181
QY	191	QAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWYSTGLNNLRGTN	250
DB	182	QAANLHLLLRDASIFGSEFGLTSQEIORYERQVERTRDSDYCVENYNTGLNSLRGTN	241
QY	251	ABSVMRYNQFRDMLTMVLDLVALFPSTYDTQMPYIKTTAQLTREYVTDATGTVHPHPSFT	310
DB	242	AASVMRYNQFRDMLTMVLDLVALFPSTYDTQMPYIKTTAQLTREYVTDATGAT--GVNMA	299
QY	311	STTWNNAPSFSAEAAVAVRNPHLLDFLEQVITYSLLSRWSTNTCYMMWGGHKLERTI	370
DB	300	SMWYNNAPSFSAEAAAIRSPHLLDFLEQVITYSLLSRWSTNTKMTYWRGHTIQSRPI	359
QY	371	GGTLNISTQGSTNTSINPVTLPFTSRDYRTESLAGLNLF--LTQPVN--VPRVDFHKEV	427
DB	360	GGGLNTSTHGAINTSINPVTLPFTSRDYRTESYAGVLLWGLYLEPIHGVPTVRNF--	416
QY	428	THP-----IASDNFYPGYAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLSASH	482
DB	417	TNPQISDRGTANYSQP--YESFGLQDKSETLPPETTERPNYESYSHRLSHIGLIQSR	475
QY	483	VKALVYSWTHRSADTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNTGT	542
DB	476	VNVVYSWTHRSADTNTIENRITQIPMKASBELPQGTTVVRGPGFTGGDILRRNTGG	535
QY	543	FGDIRVNNPPFAQRYRIRYASTTDLOFHTSINGKAINQGNFSATWNGEDLDYKTFX	602
DB	536	FGPIRVNNGPLTQRYRIGFRYASTVDFDFVSRGGTTVNNFRLTRWNSGDELKYGNFV	595
QY	603	TVGFTTPSLDQVSTFTIGAWNFSSGNEVYIDRIEFVPEVTVYEAEDFEKAQKVTAAL	662
DB	596	RRATFTPTFTQIDIRTSQGLSGNGEVIDKIEIIPVTATFEAYDLERAQAVNAL	655
QY	663	FTSTNPRGLKTDVKDYHIDQVSNLVESLSDPFYLDKKEELFEIVKYAKQLHIERNM	718

RESULT 6  
US-10-809-953-10  
; Sequence 10, Application US/10809953  
; Publication No. US200401825A1  
; GENERAL INFORMATION:

Db 656 FTNTPRLKTDVTDYHIDQVSNLVACLSDEFCLDEKRELEKVKYAKRLSDERNL 711

RESULT 7

US-09-988-462-7

; Sequence 7, Application US/09988462

; Publication No. US20030046726A1

; GENERAL INFORMATION:

APPLICANT: Koziel, Michael G.

Desai, Nalin M.

Lewis, Kelly S.

Kramer, Vance C.

Warren, Gregory W.

Evola, Stephen V.

Crossland, Lyle D.

Wright, Martha S.

Merlin, Ellis J.

Launis, Karen L.

TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED

INSECTICIDAL ACTIVITY IN MAIZE

NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:

ADDRESSEE: Syngenta Biotechnology, Inc.

STREET: 3054 Cornwallis Road

CITY: Research Triangle Park

STATE: NC

COUNTRY: USA

ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/988,462

FILING DATE: 20-NOV-2003

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/547,422

FILING DATE: 11-APR-2000

APPLICATION NUMBER: US 08/459,504

FILING DATE: 02-JUN-1995

APPLICATION NUMBER: US 07/951,715

FILING DATE: 25-SEP-1992

APPLICATION NUMBER: US 07/772,027

FILING DATE: 04-OCT-1991

ATTORNEY/AGENT INFORMATION:

NAME: Meigs, J. Timothy

REGISTRATION NUMBER: 38,241

REFERENCE/DOCKET NUMBER: S-188051

TELECOMMUNICATION INFORMATION:

TELEPHONE: (919) 541-8587

TELEFAX: (919) 541-8689

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 1207 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 7:

US-09-988-462-7

Query Match 59.6%; Score 2236; DB 10; Length 1207;

Best Local Similarity 63.9%; Pred. No. 1.2e-177;

Matches 439; Conservative 78; Mismatches 156; Indels 14; Gaps 6;

QY 40 EDCLKMSEVNPFFVSASTQIGIAGKILGTVPGAGVASTYFILGELWPKGN 99

Db 10 EDSLCIAEGNIDFFVSASTQIGIAGKILGTVPGAGVASTYFILGELWPKGN 69

QY 100 QWEIFMEHVEEIIINQKISTYARNKALTDLKLGLDALAVYHDSLVGNGNNTNARSVVK 159

Db 70 QWEIFMEHVEEIIINQKISTYARNKALTDLKLGLDALAVYHDSLVGNGNNTNARSVVK 129

QY 160 SOVIAELMFVOKLPFAVSGEVEPLLPYAAANLHLLLRDASIFGKELSSSEIST 219

Db 130 TOYIALELDFNAMEPLFAIRNOVEPLLMVYAAANLHLLLRDASLFSFSEGLTSQEIQ 189

QY 220 FYNROVERAGDYSYHCVKYSTGLNLRGTNAESVRYNQFRDMTLMVLVLFPSYD 279

Db 190 YVERQVTRDYSYDCEVYNTGLNLRGTNAESVRYNQFRDMTLMVLVLFPSYD 249

QY 280 TOMYPIKTTAQTREVVYDAIGTVHPHSFTSTWYNNAPSFSAIEAAVNVNPHLLDPL 339

Db 250 TRTYPINISAQUTREVYDAIGAT--GVNMAKMYNNAPSFSAIEAAAIRSPHLLDPL 307

QY 340 EQVTIYSLSRWSNTQYMMMGHKLFRITGGTLNISTQSTNTSINPVTLPFTSRDVI 399

Db 308 EQLTIFSSASRSWNTRHMTYWRGHTIQSRPIGGGLNTSHGATNTSINPVTLPFTSRDVI 367

QY 400 RTESLAGNLFP--LTQPVN-VPVDFHMKFVTHP-----IASDNFYFYGAGIGTQLD 451

Db 368 RTESYAGVLLWGIYLEPIHGVTVRNF---TNQNISDRGTANYQP-YESPGQLQKDS 423

QY 452 ENELPPEATQGFNYESYSHRLSHIGLISASHVKALVSWTHRSADRTNTIEFNSITQPL 511

Db 424 ETELPPETTERPNYESYSHRLSHIGLISASHVKALVSWTHRSADRTNTIEFNSITQPL 483

QY 512 VKAFNLSSGAAVVRGPGFTGGDILRRNTGTGDIRVNNINPPFAQRYRIRYASTDLO 571

Db 484 VKASELPQGTTVRGPFTGGDILRRNTGTGDIRVNNINPPFAQRYRIRYASTDLO 543

QY 572 FHTSINGKAINQGNFSAATMRGEDLDYKFTVGTGFTFPFSLDDVQSTFTIGAMNPFSSGNE 631

Db 544 FVSRGGTIVANFRFLRTMNSGDELKYGNFVRRAFTTPTFTQIQDIIRTSIQGLSGNGE 603

QY 632 VIIDRIEFVPEVVEYEAHYDFEKAQKVTAFTSTNRLGKTDYKDHIDQVSNLVESLS 691

Db 604 VYIDKIEIPVTATFEAYEDLERAQEAVALFTNPRRLKTDVTDYHIDQVSNLVACLS 663

QY 692 DEFYLDKRELFELVKVAKQLHIERNM 718

Db 664 DEFCLDEKRELEKVKYAKRLSDERNL 690

RESULT 8

US-10-428-961-63

; Sequence 63, Application US/10428961

; Publication No. US2003023711A1

; GENERAL INFORMATION:

APPLICANT: Baum, James A.

APPLICANT: Chu, Chih-Wei

APPLICANT: Donovan, William P.

APPLICANT: Gilmer, Amy J.

APPLICANT: Ruper, Amy J.

TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin

TITLE OF INVENTION: Polynucleotides, Compositions, and Methods of Use (Amended)

FILE REFERENCE: MECO201--1

CURRENT APPLICATION NUMBER: US/10/428,961

CURRENT FILING DATE: 2003-05-02

PRIOR APPLICATION NUMBER: 09/661,322

PRIOR FILING DATE: 2000-09-13

PRIOR APPLICATION NUMBER: 60/153,995

PRIOR FILING DATE: 1999-09-15

NUMBER OF SEQ ID NOS: 63

SOFTWARE: Patentin version 3.2

SEQ ID NO 63

LENGTH: 1227

TYPE: PRT

ORGANISM: Bacillus thuringiensis

US-10-428-961-63

Query Match 57.5%; Score 2156; DB 14; Length 1227;

Best Local Similarity 58.8%; Pred. No. 6.1e-171;

Matches 420; Conservative 105; Mismatches 175; Indels 14; Gaps 4;

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QY 13 SSNAKVDKISTDSLN-----ETDIELQINNHEDCLKSEYENVEPFSASTIQTIG 65
DB 7 NENEIINALSIPAVSNHSAQNLSLDARI-----EDSLCIAEGNNIDPFSASTVQTGIN 61
QY 66 IAGKILGTLPVPPAGQVASYSPILGELWPKGNQWEIFMEHVEEIIINQKISTYARNKAL 125
DB 62 IAGRILGVLGVPFAGQIASFSFLUGELWPRGRDPWEIFLEHVEHLIRQQVTTENTDALTAL 121
QY 126 TDLKGLDALAVYHDSLESWGNRNNTARSVVKSOVIALELMFVQKLPSPFVSGSEVPL 185
DB 122 ARLOGLGNSFRAYQOSLEDWLENRDARTSVLTQYIALELDFLNAMPLFAIRNQEVPL 181
QY 186 LPIYAQAANLHLLLRDASIFGKEWGLSSSISITFYNEQVERAGDYSYHCVKYSTGLNN 245
DB 182 LMVYAQAANLHLLLRDASLFGSEFGLTSQIOIYERQVEKTRYSYCARWYNTGLNN 241
QY 246 LRGTAESWRYNQFRDMLTLMVLDLVALPSPYDTOMYPIKTTAQLTREVYTDAGTVHP 305
DB 242 LRGTAESWRYNQFRDMLTLMVLDLVALPSPYDTOMYPIKTTAQLTREVYTDAGTVHP 301
QY 306 HPSFTSTWYNNAPSPSAIEAAVVRNPHLLDFLEQVTTISLSRWNTQYMMWGGHKL 365
DB 302 PSGFASWYNNAPSPSAIEAAVVRNPHLLDFLEQVTTISLSRWNTQYMMWGGHKL 361
QY 366 EFRITGGLTNTSTOGSTNTSINPVLPTSDRVYRTESLAGLNLFLTPVN-VPRVDFHW 424
DB 362 ESRITGSLSTWHTGNTSINPVLPTSDRVYRTESLAGLNLFLTPVN-VPRVDFHW 421
QY 425 KFTVTHPIASDNFYPGYAGIGTQLODSENELPPEATQPNYESYSHRLSHIGLISASHVK 484
DB 422 RNPNSLRGSLLYTIGYTGVTQGLFDSSETLPPTTERPNYESYSHRLSHIRLISGNTLR 481
QY 485 ALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRTNTCTFG 544
DB 482 APVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRTNTCTFG 541
QY 545 DIRVNINPPFAQRYRIRYASTTDLQPHTSINGKAINQGNFSAATMRGDLDTYKFTXV 604
DB 542 SMGLNFNNTSLQRYRVRVRYAASQTMVLRVTVGGSTTFDQGFPTMSANESLTSQSPFA 601
QY 605 GFTTFFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQKVTALFT 664
DB 602 EFPVGISASGSQ-TAGISISNAGRQTFHFDKIEFIPITALESDLERAKQAVNALFT 660
QY 665 STNPRGLKTDVXDYHIDOVSNLVSLSDEFYLDKRELFEIVKYAKOLHIERNM 718
DB 661 NINPRLKTGVTDXHIDVSNLVSLSDEFYLDKRELFEIVKYAKOLHIERNM 714

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RESULT 9

```

US-09-826-660-23
; Sequence 23, Application US/09826660
; Patent No. US20010026940A1
; GENERAL INFORMATION:
; APPLICANT: Cardineau, Guy A.
; APPLICANT: Stelman, Steven J.
; APPLICANT: Narva, Kenneth E.
; TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins
; FILE REFERENCE: MA-714XC2D1
; CURRENT APPLICATION NUMBER: US/09/826,660
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/178,252
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: 60/065,215
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/076,445
; PRIOR FILING DATE: 1998-03-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 23
; LENGTH: 1186
; TYPE: PRT
; ORGANISM: Artificial Sequence

```

FEATURE:

OTHER INFORMATION: Toxin encoded by synthetic B.t. gene

US-09-826-660-23

Query Match 57.1%; Score 2141; DB 9; Length 1183;

Best Local Similarity 58.5%; Pred. No. 1e-169;

Matches: 418; Conservative 108; Mismatches 174; Indels 14; Gaps 4;

```

QY 13 SSNAKVDKISTDSLN-----ETDIELQINNHEDCLKSEYENVEPFSASTIQTIG 65
DB 7 NENEIINALSIPAVSNHSAQNLSLDARI-----EDSLCIAEGNNIDPFSASTVQTGIN 61
QY 66 IAGKILGTLPVPPAGQVASYSPILGELWPKGNQWEIFMEHVEEIIINQKISTYARNKAL 125
DB 62 IAGRILGVLGVPFAGQIASFSFLUGELWPRGRDPWEIFLEHVEHLIRQQVTTENTOTAL 121
QY 126 TDLKGLDALAVYHDSLESWGNRNNTARSVVKSOVIALELMFVQKLPSPFVSGSEVPL 185
DB 122 ARLOGLGNSFRAYQOSLEDWLENRDARTSVLTQYIALELDFLNAMPLFAIRNQEVPL 181
QY 186 LPIYAQAANLHLLLRDASIFGKEWGLSSSISITFYNEQVERAGDYSYHCVKYSTGLNN 245
DB 182 LMVYAQAANLHLLLRDASLFGSEFGLTSQIOIYERQVEKTRYSYCARWYNTGLNN 241
QY 246 LRGTAESWRYNQFRDMLTLMVLDLVALPSPYDTOMYPIKTTAQLTREVYTDAGTVHP 305
DB 242 LRGTAESWRYNQFRDMLTLMVLDLVALPSPYDTOMYPIKTTAQLTREVYTDAGTVHP 301
QY 306 HPSFTSTWYNNAPSPSAIEAAVVRNPHLLDFLEQVTTISLSRWNTQYMMWGGHKL 365
DB 302 PSGFASWYNNAPSPSAIEAAVVRNPHLLDFLEQVTTISLSRWNTQYMMWGGHKL 361
QY 366 EFRITGGLTNTSTOGSTNTSINPVLPTSDRVYRTESLAGLNLFLTPVN-VPRVDFHW 424
DB 362 ESRITGSLSTWHTGNTSINPVLPTSDRVYRTESLAGLNLFLTPVN-VPRVDFHW 421
QY 425 KFTVTHPIASDNFYPGYAGIGTQLODSENELPPEATQPNYESYSHRLSHIGLISASHVK 484
DB 422 RNPNSLRGSLLYTIGYTGVTQGLFDSSETLPPTTERPNYESYSHRLSHIRLISGNTLR 481
QY 485 ALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRTNTCTFG 544
DB 482 APVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRTNTCTFG 541
QY 545 DIRVNINPPFAQRYRIRYASTTDLQPHTSINGKAINQGNFSAATMRGDLDTYKFTXV 604
DB 542 SMGLNFNNTSLQRYRVRVRYAASQTMVLRVTVGGSTTFDQGFPTMSANESLTSQSPFA 601
QY 605 GFTTFFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQKVTALFT 664
DB 602 EFPVGISASGSQ-TAGISISNAGRQTFHFDKIEFIPITALESDLERAKQAVNALFT 660
QY 665 STNPRGLKTDVXDYHIDOVSNLVSLSDEFYLDKRELFEIVKYAKOLHIERNM 718
DB 661 NINPRLKTGVTDXHIDVSNLVSLSDEFYLDKRELFEIVKYAKOLHIERNM 714

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RESULT 10

```

US-10-428-961-38
; Sequence 38, Application US/10428961
; Publication No. US20030237111A1
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Chu, Chih-Rei
; APPLICANT: Donovan, William P.
; APPLICANT: Gilmer, Amy J.
; APPLICANT: Rupar, Mark J.
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin
; FILE REFERENCE: MECO201-1
; CURRENT APPLICATION NUMBER: US/10/428,961
; CURRENT FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: 09/661,322

```



; PRIOR FILING DATE: 2000-09-13  
 ; PRIOR APPLICATION NUMBER: 60/153,995  
 ; PRIOR FILING DATE: 1999-09-15  
 ; NUMBER OF SEQ ID NOS: 63  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 38  
 ; LENGTH: 1228  
 ; TYPE: PR1  
 ; ORGANISM: Bacillus thuringiensis  
 ; US-10-428-961-38

Query Match 55.6%; Score 2085.5; DB 14; Length 1228;  
 Best Local Similarity 59.0%; Pred. No. 4.9e-165;  
 Matches 421; Conservative 98; Mismatches 183; Indels 11; Gaps 8;

QY	13	SSNAKVDKISTDSLKN-ETDIEIQ-NINHEDCMKSEYENVEFPVSASTIQTGIGIAGKI	70
DB	7	NENEIINALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGINIAGRI	66
QY	71	LGTLGVPFAGQVASYLSFILGELWPKGNOWEIFMEHVEEIIINOKISTVARNKALTDLKG	130
DB	67	LGVLGVFPFAGQIASFSYFLVGEIWPGRGDQWEIFLEHVEQLINQOITENARNALALRQOG	126
QY	131	LGDAVAVHDSLSWGNRNNTARSVVKSYQYIALELMFVQKLPSPFVSGEVEVLLPIYA	190
DB	127	LGDSFRAYQOSLEDWLENRDARTSVLYTOYIALELDPLNAMPLEFAIRNQEVEVLLMVA	186
QY	191	QAANLHLLLDASITGKWLGSSEISSTFYNQVERAGDYSYHCVKYSTGLNLRGTN	250
DB	187	QAANLHLLLDASLFGSEFGLTSQEIQRYYERQVQETRDYSDYCVENYNTGLNLRGTN	246
QY	251	AESWRYNQPRRDMTLMVLVALFPSSYDTQMPYIKTTAQLTREVTYDAIGTVHPHPSFT	310
DB	247	AASWRYNQPRRDLTLGVLDLVALFPSSYDTRTYPINTSAQLTREVTYDAIGAT--GVNVA	304
QY	311	STTWYNNAPSAFAIEAAVVRNPHLLDFLEQVITYLSLRWSNTQYNNMWSGHKLEFRTI	370
DB	305	SMWYNNAPSAFAIETAVIRSPHLLDFLEQVITYLSLRWSNTQYNNMWSGHKLEFRTI	364
QY	371	GGTLNISTQGSTNTSINPVLTPFTSRDYRTESLAGLNL--LTQPVN-VPRVDFHMKFV	427
DB	365	GGGLNTSTHGSTNTSINPVLTPFTSRDYRTESLAGLNL--LTQPVN-VPRVDFHMKFV	424
QY	428	--THPIASDNFYPGYAGIGTQLQDSNELPPEATGQPNYESYSHRSLSHIGLISASHVKA	485
DB	544	MGLFNNTSLQRYVRVRYAASQTMVLRTVVGSTTFDQGFPTMSANESLTSQSPFAE	603
QY	606	FTTFFSLDVQSTTIGAMNFSNGNEVYIDRIEFVPEVTEYAEYDFEKAQKVTALFTS	665
DB	604	FPVGISASGQ--TAGISISNAGRQTFHFQKIEFIPITATFEAEYDLERAQAVNALFTN	662
QY	666	TNPRGLKTDVYDHIQVSNLVSDEFLYDEKRELFEIVKYAKOLHIERNM	718
DB	663	TNPRRLKTDVYDHIQVSNLVSDEFLYDEKRELFEIVKYAKOLHIERNM	715

RESULT 11  
 US-10-614-524-2  
 ; Sequence 2, Application US/10614524  
 ; Publication No. US20040016020A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Arnaud, Greta  
 ; APPLICANT: Boets, Annemie  
 ; APPLICANT: Damme, Nicole  
 ; APPLICANT: Mathieu, Eva

; APPLICANT: Vanneste, Stijn  
 ; APPLICANT: Van Rie, Jeroen  
 ; TITLE OF INVENTION: Insecticidal proteins from Bacillus thuringiensis.  
 ; FILE REFERENCE: NEWBTSUS2  
 ; CURRENT APPLICATION NUMBER: US/10/614,524  
 ; CURRENT FILING DATE: 2003-07-09  
 ; PRIOR APPLICATION NUMBER: US/09/739,243  
 ; PRIOR FILING DATE: 2000-12-19  
 ; PRIOR APPLICATION NUMBER: 60/173387  
 ; PRIOR FILING DATE: 1999-12-28  
 ; NUMBER OF SEQ ID NOS: 13  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 2  
 ; LENGTH: 1228  
 ; TYPE: PR1  
 ; ORGANISM: Bacillus thuringiensis  
 ; US-10-614-524-2

QY	13	SSNAKVDKISTDSLKN-ETDIEIQ-NINHEDCMKSEYENVEFPVSASTIQTGIGIAGKI	70
DB	7	NENEIINALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGINIAGRI	66
QY	71	LGTLGVPFAGQVASYLSFILGELWPKGNOWEIFMEHVEEIIINOKISTVARNKALTDLKG	130
DB	67	LGVLGVFPFAGQIASFSYFLVGEIWPGRGDQWEIFLEHVEQLINQOITENARNALALRQOG	126
QY	131	LGDAVAVHDSLSWGNRNNTARSVVKSYQYIALELMFVQKLPSPFVSGEVEVLLPIYA	190
DB	127	LGDSFRAYQOSLEDWLENRDARTSVLYTOYIALELDPLNAMPLEFAIRNQEVEVLLMVA	186
QY	191	QAANLHLLLDASITGKWLGSSEISSTFYNQVERAGDYSYHCVKYSTGLNLRGTN	250
DB	187	QAANLHLLLDASLFGSEFGLTSQEIQRYYERQVQETRDYSDYCVENYNTGLNLRGTN	246
QY	251	AESWRYNQPRRDMTLMVLVALFPSSYDTQMPYIKTTAQLTREVTYDAIGTVHPHPSFT	310
DB	247	AASWRYNQPRRDLTLGVLDLVALFPSSYDTRTYPINTSAQLTREVTYDAIGAT--GVNVA	304
QY	311	STTWYNNAPSAFAIEAAVVRNPHLLDFLEQVITYLSLRWSNTQYNNMWSGHKLEFRTI	370
DB	305	SMWYNNAPSAFAIETAVIRSPHLLDFLEQVITYLSLRWSNTQYNNMWSGHKLEFRTI	364
QY	371	GGTLNISTQGSTNTSINPVLTPFTSRDYRTESLAGLNL--LTQPVN-VPRVDFHMKFV	427
DB	365	GGGLNTSTHGSTNTSINPVLTPFTSRDYRTESLAGLNL--LTQPVN-VPRVDFHMKFV	424
QY	428	--THPIASDNFYPGYAGIGTQLQDSNELPPEATGQPNYESYSHRSLSHIGLISASHVKA	485
DB	425	QNTFERGTANYSQP--YESPGQLKDSSETLPPETTERPNYESYSHRSLSHIGLISASHVKA	483
QY	486	LVYSWTHRSADRTNIEPNSITQIPLVKFNLSGAAVVRGPGFTGGDILRTNTGTFGD	545
DB	484	PVYSWTHRSADRTNIEPNSITQIPLVKFNLSGAAVVRGPGFTGGDILRTNTGTFGD	543
QY	546	IRVINPPFAQRYVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDDLYKTFXTVG	605
DB	544	MGLFNNTSLQRYVRVRYAASQTMVLRTVVGSTTFDQGFPTMSANESLTSQSPFAE	603
QY	606	FTTFFSLDVQSTTIGAMNFSNGNEVYIDRIEFVPEVTEYAEYDFEKAQKVTALFTS	665
DB	604	FPVGISASGQ--TAGISISNAGRQTFHFQKIEFIPITATFEAEYDLERAQAVNALFTN	662
QY	666	TNPRGLKTDVYDHIQVSNLVSDEFLYDEKRELFEIVKYAKOLHIERNM	718
DB	663	TNPRRLKTDVYDHIQVSNLVSDEFLYDEKRELFEIVKYAKOLHIERNM	715

RESULT 12  
 US-09-826-660-25

```

RESULT 13
US-10-089-678-1
; Sequence 1, Application US/10089678
; Publication NO. US20030017967A1
; GENERAL INFORMATION:
; APPLICANT: ASANO, Shinichiro
; TITLE OF INVENTION: PROTEIN HAVING INSECTICIDAL ACTIVITY, DNA ENCODING THE PROTEIN, AN
; TITLE OF INVENTION: NOXIOUS ORGANISM-CONTROLLING AGENT AND METHOD
; FILE REFERENCE: Q68821
; CURRENT APPLICATION NUMBER: US/10/089,678
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: JP 2000-236140
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: PCT/JP01/06660
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1167
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-089-678-1
Query Match 45.6% Score 1708; DB 14; Length 1167;

```

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; Sequence 25, Application US/09826660
; Patent No.: US20010026940A1
; GENERAL INFORMATION:
; APPLICANT: Cardineau, Guy A.
; APPLICANT: Stelman, Steven J.
; APPLICANT: Narva, Kenneth E.
; TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins
; FILE REFERENCE: MA-714XC2D1
; CURRENT APPLICATION NUMBER: US/09/826,660
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/178,252
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: 60/065,215
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/076,445
; PRIOR FILING DATE: 1998-03-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 643
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Toxin encoded by synthetic B.t. gene
; US-09-826-660-25

Query Match          50.7%; Score 1902; DB 9; Length 643;
Best Local Similarity 57.2%; Pred. No. 4.2e-150;
Matches 368; Conservative 100; Mismatches 161; Indels 14; Gaps 4

QY      13  SSNAKVDKISTDSLKN-----ETDIELQINHEPCLKMSEYENVEPVFVASTIQTGIG 65
DB      7  NENEIINALSPAVNSHSAQNLSTDARI-----EDSLCIAEGNIDPFVSASTVQTGIN 61

QY      66  IAGKILGTGVPPAGQAVASLYSPFLIGELWPKGNQWEIFMEHVEEILINOKISTVARNKAL 125
DB      62  IAGRILGTVLGVPPAGQIASFVSFLVGLBNPRGRDMEIFLEHVEEILIRQQVTVNTRDTAL 121

QY      126  TDLKGLGDALAVYHDSLSBSWNGNENNRTRASVVKSQSVIALLELMFVKQLPSFAVSGEEVPL 185
DB      122  ARLOGLGNSFRAYQOQSLIEDWLENRDDARTSRSLVTVQVIALELDPLNAMPFLAIRNQEVPL 181

QY      186  LPIYQAANLHLLLRDASIIEKRWGLSSSEISTFYNNQVERAGDYSYHCKWYSTGLNN 245
DB      182  LMVYQAANLHLLLRDASLSEFGTSGEIQRYERQVEKTRTESDTCARWYNIGLNN 241

QY      246  LRGTTNAESWVRNQPFRRDMLMLDLVALPFSYDTQMPYIKTTAQTREYVYTDAGTVHP 305
DB      242  LRGTTNAESWLRNQPFRRDLTLGLDLVALPFSYDVRVPMNTSAQLTREIYTDPIGRTA 301

QY      306  HPSFTSTWYNNAPSAIEAAVVRPHLLDPLEQVITYSLSRMSNTQYNNMGSHKL 365
DB      302  PGSPFATWNNFNAPSAIEAAVVRPHLLDPPQETIIEVLSRMSNTQYNNYVWGHKL 361

QY      366  EFRITGGTLNISTQGSTNTSINPVLTPTSRDVYRTESLAGNLFLUTQPVN-VPVRVDFHW 424
DB      362  ESKTIRGSLSTHGNTNTSINPVLTQFTSRDVYRTESFAGINILLTTPVNGVPWAFENW 421

QY      425  KFTVTHPIASDNFYGYAGITQLODSENELPPEATQCPNVESYSHLSHIGLISASHVK 484
DB      422  RNPLNSLRGLSLTYTGYGVGTQQLFDSETELPPTTERPNVESYSHLSNIRLISGNTLR 481

QY      485  ALVYSWTHRSADRTNTIEPNSITQPLVKAPNLSSGAAVVRGPGFTGGDILRNTNTGTFG 544
DB      482  APVYSWTHRSADRTNTISSDITQPLVKSFNLSNGTSVVSQSGPFTGGDIIRTNVNGSVL 541

QY      545  DIRVAINPFFAORYVRIRYASTTDLPQHTSINGKAINQGNFSATNMWRGSDLDYKCTFTV 604
DB      542  SMGLNFNTSLORYVRVRYAASQTMVLRVTVGSGTFTDQGFSTMSANESLTSQSFRFA 601

QY      605  GTTFPSLLDVQSTTFIGAWNFSSGNEVYIDRIEFVPEVYTYE 647
DB      602  EFPVGIASGSGO-TAGISLNSNAGSQTFHFPIKIFIDITATLE 643

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Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	3718.5	99.2	719	3	US-08-286-870A-8	Sequence 8, Appli
2	3439	91.7	710	4	US-09-661-322A-42	Sequence 42, Appli
3	3360.5	89.6	548	3	US-08-286-870A-4	Sequence 4, Appli
4	3358.5	89.6	719	2	US-09-003-217-2	Sequence 2, Appli
5	3356.5	89.5	719	3	US-09-218-943-2	Sequence 2, Appli
6	2778.5	74.1	535	3	US-08-286-870A-6	Sequence 6, Appli
7	2415	64.4	1239	1	US-08-100-709-4	Sequence 4, Appli
8	2415	64.4	1229	1	US-08-176-865-4	Sequence 4, Appli
9	2415	64.4	1229	1	US-08-474-038-4	Sequence 4, Appli
10	2415	64.4	1229	2	US-08-779-036-4	Sequence 4, Appli
11	2415	64.4	1229	2	US-08-881-340-4	Sequence 4, Appli
12	2319	61.9	488	1	US-08-448-170-10	Sequence 10, Appli
13	2319	61.9	488	3	US-08-961-803-10	Sequence 10, Appli
14	2236	59.6	1207	1	US-07-951-715A-7	Sequence 7, Appli
15	2236	59.6	1207	2	US-08-459-448A-7	Sequence 7, Appli
16	2236	59.6	1207	3	US-08-459-595A-7	Sequence 7, Appli
17	2236	59.6	1207	3	US-08-459-504B-7	Sequence 7, Appli
18	2236	59.6	1207	3	US-08-459-444-7	Sequence 7, Appli
19	2236	59.6	1207	3	US-09-053-549-8	Sequence 8, Appli
20	2236	59.6	1207	3	US-09-547-423-7	Sequence 8, Appli
21	2236	59.6	1207	4	US-09-988-463-7	Sequence 7, Appli
22	2236	59.6	1207	3	US-09-053-549-2	Sequence 2, Appli
23	2165	57.7	1237	1	US-08-448-170-8	Sequence 8, Appli
24	2165	57.7	1237	3	US-08-448-170-8	Sequence 8, Appli
25	2156	57.5	1227	4	US-09-661-322A-63	Sequence 9, Appli
26	2141	57.1	1186	3	US-09-178-253-23	Sequence 63, Appli
27	2141	57.1	1186	4	US-09-826-660-23	Sequence 23, Appli

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Query Match      99.2%; Score 3718.5; DB 3; Length 719;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 714; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 1 M K L N Q D K H Q S F S S N A K V D K I S T S L K N E T D I E L Q N I N H E D C L K S E Y E N V E P F V S A S T I 60
DB 1 M K L N Q D K H Q S F S S N A K V D K I S T S L K N E T D I E L Q N I N H E D C L K S E Y E N V E P F V S A S T I 60

QY 61 Q T G I G I A K I L G T L G V P P A G Q V A S L Y S F I L G E L W P K G K N Q W E I F M E H V E E I I N Q K I S T Y A 120
DB 61 Q T G I G I A K I L G T L G V P P A G Q V A S L Y S F I L G E L W P K G K N Q W E I F M E H V E E I I N Q K I S T Y A 120

QY 61 Q T G I G I A K I L G T L G V P P A G Q V A S L Y S F I L G E L W P K G K N Q W E I F M E H V E E I I N Q K I S T Y A 120
DB 61 Q T G I G I A K I L G T L G V P P A G Q V A S L Y S F I L G E L W P K G K N Q W E I F M E H V E E I I N Q K I S T Y A 120

QY 121 R N K A L T D L K G L D A L A V H D S L E S W G N R N N T R A R S V V K S Q I A L E L M F V Q K L P S F A V S G 180
DB 121 R N K A L T D L K G L D A L A V H D S L E S W G N R N N T R A R S V V K S Q I A L E L M F V Q K L P S F A V S G 180

QY 181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S E I S T F Y N Q V E R A G D Y S Y H C V K W Y S 240
DB 181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S E I S T F Y N Q V E R A G D Y S Y H C V K W Y S 240

QY 241 T G L N L R G T N A E S W Y R N Q F R D M T L M V L D I A L V P S Y D T Q M P I K T A Q L T R E V Y T D A I 300
DB 241 T G L N L R G T N A E S W Y R N Q F R D M T L M V L D I A L V P S Y D T Q M P I K T A Q L T R E V Y T D A I 300

QY 301 G T V H P H P S F T S T T W Y N N N A P S F S A I E A A V V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y N M W 360
DB 301 G T V H P H P S F T S T T W Y N N N A P S F S A I E A A V V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y N M W 360

QY 361 G G H K L E F R T I G T L N I S T Q G S T N T S I N P V T L P F T S R D V Y R T E S L A G N L F L T Q P V N - V P R 419
DB 361 G G H K L E F R T I G T L N I S T Q G S T N T S I N P V T L P F T S R D V Y R T E S L A G N L F L T Q P V N G V P R 420

QY 420 V D F H W K F V T H P I A S D N F Y P G Y A G I G T Q L O D S E N E L P E A T G Q P N Y E S Y S H R L S H I G L I S 479
DB 421 V D F H W K F V T H P I A S D N F Y P G Y A G I G T Q L O D S E N E L P E A T G Q P N Y E S Y S H R L S H I G L I S 480

QY 480 A S H V K A L Y S W T H R S A D R T N I E P N S I T Q I P L V K A F N L S S G A A V V R G P F T G D I L R T N 539
DB 481 A S H V K A L Y S W T H R S A D R T N I E P N S I T Q I P L V K A F N L S S G A A V V R G P F T G D I L R T N 540

QY 540 T G T F G D I R V N I N P P A Q R Y R V R I R Y A S T T D L Q F H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 599
DB 541 T G T F G D I R V N I N P P A Q R Y R V R I R Y A S T T D L Q F H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 600

QY 600 T F X T V G F T T P F S L D V Q S T F T I G A W N F S S G N E V I D R I E F V P V E V T Y E A E Y D P E K A Q E K V 659
DB 601 T F R T V G F T T P F S L D V Q S T F T I G A W N F S S G N E V I D R I E F V P V E V T Y E A E Y D P E K A Q E K V 660

QY 660 T A L F T S T N P R G L K T D V Q D H I D Q V S N L V E S L D E F Y L D E K R E L F E I V K Y A K Q L H I E R N M 718
DB 661 T A L F T S T N P R G L K T D V Q D H I D Q V S N L V E S L D E F Y L D E K R E L F E I V K Y A K Q L H I E R N M 719

RESULT 2
US-09-661-322A-42
; Sequence 42, Application US/09661322A
; Patent No. 6593293
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Chu, Chih-Rei
; APPLICANT: Donovan, William P.
; APPLICANT: Gilmer, Amy J.
; APPLICANT: Ruper, Mark J.
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin Compo
; FILE REFERENCE: MECO201
; CURRENT APPLICATION NUMBER: US/09/661.322A
; CURRENT FILING DATE: 2000-09-13
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 42
; LENGTH: 710
; TYPE: PRT

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; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (200)..(200)
; OTHER INFORMATION: No. 6593293-Coding
US-09-661-322A-42

Query Match      91.7%; Score 3439; DB 4; Length 710;
Best Local Similarity 91.9%; Pred. No. 1.1e-299;
Matches 661; Conservative 15; Mismatches 33; Indels 10; Gaps 2;

QY 1 M K L N Q D K H Q S F S S N A K V D K I S T S L K N E T D I E L Q N I N H E D C L K S E Y E N V E P F V S A S T I 60
DB 1 M K S K N Q N H Q S L S N N A T V D K N F T G S L E N T N T E L Q N F N H -----E G I E P F V S V S T I 51

QY 61 Q T G I G I A K I L G T L G V P P A G Q V A S L Y S F I L G E L W P K G K N Q W E I F M E H V E E I I N Q K I S T Y A 120
DB 52 Q T G I G I A K I L G T L G V P P A G Q V A S L Y S F I L G E L W P K G K S O W E I F M E H V E E I I N Q K I S T Y A 111

QY 121 R N K A L T D L K G L D A L A V H D S L E S W G N R N N T R A R S V V K S Q I A L E L M F V Q K L P S F A V S G 180
DB 112 R N K A L A D L K G L D A L A V H S L E S W I E N R N T R I F S V V K S Q I T I L E L M F V Q S L P S F A V S G 171

QY 181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S E I S T F Y N Q V E R A G D Y S Y H C V K W Y S 240
DB 172 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K X W G L S D S E I S T F Y N R Q S G K S E Y S D H C V K W Y N 231

QY 241 T G L N L R G T N A E S W Y R N Q F R D M T L M V L D I A L V P S Y D T Q M P I K T A Q L T R E V Y T D A I 300
DB 232 T G L N L M G N N A E S W Y R N Q F R D M T L M V L D I A L V P S Y D T Q M P I K T A Q L T R E V Y T D A I 291

QY 301 G T V H P H P S F T S T T W Y N N N A P S F S A I E A A V V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y N M W 360
DB 292 G T V H P H P S F T S T T W Y N N N A P S F T I E A A V V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y N M W 351

QY 361 G G H K L E F R T I G T L N I S T Q G S T N T S I N P V T L P F T S R D V Y R T E S L A G N L F L T Q P V N - V P R 419
DB 352 G G H K L E F R T I G T L N T S T Q G S T N T S I N P V T L P F T S R D V Y R T E S L A G N L F L T Q P V N G V P R 411

QY 420 V D F H W K F V T H P I A S D N F Y P G Y A G I G T Q L O D S E N E L P E A T G Q P N Y E S Y S H R L S H I G L I S 479
DB 412 V D F H W K F V T H P I A S D N F Y P G Y A G I G T Q L O D S E N E L P E A T G Q P N Y E S Y S H R L S H I G L I S 471

QY 480 A S H V K A L Y S W T H R S A D R T N I E P N S I T Q I P L V K A F N L S S G A A V V R G P F T G D I L R T N 539
DB 472 A S H V K A L Y S W T H R S A D R T N I E P N S I T Q I P L V K A F N L S S G A A V V R G P F T G D I L R R N 531

QY 540 T G T F G D I R V N I N P P A Q R Y R V R I R Y A S T T D L Q F H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 599
DB 532 T G T F G D I R V N I N P P A Q R Y R V R I R Y A S T T D L Q F H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 591

QY 600 T F X T V G F T T P F S L D V Q S T F T I G A W N F S S G N E V I D R I E F V P V E V T Y E A E Y D P E K A Q E K V 659
DB 592 T F R T V G F T T P F S D V Q S T F T I G A W N F S S G N E V I D R I E F V P V E V T Y E A E Y D P E K A Q E V 651

QY 660 T A L F T S T N P R G L K T D V Q D H I D Q V S N L V E S L D E F Y L D E K R E L F E I V K Y A K Q L H I E R N M 718
DB 652 T A L F T S T N P R G L K T D V Q D H I D Q V S N L V E S L D K F Y L D E K R E L F E I V K Y A K Q L H I E R N M 710

RESULT 3
US-08-286-870A-4
; Sequence 4, Application US/08286870A
; Patent No. 603605
; GENERAL INFORMATION:
; APPLICANT: Ely, S
; APPLICANT: TAILOR, RH
; APPLICANT: TIPPETT, JM
; APPLICANT: BLENN, RG
; TITLE OF INVENTION: BACTERIAL GENES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DABBY & CUSHMAN

```

ADDRESSEE: Intellectual Property Group of  
ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP  
STREET: 1100 New York Avenue, N.W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3918  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/286,870A  
FILING DATE: 05-AUG-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/520228  
FILING DATE: 09-MAY-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 8910624.9  
FILING DATE: 09-MAY-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: PAUL N. KOKULIS  
REGISTRATION NUMBER: 16,773  
REFERENCE/DOCKET NUMBER: 70608/220720  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 861-3000  
TELEFAX: (202) 822-0944  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 648 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-286-870A-4

Query Match 89.6%; Score 3360.5; DB 3; Length 648;  
Best Local Similarity 99.4%; Pred. No. 1e-292;  
Matches 644; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 MKLKNQDKHQSFSNAKVDKISTSLKNETDIELQINHEDECLKMSEYENVEPFVSASTI 60  
DB 1 MKLKNQDKHQSFSNAKVDKISTSLKNETDIELQINHEDECLKMSEYENVEPFVSASTI 60  
QY 61 QTGIGIAGKILGTGVPPFAGQVASYLSPILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
DB 61 QTGIGIAGKILGTGVPPFAGQVASYLSPILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
QY 121 RNKALTDLKGDLAVYHDSLSWGNRNNTARSVVKSQYIALBELMFVKLPSPAVSG 180  
DB 121 RNKALTDLKGDLAVYHDSLSWGNRNNTARSVVKSQYIALBELMFVKLPSPAVSG 180  
QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTEYFNQVERAGDYSYHCVKWYS 240  
DB 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTEYFNQVERAGDYSYHCVKWYS 240  
QY 241 TGLNNLGTNAESWVRYNQFRDWTLMVLDLVALFSPSYDTQMPYIKTTAQLTREVTDAI 300  
DB 241 TGLNNLGTNAESWVRYNQFRDWTLMVLDLVALFSPSYDTQMPYIKTTAQLTREVTDAI 300  
QY 301 GTVHPHPSFTSTWYNNNAPSEGAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMNW 360  
DB 301 GTVHPHPSFTSTWYNNNAPSEGAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMNW 360  
QY 361 GGHKLEFRTIGGTINISQTSTNTSINPVLPTFSRDVYRTESLAGINLFLTPVNV-VP 419  
DB 361 GGHKLEFRTIGGTINISQTSTNTSINPVLPTFSRDVYRTESLAGINLFLTPVNVGP 420  
QY 420 VDFHWKVTPIASDNPYFGYAGIGTQLODSENELPPEATGPNYESYSHRLSHGLIS 479  
DB 421 VDFHWKVTPIASDNPYFGYAGIGTQLODSENELPPEATGPNYESYSHRLSHGLIS 480

QY 480 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGSGFTGGDILRRTN 539  
DB 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGSGFTGGDILRRTN 540  
QY 540 TGTGDIRVWINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATVNRGSDLYK 599  
DB 541 TGTGDIRVWINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATVNRGSDLYK 600  
QY 600 TFXTVGFTTTPFSLDVQSTFTIGAMNPFSSGNEVYIDRIEFVPEVITYE 647  
DB 601 TERTVGTTPFSLDVQSTFTIGAMNPFSSGNEVYIDRIEFVPEVITYE 648

RESULT 4  
US-09-003-217-2  
; Sequence 2, Application US/09003217  
; Patent No. 5986177  
; GENERAL INFORMATION:  
; APPLICANT: Osman, Yehia A.  
; APPLICANT: Madkour, Magdy A.  
; APPLICANT: Bulla, Lee A.  
; TITLE OF INVENTION: BACILLUS THURINGIENSIS ISOLATES WITH  
; TITLE OF INVENTION: BACILLUS THURINGIENSIS ISOLATES WITH  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: W. Murray Spruill (Alston & Bird, LLP)  
; STREET: 3605 Glenwood Ave. Suite 310  
; CITY: Raleigh  
; STATE: NC  
; COUNTRY: US  
; ZIP: 27622  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/003,217  
; FILING DATE:  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Spruill, W. Murray  
; REGISTRATION NUMBER: 32,943  
; REFERENCE/DOCKET NUMBER: 5718-3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 919 420 2202  
; TELEFAX: 919 881 3175  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 719 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-09-003-217-2

Query Match 89.6%; Score 3358.5; DB 2; Length 719;  
Best Local Similarity 89.6%; Pred. No. 1.9e-292;  
Matches 644; Conservative 33; Mismatches 41; Indels 1; Gaps 1;

QY 1 MKLKNQDKHQSFSNAKVDKISTSLKNETDIELQINHEDECLKMSEYENVEPFVSASTI 60  
DB 1 MKLKNQDKHQSFSNAKVDKISTSLKNETDIELQINHEDECLKMSEYENVEPFVSASTI 60  
QY 61 QTGIGIAGKILGTGVPPFAGQVASYLSPILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
DB 61 QTGIGIAGKILGTGVPPFAGQVASYLSPILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
QY 121 RNKALTDLKGDLAVYHDSLSWGNRNNTARSVVKSOYIALBELMFVKLPSPAVSG 180  
DB 121 RNKALTDLKGDLAVYHDSLSWGNRNNTARSVVKSOYIALBELMFVKLPSPAVSG 180  
QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTEYFNQVERAGDYSYHCVKWYS 240  
DB 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTEYFNQVERAGDYSYHCVKWYS 240

191 EVVPLPIYAQAANHLHLLLDASIFKNGGLSASEISTFYNROVERAGDYSYHCVKWN 240  
 241 TGLNLRGTNAESWVRNQFRDMLVLDLVALFPSSYDTQMPYIKTTAQLTREYVYDAI 300  
 241 TGLNLRGTNAESWVRNQFRDMLVLDLVALFPSSYDTQMPYIKTTAQLTREYVYDAI 300  
 241 TGLNLRGTNAESWVRNQFRDMLVLDLVALFPSSYDTQMPYIKTTAQLTREYVYDAI 300  
 301 GTVPHPSFTSTWNNNAPSFAIEAAVVRNPHLLDFLEQVYIYLLSRWSNTQYNNMW 360  
 301 GTVDPNQALRSTWNNNAPSFAIEAAVVRNPHLLDFLEQVYIYLLSRWSNTQYNNMW 360  
 361 GGHLEFRTIGTLNISTQGSTNTSINPVTLPFTSRDVRYSAGLNLFLTQPVN-VPR 419  
 361 GGHLESPICGALNTSTQGSTNTSINPVTLPFTSRDVRYSAGLNLFLTQPVN-VPR 420  
 420 VDFHWKFTPIASDNFYYPGAGIGTQLOQSENELPPEATGQPNYESYSHRSHIGLIS 479  
 421 VDFHWKFTPIASDNFYYPGAGIGTQLOQSENELPPEATGQPNYESYSHRSHIGLIS 480  
 480 ASHVKALVYSWTHRSADRTNIEPNSITQIPLVAFNLSGAAVVRGPGTGGDILRTN 539  
 481 GSHVVALVYSWTHRSADRTNIEPNSITQIPLVAFNLSGAAVVRGPGTGGHILRTK 540  
 540 TGTFGDIRVNIINPPFAQRYRIRIYASTDLOFHTSINGKAINQGNFSATNMGEDLDYK 599  
 541 SGTFCHIRVNIINPPFAQRYRIRIYASTDLOFHTSINGKAINQGNFSATNMGEDLDYK 600  
 600 TFXTVGFTTPSLLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVYEAEDFEKAQEKV 659  
 601 TFRTVGFTTPSFSQVSTFTIGAWNFSSGNEVYIGRIEFVPEVYEAEDFEKAQEKV 660  
 660 TALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDYLFDEKELFEIVKYAKQIHERNM 718  
 661 TALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDYLFDEKELFEIVKYAKQIHERNM 719

RESULT 5  
 US-09-218-942-2  
 ; Sequence 2, Application US/09218942  
 ; Patent No. 6232439  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Oman, Yehia  
 ; TITLE OF INVENTION: Bacillus Thuringiensis Isolates with Broad Spectrum  
 ; FILE REFERENCE: Cry1I  
 ; CURRENT APPLICATION NUMBER: US/09/218,942  
 ; EARLIER FILING DATE: 1998-12-22  
 ; EARLIER APPLICATION NUMBER: 60/035,361  
 ; EARLIER FILING DATE: 1997-01-10  
 ; EARLIER APPLICATION NUMBER: 09/003,217  
 ; EARLIER FILING DATE: 1998-01-06  
 ; NUMBER OF SEQ ID NOS: 2  
 ; SOFTWARE: Patent In Ver. 2.0  
 ; SEQ ID NO 2  
 ; LENGTH: 719  
 ; TYPE: PRT  
 ; ORGANISM: Bacillus thuringiensis  
 US-09-218-942-2

Query Match 89.5%; Score 3356.5; DB 3; Length 719;  
 Best Local Similarity 89.6%; Pred. No. 2.8e-292;  
 Matches 644; Conservative 33; Mismatches 41; Indels 1; Gaps 1;

1 MKLKNDQHQSFSSNAKVDKISTDLSKNETDIELQININHDCLKMSVENVEPVASATI 60  
 1 MKLKNDQHQSFSSNAKVDKISTDLSKNETDIELQININHDCLKMSVENVEPVASATI 60  
 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEIEMHVEEILNOKISTYA 120  
 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEIEMHVEEILNOKISTYA 120  
 121 RNKALTDLKGDLAVLHDSLESWGVRNNTARSVVKSOYIALELMFVKLPSPAVSG 180  
 121 RNKALTDLKGDLAVLHDSLESWGVRNNTARSVVKSOYIALELMFVKLPSPAVSG 180

181 EVVPLPIYAQAANHLHLLLDASIFKNGGLSASEISTFYNROVERAGDYSYHCVKWN 240  
 181 EVVPLPIYAQAANHLHLLLDASIFKNGGLSASEISTFYNROVERAGDYSYHCVKWN 240  
 241 TGLNLRGTNAESWVRNQFRDMLVLDLVALFPSSYDTQMPYIKTTAQLTREYVYDAI 300  
 241 TGLNLRGTNAESWVRNQFRDMLVLDLVALFPSSYDTQMPYIKTTAQLTREYVYDAI 300  
 301 GTVPHPSFTSTWNNNAPSFAIEAAVVRNPHLLDFLEQVYIYLLSRWSNTQYNNMW 360  
 301 GTVDPNQALRSTWNNNAPSFAIEAAVVRNPHLLDFLEQVYIYLLSRWSNTQYNNMW 360  
 361 GGHLEFRTIGTLNISTQGSTNTSINPVTLPFTSRDVRYSAGLNLFLTQPVN-VPR 419  
 361 GGHLESPICGALNTSTQGSTNTSINPVTLPFTSRDVRYSAGLNLFLTQPVN-VPR 420  
 420 VDFHWKFTPIASDNFYYPGAGIGTQLOQSENELPPEATGQPNYESYSHRSHIGLIS 479  
 421 VDFHWKFTPIASDNFYYPGAGIGTQLOQSENELPPEATGQPNYESYSHRSHIGLIS 480  
 480 ASHVKALVYSWTHRSADRTNIEPNSITQIPLVAFNLSGAAVVRGPGTGGDILRTN 539  
 481 ASHVKALVYSWTHRSADRTNIEPNSITQIPLVAFNLSGAAVVRGPGTGGHILRTK 540  
 540 TGTFGDIRVNIINPPFAQRYRIRIYASTDLOFHTSINGKAINQGNFSATNMGEDLDYK 599  
 541 SGTFCHIRVNIINPPFAQRYRIRIYASTDLOFHTSINGKAINQGNFSATNMGEDLDYK 600  
 600 TFXTVGFTTPSLLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVYEAEDFEKAQEKV 659  
 601 TFRTVGFTTPSFSQVSTFTIGAWNFSSGNEVYIGRIEFVPEVYEAEDFEKAQEKV 660  
 660 TALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDYLFDEKELFEIVKYAKQIHERNM 718  
 661 TALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDYLFDEKELFEIVKYAKQIHERNM 719

RESULT 6  
 US-08-286-870A-6  
 ; Sequence 6, Application US/08286870A  
 ; Patent No. 6063605  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ely, S  
 ; APPLICANT: TAILOR, RH  
 ; APPLICANT: TIPPETT, JM  
 ; APPLICANT: BLENN, RG  
 ; TITLE OF INVENTION: BACTERIAL GENES  
 ; NUMBER OF SEQUENCES: 10  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: CUSHMAN DABY & CUSHMAN  
 ; ADDRESSEE: Intellectual Property Group of  
 ; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP  
 ; STREET: 1100 New York Avenue, N.W.  
 ; CITY: Washington  
 ; STATE: DC  
 ; COUNTRY: USA  
 ; ZIP: 20005-3918  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/286,870A  
 ; FILING DATE: 05-AUG-1994  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/520228  
 ; FILING DATE: 09-MAY-1990  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: GB 8910624.9  
 ; FILING DATE: 09-MAY-1989



ATTORNEY/AGENT INFORMATION:  
NAME: PAUL N. KOKULIS  
REGISTRATION NUMBER: 16,773  
REFERENCE/DOCKET NUMBER: 70608/220720  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 861-3000  
TELEFAX: (202) 822-0944  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 535 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-286-870A-6

Query Match 74.1%; Score 2778.5; DB 3; Length 535;  
Best Local Similarity 99.6%; Pred. No. 1.4e-240;  
Matches 533; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 MKLKNQDKHOSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMEYENVPFVSASTI 60  
DB 1 MKLKNQDKHOSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMEYENVPFVSASTI 60  
QY 61 QTGIGIAGKILGTGVPFAGQVSLYSFILGELWPKGKQWEIFMEHVEEIIINQKISTYA 120  
DB 61 QTGIGIAGKILGTGVPFAGQVSLYSFILGELWPKGKQWEIFMEHVEEIIINQKISTYA 120  
QY 121 RNKALTDLKLGDALAVYHDSLESVGNRNNTARSVKQSYIALELMFVKLPSPAVSG 180  
DB 121 RNKALTDLKLGDALAVYHDSLESVGNRNNTARSVKQSYIALELMFVKLPSPAVSG 180  
QY 181 EYVPLPIYAQAANLHLLLRDASIFGKEWGLSSSISITFYNQVERAGDYSVHCVKWYS 240  
DB 181 EYVPLPIYAQAANLHLLLRDASIFGKEWGLSSSISITFYNQVERAGDYSVHCVKWYS 240  
QY 241 TGLNLRGTNAESWRYNQRRDMLVLDLVALFPSYDTQMPYIKTTAQLTREYVTDI 300  
DB 241 TGLNLRGTNAESWRYNQRRDMLVLDLVALFPSYDTQMPYIKTTAQLTREYVTDI 300  
QY 301 GTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDFLEQVITYSLLSKWSNTQMNW 360  
DB 301 GTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDFLEQVITYSLLSKWSNTQMNW 360  
QY 361 GGHKLEFRITGGLTNTSTQSTNTSINPVTLPFTSRDVRVYTESLAGLNFLTPQVNVGR 420  
DB 361 GGHKLEFRITGGLTNTSTQSTNTSINPVTLPFTSRDVRVYTESLAGLNFLTPQVNVGR 420  
QY 420 VDFHKEVTHPIASDNFYPGYAGIGTQLODSENELPPEATGQPNYESYSHRSLSHIGLIS 479  
DB 420 VDFHKEVTHPIASDNFYPGYAGIGTQLODSENELPPEATGQPNYESYSHRSLSHIGLIS 479  
QY 480 ASHKALVYSWTHRSADRTNTIENPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDI 534  
DB 480 ASHKALVYSWTHRSADRTNTIENPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDI 534

RESULT 7  
US-08-100-709-4  
Sequence 4, Application US/08100709  
Patent No. 5323687  
GENERAL INFORMATION:  
APPLICANT: Dorovan, William P.  
APPLICANT: Tan, Yuting  
APPLICANT: Jany, Christine S.  
APPLICANT: Gonzalez Jr., Jose M.  
TITLE OF INVENTION: BACILLUS THURINGIENSIS CYVET4 AND CYVETS  
TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.  
ADDRESSEE: Nadel  
STREET: 1601 Market Street, 36th Floor  
City: Philadelphia

STATE: Pennsylvania  
COUNTRY: U.S.A.  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/100.709  
FILING DATE: 19930729  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Egoft, Christopher  
REGISTRATION NUMBER: 27633  
REFERENCE/DOCKET NUMBER: 7205-49  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-757-1590  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1229 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-100-709-4

Query Match 64.4%; Score 2415; DB 1; Length 1229;  
Best Local Similarity 65.1%; Pred. No. 2.3e-207;  
Matches 467; Conservative 91; Mismatches 141; Indels 18; Gaps 7;

QY 13 SSNAKVDKISTDSLKNETDIELQ-NINHEDCLKMEYENVPFVSASTIQTGIGIAGKI 70  
DB 7 NENEIINALSIPTVSNPSTQNLSPDARIEDSLCVAEVNNDIPFVSASTVQTGINIAGRI 66  
QY 71 LGTGVPPAGQVSLYSFILGELWPKGKQWEIFMEHVEEIIINQKISTYARKALTDLKG 130  
DB 67 LGVLGVPFAGQVSLYSFILGELWPKGKQWEIFMEHVEEIIINQKISTYARKALTDLKG 126  
QY 131 LGDALAVYHDSLESVGNRNNTARSVKQSYIALELMFVKLPSPAVSGEVEPLPTIYA 190  
DB 127 LGRGYSYQQALETWLDNENDARSIIILERYVALELDITTAIFLFRINEEVEPLMUYA 186  
QY 191 QAANLHLLLRDASIFGKEWGLSSSISITFYNQVERAGDYSVHCVKWYSTGLANLRGTN 250  
DB 187 QAANLHLLLRDASIFGKEWGLSSSISITFYNQVERAGDYSVHCVKWYSTGLANLRGTN 246  
QY 251 AESWRYNQRRDMLVLDLVALFPSYDTQMPYIKTTAQLTREYVTDIATVHPHPSFT 310  
DB 247 AESWRYNQRRDMLVLDLVALFPSYDTQMPYIKTTAQLTREYVTDIATVHPHPSFT 306  
QY 311 STTWYNNAPSFSAIEAAVVRNPHLLDFLEQVITYSLLSKWSNTQYMMWGGHKLPRTI 370  
DB 307 STTWYNNAPSFSAIEAAVVRNPHLLDFLEQVITYSLLSKWSNTQYMMWGGHKLPRTI 366  
QY 371 GGTNLNISTQGST-NTSINPVTLPFTSRDVRVYTESLAGLNFLTPQVNV-VPRVDFHKEV 428  
DB 367 GGTNLNISTQGST-NTSINPVTLPFTSRDVRVYTESLAGLNFLTPQVNV-VPRVDFHKEV 422  
QY 429 HPIASDNFYPGYAGIGTQLODSENELPPEATGQPNYESYSHRSLSHIGLISAS 481  
DB 423 --INPQNIYERGAITYSQYQGVGLFDSSETLPETTERPENYESYSHRSLSHIGLIIGN 480  
QY 482 HVKALVYSWTHRSADRTNTIENPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDIIRRTNG 541  
DB 481 TIRAFVYSWTHRSADRTNTIENPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDIIRRTNG 540  
QY 542 TFGDIRVNNPFAQRVVRIRVYASTTDLQPHSTINGKAINQGNFSAATMGEDELDTKVF 601  
DB 541 TFGDIRVNNPFAQRVVRIRVYASTTDLQPHSTINGKAINQGNFSAATMGEDELDTKVF 600  
QY 602 XTVGTTTPFSLDQVSTFTTCIAMNPFSSGNEVYIDRIEFVPPVEVYIEAYEPEKAQKVTA 661  
DB 601 RTAGFSTPFNLNAQSTFTLGAQFSN-QEYVIDRVEFVPAEVTFEAYDLERAQKAVNA 659

QY 662 LFTSTNPRGLKTDVYKHIDOVSNLVESLSDSEFFVLDKRELFELVYKAKOLHIERNM 718  
 DB 660 LFTSTNPRRLKTDVYKHIDOVSNVACLSDSEFFVLDKRELFELVYKAKOLHIERNL 716

RESULT 8  
 US-08-176-865-4  
 ; Sequence 4, Application US/08176865  
 ; Patent No. 5616319  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Donovan, William P.  
 ; APPLICANT: Tan, Yiping  
 ; APPLICANT: Jan, Christine S.  
 ; APPLICANT: Gonzalez Jr., Jose M.  
 ; TITLE OF INVENTION: BACILLUS THURINGIENSIS cryET4 AND cryET5  
 ; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS  
 ; NUMBER OF SEQUENCES: 5  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.  
 ; STREET: 1601 Market Street, 36th Floor  
 ; CITY: Philadelphia  
 ; STATE: Pennsylvania  
 ; COUNTRY: U.S.A.  
 ; ZIP: 19103  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent in Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/176.865  
 ; FILING DATE: 30-DEC-1993  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/100,709  
 ; FILING DATE: 29-JUL-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Egolf, Christopher  
 ; REGISTRATION NUMBER: 27633  
 ; REFERENCE/DOCKET NUMBER: 7205-49  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 215-757-1590  
 ; INFORMATION FOR SEQ ID NO: 4:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1229 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-176-865-4

Query Match 64.4%; Score 2415; DB 1; Length 1229;  
 Best Local Similarity 65.1%; Pred. No. 2.3e-207;  
 Matches 467; Conservative 91; Mismatches 141; Indels 18; Gaps 7;

QY 13 SSNAKVDKISDLSKN-ETDTELQ-NINHECLAKSEVENVEPVASSTIQTGTGAGKI 70  
 DB 7 NENEINALSIPVSNSTONLSFDARIEDSLCAEVNNDIPVVSASTVQTGINIAGRI 66

QY 71 LGTLGVPPAGVAGLYFGLGELWPKGNQWEIFMEHVEEIIINQKISTYARNKALDLKG 130  
 DB 67 LGVLGVPPAGVAGLYFGLGELWPKGNQWEIFMEHVEEIIINQKISTYARNKALDLKG 126

QY 131 LGDALVYHDSLEWGNVGNRNRARSVVKSYIALELMFVKLPSPFAVSGEEVPLPIYA 190  
 DB 127 LGRGVRVYQQALETWLNDRNRDARSIIILERYVALELDITTAIFLRNEEVPLLMVYA 186

QY 191 QAANLHLLLLLDASIFGKRWGLSSEISTFTYRQVERAGDYSHCVKWKYSTGLNNLRGTN 250  
 DB 187 QAANLHLLLLLDASIFGSEWGMASSDVQYQEQIRVTEEYSHCVQWYNTGLNNLRGTN 246

QY 251 AESWVRVYQQRDMTLVLDLVALFPSTQDQMYPIKTAQLTREYVYDALTGVHPHSFT 310

DB 247 AESWVRVYQQRDMTLVLDLVALFPSTQDQMYPIKTAQLTREYVYDALTGVHPHSFT 306  
 QY 311 STTWNNAPSFSAIEAAVVRNPHLLDFLEQVITYLLSRWSNTQYVWVWGGHKLERTI 370  
 DB 307 STWNNAPSFSAIEAAVVRNPHLLDFLEQVITYLLSRWSNTQYVWVWGGHKLERTI 366

QY 371 GGTLMISTQGST-NTSINPVTLPFTSRDVRVYTESLAGNLNLELTPQVNV-VRPVDVFWKFTV 428  
 DB 367 GGTLMISTQGST-NTSINPVTLPFTSRDVRVYTESLAGNLNLELTPQVNV-VRPVDVFWKFTV 422

QY 429 HPIASDNFYYPG-----YAGIGTQLODSNEILPEATGQPNVYESYSHRSLHIGLISAS 481  
 DB 423 --INPQTYERGATTYSQYQVGIQDFDSETELPETTERPNVYESYSHRSLHIGLIGN 480

QY 482 HVKALVYSWTHRSADRTNTIBPNSITQIPKAFNLSSGAAVVRGPGFTGGDILRRNTG 541  
 DB 481 TURAPVYSWTHRSADRTNTIBPNSITQIPKAFNLSSGAAVVRGPGFTGGDILRRNTG 540

QY 542 TFGDIRVNNPPFAQRYRVRIRYASTTDLQPHTSINGKAINQGNFSATMNGEDLDYKTF 601  
 DB 541 TFGDIRVNNPPFAQRYRVRIRYASTTDLQPHTSINGKAINQGNFSATMNGEDLDYKTF 600

QY 602 XTVGTTTFFSLDQSTTIGAWNPFSSGNEVYIDRIEFVPEVTVYEAEDYFEKAEKVTA 661  
 DB 601 RTAGFTSTFFNLNAGSTFTLGAQSPSN-QEYVIDRVEFVPAEVTFAEDYFEKAEKVTA 659

QY 662 LFTSTNPRGLKTDVYKHIDOVSNLVESLSDSEFFVLDKRELFELVYKAKOLHIERNM 718  
 DB 660 LFTSTNPRRLKTDVYKHIDOVSNVACLSDSEFFVLDKRELFELVYKAKOLHIERNL 716

RESULT 9  
 US-08-474-038-4  
 ; Sequence 4, Application US/08474038  
 ; Patent No. 5679343  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Donovan, William P.  
 ; APPLICANT: Tan, Yiping  
 ; APPLICANT: Jan, Christine S.  
 ; APPLICANT: Gonzalez Jr., Jose M.  
 ; TITLE OF INVENTION: BACILLUS THURINGIENSIS cryET4 AND cryET5  
 ; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS  
 ; NUMBER OF SEQUENCES: 5  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.  
 ; STREET: 1601 Market Street, 36th Floor  
 ; CITY: Philadelphia  
 ; STATE: Pennsylvania  
 ; COUNTRY: U.S.A.  
 ; ZIP: 19103  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent in Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/474,038  
 ; FILING DATE: 07-JUN-1995  
 ; CLASSIFICATION: 514  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/176,865  
 ; FILING DATE: 30-DEC-1993  
 ; APPLICATION NUMBER: US 08/100,709  
 ; FILING DATE: 29-JUL-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Egolf, Christopher  
 ; REGISTRATION NUMBER: 27633  
 ; REFERENCE/DOCKET NUMBER: 7205-49  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 215-757-1590  
 ; INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 1229 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-474-038-4

Query March 64.4%; Score 2415; DB 1; Length 1229;  
 Best Local Similarity 65.1%; Pred. No. 2.3e-207;  
 Matches 467; Conservative 91; Mismatches 141; Indels 18; Gaps 7;  
 QY 13 SSNAKVDKISTDSLKN-ETDIELQ-NINHEDCMKSEYENVEPFVSGASTIQTGIGIAGKI 70  
 DB 7 NENEINALSIPTVSNSTQWLSDPDARIEDSLCVAEVNNDIPFVSASTVQTGINIAGRI 66  
 QY 71 LGTLGVFPAGVASLYSFLIGELWPKGNQWEIEMHVEEIIINOKISTYARNKALTDLKG 130  
 DB 67 LGVLGVFPAGVASFYFLVGLWPSGRDPEIFLEHVEQILRQOVNTENTAIARLEG 126  
 QY 131 LGDALAVYHDSLSWVGNRNTRARSVVVKQSYIALELMFVQKLPSPAVSGEEVPLPIYA 190  
 DB 127 LGRGYRSYQQALETWLDNRNDARSIIILERYVALELDITTAIPLFRIRNEEVPLLMVYA 186  
 QY 191 QAAHLHLLLRDASIFGKXWGLSSSEISTFYNQVERAGDYSYHCVKWYSTGLNNLRGTN 250  
 DB 187 QAAHLHLLLRDASLFGSEWGNASSDVNQYQEQIRYTEESYHCVQWYNTGLNNLRGTN 246  
 QY 251 AESWRYNQRRDWTMLVLDLVALFPSYDTQWYPIKTTAQLTREYVTDALGTVHPHPSFT 310  
 DB 247 AESWRYNQRRDWTMLVLDLVALFPSYDTQWYPIKTTAQLTREYVTDALGTVHPHPSFT 306  
 QY 311 STWYNNNAPSFAIAEAAVVRNPHLLDFLEQVITYSLLSWSNTQYNNMMWGHKLFRFTI 370  
 DB 307 STWYNNNAPSFAIAEAAVVRNPHLLDFLEQVITYSLLSWSNTQYNNMMWGHKLFRFTI 366  
 QY 371 GGTINISTQGST-NTSINPVTLPFTSRDVRRTESLAGNLPLTQPVN-VPVDFHKKFVT 428  
 DB 367 GGTINTSTQGLTNNTSINPVTLPFTSRDVRRTESLAGNLPLTQPVN-VPVDFHKKFVT 422  
 QY 429 HPIASDNFYYPG-----YAGIGTQLQDSSENLPEATGQPNVSEYSHRLSHIGLISAS 481  
 DB 423 --INPQNIYERGATTYSQYQGVGIQLFDSSETLPETTERPNVSEYSHRLSHIGLIGN 480  
 QY 482 HVKALVYSWTHRSADRNTIENSTQIPLVKAFNLSGAAVVRGPGTGGDILRRNTNG 541  
 DB 481 TLRAVPYSWTHRSADRNTIENSTQIPLVKALNLSHGVTVVGGPFTGGDILRRNTNG 540  
 QY 542 TFGDIRVNIINPPAQRVVRIRYASTTDLQFHTSINGKALNQGNSFATMNGEDLDYKTF 601  
 DB 541 TFGDIRVNIINPPAQRVVRIRYASTTDLQFHTSINGKALNQGNSFATMNGEDLDYKTF 600  
 QY 602 XTGVFTTFFSLDLVQSTFTTCAMNFFSGNEVYIDRIEFVPEVITYEAEYDPEKAQEKVTA 661  
 DB 601 RTAGFSTPFNLAQSTFTLGAQSFNS-QEVIYIDRVEFVPAEVTFAEYDLERAQKAVNA 659  
 QY 662 LFTSTNRLKTDVYKHYDQVSNLVESLSDPEYDLDEKRELFEIVYAKOLHIERNM 718  
 DB 660 LFTSTNRLKTDVYKHYDQVSNLVESLSDPEYDLDEKRELFEIVYAKOLHIERNM 716

RESULT 10  
 US-08-779-046-4  
 Sequence 4, Application US/08779046  
 Patent No. 5834053  
 GENERAL INFORMATION:  
 APPLICANT: Donovan, William P.  
 APPLICANT: Tan, Yiping  
 APPLICANT: Jan, Christine S.  
 APPLICANT: Gonzalez Jr., Jose M.  
 TITLE OF INVENTION: BACILLUS THURINGIENSIS CRYET4 AND CRYETS  
 TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS  
 NUMBER OF SEQUENCES: 5  
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.  
 ADDRESSEE: Nadel  
 STREET: 1601 Market Street, 36th Floor  
 CITY: Philadelphia  
 STATE: Pennsylvania  
 COUNTRY: U.S.A.  
 ZIP: 19103  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/779,046  
 FILING DATE: 06-JAN-1997  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/100,709  
 FILING DATE: 29-JUL-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Egolf, Christopher  
 REGISTRATION NUMBER: 27633  
 REFERENCE/DOCKET NUMBER: 7205-49  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 215-757-1590  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1229 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-779-046-4

Query March 64.4%; Score 2415; DB 2; Length 1229;  
 Best Local Similarity 65.1%; Pred. No. 2.3e-207;  
 Matches 467; Conservative 91; Mismatches 141; Indels 18; Gaps 7;  
 QY 13 SSNAKVDKISTDSLKN-ETDIELQ-NINHEDCMKSEYENVEPFVSGASTIQTGIGIAGKI 70  
 DB 7 NENEINALSIPTVSNSTQWLSDPDARIEDSLCVAEVNNDIPFVSASTVQTGINIAGRI 66  
 QY 71 LGTLGVFPAGVASLYSFLIGELWPKGNQWEIEMHVEEIIINOKISTYARNKALTDLKG 130  
 DB 67 LGVLGVFPAGVASFYFLVGLWPSGRDPEIFLEHVEQILRQOVNTENTAIARLEG 126  
 QY 131 LGDALAVYHDSLSWVGNRNTRARSVVVKQSYIALELMFVQKLPSPAVSGEEVPLPIYA 190  
 DB 127 LGRGYRSYQQALETWLDNRNDARSIIILERYVALELDITTAIPLFRIRNEEVPLLMVYA 186  
 QY 191 QAAHLHLLLRDASIFGKXWGLSSSEISTFYNQVERAGDYSYHCVKWYSTGLNNLRGTN 250  
 DB 187 QAAHLHLLLRDASLFGSEWGNASSDVNQYQEQIRYTEESYHCVQWYNTGLNNLRGTN 246  
 QY 251 AESWRYNQRRDWTMLVLDLVALFPSYDTQWYPIKTTAQLTREYVTDALGTVHPHPSFT 310  
 DB 247 AESWRYNQRRDWTMLVLDLVALFPSYDTQWYPIKTTAQLTREYVTDALGTVHPHPSFT 306  
 QY 311 STWYNNNAPSFAIAEAAVVRNPHLLDFLEQVITYSLLSWSNTQYNNMMWGHKLFRFTI 370  
 DB 307 STWYNNNAPSFAIAEAAVVRNPHLLDFLEQVITYSLLSWSNTQYNNMMWGHKLFRFTI 366  
 QY 371 GGTINISTQGST-NTSINPVTLPFTSRDVRRTESLAGNLPLTQPVN-VPVDFHKKFVT 428  
 DB 367 GGTINTSTQGLTNNTSINPVTLPFTSRDVRRTESLAGNLPLTQPVN-VPVDFHKKFVT 422  
 QY 429 HPIASDNFYYPG-----YAGIGTQLQDSSENLPEATGQPNVSEYSHRLSHIGLISAS 481  
 DB 423 --INPQNIYERGATTYSQYQGVGIQLFDSSETLPETTERPNVSEYSHRLSHIGLIGN 480  
 QY 482 HVKALVYSWTHRSADRNTIENSTQIPLVKAFNLSGAAVVRGPGTGGDILRRNTNG 541  
 DB 481 TLRAVPYSWTHRSADRNTIENSTQIPLVKALNLSHGVTVVGGPFTGGDILRRNTNG 540

QY 542 TFGDIRVNINPPFAQRYVRIRYASTTDLQPHITSINGKAINQGNFSATMARGEDLDYKTF 601  
 DB 541 TFGDIRVNINPVSQRYVRIRYASTTDLQPHITSINGKAINQGNFSATMARGEDLDYKTF 600  
 QY 602 XTGVFTTFFSLDQSTFTICAMNPFSSGNEVYIDRIEFPVPEVTEYAEYDFEKAQEKVIA 661  
 DB 601 RTAGESTPFENLAGSTFTILGAQFSN-QEYVIDRVEFVPAEVTFEAEYDLERAQKAVNA 659  
 QY 662 LFTSTNPRGLKTDVKYHIDQVSNLVESLSEDEFYLDKRELFELVYKAKQLHIERNM 718  
 DB 660 LFTSTNPRRLKTDVTDYHIDQVSNVACLSEDEFCLDKRELFELVYKAKRLSDERNL 716  
 RESULT 11  
 US-08-881-340-4  
 ; Sequence 4, Application US/08881340  
 ; Patent No. 5942658  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Donovan, William P.  
 ; APPLICANT: Tan, Yeping  
 ; APPLICANT: Jany, Christine S.  
 ; APPLICANT: Gonzalez Jr., Jose M.  
 ; TITLE OF INVENTION: BACILLUS THURINGIENSIS cryET4 AND cryET5  
 ; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS  
 ; NUMBER OF SEQUENCES: 5  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.  
 ; ADDRESSEE: Nadel  
 ; STREET: 1601 Market Street, 36th Floor  
 ; CITY: Philadelphia  
 ; STATE: Pennsylvania  
 ; COUNTRY: U.S.A.  
 ; ZIP: 19103  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/881,340  
 ; FILING DATE: 24-JUN-1997  
 ; CLASSIFICATION: 424  
 ; PRIORITY APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/100,709  
 ; FILING DATE: 29-JUL-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Egolf, Christopher  
 ; REGISTRATION NUMBER: 27633  
 ; REFERENCE/DOCKET NUMBER: 7205-49  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 215-757-1590  
 ; INFORMATION FOR SEQ ID NO: 4:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1229 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-881-340-4  
 Query Match 64.4%; Score 2415; DB 2; Length 1229;  
 Best Local Similarity 65.1%; Pred. No. 2.3e-207;  
 Matches 467; Conservative 91; Mismatches 141; Indels 18; Gaps 7;  
 QY 13 SSNAKVDKISTSLKN-ETDIELQ-NINHEBCLKXSEVENVEPVASSTQTGTGIGAKI 70  
 DB 7 NENEINALSITVSNPSTQNLSPDARIEDSLCVAEVNNDPVSASTVGTGINIAGRI 66  
 QY 71 LGLTGVPPAGVVASISYFSLGELWPKGNQWEIFMEHVEEIIINQISTYARNKALTDLKG 130  
 DB 67 LGVLGVPPAGQLASFSYFLVGLWPSGRDPWEIFLHVQLIRQVQVNTENTTAIRLEG 126  
 QY 131 LGDALLVTHDSLESVWGNHNTNRAISVYKSVIALELMFVOKLSPAVSGEEVPLLIYA 190

DB 127 LGRGYSYQOALLETWLDNRNDARSIIILERYVALELDITTAIPLFIRNBEVPLLMVYA 186  
 QY 191 QANLHLLLLRLDASIFGKEMGLSSSEISTFYNRQVERAGDYSYHCVKWSYGLNLRGTN 250  
 DB 187 QANLHLLLLRLDASIFGSEWGNASSDVNQYQEQIRYTEEYNSHNHCQWYNTGLNLRGTN 246  
 QY 251 ASWVYVQCFRDMTLMVLDLVALFPSTDTOMYPIKTTAQLTREYVTDATGIVPHPSFT 310  
 DB 247 ASWLYVQCFRDLTILGVLDLVALFPSTDTYTPINTSAQLTREYVTDPIGRTNAPSFA 306  
 QY 311 STTWYNNAPSAIEAAVVRNPHLLDFLEQVTVYLSLSRWSNTQYMMWGHKLEPFTI 370  
 DB 307 STWYNNAPSAIEAAIFRPHLLDFPEQLTIYSASSRWSSTQHMVYVWGHRLNFPPI 366  
 QY 371 GGTALISTOGST-NTSINPVTLPPTSVDYRTPESLAGLNLFLTQPVN-VPRVDFHWKFTV 428  
 DB 367 GGTALISTOGLTNNISINPVTLPPTSVDYRTPESLAGLNLFLTQPVNVPWAFNF- 422  
 QY 429 HPIASDNFYPG-----YAGIGTQLQDSNELPEATGQPNYESYSHRLSHIGLISAS 481  
 DB 423 --INPQNIYERGATTYSQPYQVGIQLFDESELPETTERPNYESYSHRLSHIGLIIEN 480  
 QY 482 HVKALVYTHSADRTNIBNSITQPLVKAFNLSSGAAVVRGPGTGGDILRTWTG 541  
 DB 481 TLRAPYVYTHSADRTNITGNRITQPLVKALNLHSGVTVVGGPGTGGDILRTWTG 540  
 QY 542 TFGDIRVNINPPFAQRYVRIRYASTTDLQPHITSINGKAINQGNFSATMARGEDLDYKTF 601  
 DB 541 TFGDIRVNINPVSQRYVRIRYASTTDLQPHITSINGKAINQGNFSATMARGEDLDYKTF 600  
 QY 602 XTGVFTTFFSLDQSTFTICAMNPFSSGNEVYIDRIEFPVPEVTEYAEYDFEKAQEKVIA 661  
 DB 601 RTAGESTPFENLAGSTFTILGAQFSN-QEYVIDRVEFVPAEVTFEAEYDLERAQKAVNA 659  
 QY 662 LFTSTNPRGLKTDVKYHIDQVSNLVESLSEDEFYLDKRELFELVYKAKQLHIERNM 718  
 DB 660 LFTSTNPRRLKTDVTDYHIDQVSNVACLSEDEFCLDKRELFELVYKAKRLSDERNL 716  
 RESULT 12  
 US-08-448-170-10  
 ; Sequence 10, Application US/08448170  
 ; Patent No. 5723758  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Payne, Jewel  
 ; APPLICANT: Cummings, David A.  
 ; APPLICANT: Cannon, Raymond J.C.  
 ; APPLICANT: Narva, Kenneth E.  
 ; APPLICANT: Stelman, Steve  
 ; TITLE OF INVENTION: No. 5723758el Bacillus thuringiensis Isolate Denoted  
 ; TITLE OF INVENTION: B.t. PS158C2, Active Against Lepidopteran Pests, and Genes  
 ; TITLE OF INVENTION: Encoding Lepidopteran-Active Toxins  
 ; NUMBER OF SEQUENCES: 10  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: David R. Saliwanchik  
 ; STREET: 2421 N.W. 41st Street, Suite A-1  
 ; CITY: Gainesville  
 ; STATE: Florida  
 ; COUNTRY: USA  
 ; ZIP: 32606  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/448,170  
 ; FILING DATE:  
 ; CLASSIFICATION: 424  
 ; PRIORITY APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/069,902  
 ; FILING DATE: 01-JUNE-1993  
 ; CLASSIFICATION: 424

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/759,247
; FILING DATE: 13-SEPT-1991
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: M/S 102D.C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 488 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-448-170-10

Query Match 61.9%; Score 2319; DB 1; Length 488;
Best Local Similarity 89.3%; Pred. No. 2.1e-199;
Matches 444; Conservative 13; Mismatches 30; Indels 10; Gaps 2;

QY 1 MKLNQDKHQSFSNAKVDKISTDSLKNETDIELQINHEDECKMSEYENVEPVSASTI 60
DB 1 MKSKNQNHQSLSNNAVDKNTGSLNNTNTELQNFH-----EGIEPVSVSTI 51
QY 61 QTGIGIAGKILGTGVPPAGQVASYLSPILGELMPKQKQWEIFMEHVEEIIINOKISTYA 120
DB 52 QTGIGIVGKILGNLGVPPAGQVASYLSPILGELMPKQKQWEIFMEHVEEIIINOKISTYA 111
QY 121 RNKALTDLKGDLAVYHDSLEWGNRNNTARSVVKSOYIALELMFVKQLPSFAVSG 180
DB 112 RNKALADLKGDLAVYHDSLEWNIENRNTTRSVVKSQYITLBMFVQSLPSFAVSG 171
QY 181 EEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVRAGDYSYHCVKWS 240
DB 172 EEVPLPIYAQAANLHLLLRDASIFGKXWGLSDSEISTFYNRQSGKSEYSDHCWKYN 231
QY 241 TGLNLRGTVNAESWVRVYQFQERDMLVLDLVALFBSYDTOMYPIKTTAQLTREYVTDI 300
DB 232 TGLNRLMGNNAESWVRVYQFQERDMLVLDLVALFBSYDTOMYPIKTTAQLTREYVTDI 291
QY 301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYNNMW 360
DB 292 GTVHPHPSFTSTWYNNNAPSFTIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYNNMW 351
QY 361 GGHKLEFRTTIGTLINISTQGSTNTSINPVTLPFTSRDVRVYTESLAGINLFLTPQVNV 419
DB 352 GGHKLEFRTTIGTLINISTQGSTNTSINPVTLPFTSRDVRVYTESLAGINLFLTPQVNGVR 411
QY 420 VDFHWKVTPIASDNFYYPGYAGIGTOLQDSNELPPEATGQPNYESYSHRLSHIGLIS 479
DB 412 VDFHWKVTPIASDNFYYPGYAGIGTOLQDSNELPPEATGQPNYESYSHRLSHIGLIS 471
QY 480 ASHKALVYSWTHRSAD 496
DB 472 ASHKALVYSWTHRSAD 488

RESULT 13
US-08-961-803-10
; Sequence 10, Application US/08961803
; Patent No. 6150589
; GENERAL INFORMATION:
; APPLICANT: Payne, Jewel
; APPLICANT: Cummings, David A.
; APPLICANT: Cannon, Raymond J.C.
; APPLICANT: Narva, Kenneth E.
; APPLICANT: Stelman, Steve
; TITLE OF INVENTION: No. 6150589e1 Bacillus thuringiensis Isolate Denoted
; TITLE OF INVENTION: B.t. PSI58C2, Active Against Lepidopteran Pests, and Genes

```

```

; TITLE OF INVENTION: Encoding Lepidopteran-Active Toxins
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jay M. Sanders
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,803
; FILING DATE: 31-OCT-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/069,902
; FILING DATE: 01-JUNE-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/759,247
; FILING DATE: 13-SEPT-1991
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/448,170
; FILING DATE: 23-MAY-1995
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Sanders, Jay M.
; REGISTRATION NUMBER: 39,355
; REFERENCE/DOCKET NUMBER: M/S 102DCD1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 488 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-961-803-10

Query Match 61.9%; Score 2319; DB 3; Length 488;
Best Local Similarity 89.3%; Pred. No. 2.1e-199;
Matches 444; Conservative 13; Mismatches 30; Indels 10; Gaps 2;

QY 1 MKLNQDKHQSFSNAKVDKISTDSLKNETDIELQINHEDECKMSEYENVEPVSASTI 60
DB 1 MKSKNQNHQSLSNNAVDKNTGSLNNTNTELQNFH-----EGIEPVSVSTI 51
QY 61 QTGIGIAGKILGTGVPPAGQVASYLSPILGELMPKQKQWEIFMEHVEEIIINOKISTYA 120
DB 52 QTGIGIVGKILGNLGVPPAGQVASYLSPILGELMPKQKQWEIFMEHVEEIIINOKISTYA 111
QY 121 RNKALTDLKGDLAVYHDSLEWGNRNNTARSVVKSOYIALELMFVKQLPSFAVSG 180
DB 112 RNKALADLKGDLAVYHDSLEWNIENRNTTRSVVKSQYITLBMFVQSLPSFAVSG 171
QY 181 EEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVRAGDYSYHCVKWS 240
DB 172 EEVPLPIYAQAANLHLLLRDASIFGKXWGLSDSEISTFYNRQSGKSEYSDHCWKYN 231
QY 241 TGLNLRGTVNAESWVRVYQFQERDMLVLDLVALFBSYDTOMYPIKTTAQLTREYVTDI 300
DB 232 TGLNRLMGNNAESWVRVYQFQERDMLVLDLVALFBSYDTOMYPIKTTAQLTREYVTDI 291
QY 301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYNNMW 360
DB 292 GTVHPHPSFTSTWYNNNAPSFTIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYNNMW 351

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361 GGHKLEFETIGTGLNISTQSTNTSINPVTLPFTSRDVRVRESLAGNLFLOPVN-VPR 419  
 352 GGHKLEFETIGTGLNISTQSTNTSINPVTLPFTSRDVRVRESLAGNLFLOPVN-VPR 411  
 420 VDPHMKFVTHPIASDNFYFPGYAGIGTQLODSENELPPEATGQPNYSYSHRLSHIGLIS 479  
 412 VDPHMKFVTHPIASDNFYFPGYAGIGTQLODSENELPPEATGQPNYSYSHRLSHIGLIS 471  
 480 ASHVKALVSWTHRSAD 496  
 472 ASHVKALVSWTHRSAD 488

RESULT 14  
 US-07-951-715A-7  
 ; Sequence 7, Application US/07951715A  
 ; Patent No. 5625136

GENERAL INFORMATION:  
 APPLICANT: Koziel, Michael G.  
 APPLICANT: Desai, Nalini M.  
 APPLICANT: Lewis, Kelly S.  
 APPLICANT: Kramer, Vance C.  
 APPLICANT: Warren, Gregory W.  
 APPLICANT: Evola, Stephen V.  
 APPLICANT: Crossland, Lyle D.  
 APPLICANT: Wright, Martha S.  
 APPLICANT: Merlin, Ellis J.  
 APPLICANT: Launis, Karen L.  
 APPLICANT: Rothstein, Steven J.  
 APPLICANT: Bowman, Cindy G.  
 APPLICANT: Dawson, John L.  
 APPLICANT: Dunder, Erik M.  
 APPLICANT: Pace, Gary M.  
 APPLICANT: Suttie, Janet L.  
 TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
 TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE  
 NUMBER OF SEQUENCES: 94  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: CIBA-GEIGY Corporation  
 STREET: 7 Skyline Drive  
 CITY: Hawthorne  
 STATE: New York  
 COUNTRY: USA  
 ZIP: 10532

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.30B  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/07/951,715A  
 FILING DATE: 25-SEP-1992  
 CLASSIFICATION: 800  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/772,027  
 FILING DATE: 04-OCT-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Spriull, W. Murray  
 REGISTRATION NUMBER: 32,943  
 REFERENCE/DOCKET NUMBER: S-18805/A/CSC 1577/CIP  
 TELEPHONE: (919) 541-8615  
 TELEFAX: (919) 541-8689  
 INFORMATION FOR SEQ ID NO: 7:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1207 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-07-951-715A-7

Query Match 59.6%; Score 2236; DB 1; Length 1207;

Best Local Similarity 63.9%; Pred. No. 2.6e-191;  
 Matches 439; Conservative 78; Mismatches 156; Indels 14; Gaps 6;  
 QY 40 EBLCKMSEVENPEFVSASTIQTGIGIAGKILGTGVFFAGQVSLYFIFLGLWPKGKN 99  
 Db 10 EBLCKIAGNNDPVSASTVQTGINIAGRILGVGVFAQLASFYGFVLGLWPKGRD 69  
 QY 100 QWEIFMEHVEEINQKISTYARNKALTDLKGIDALAVYHDSLSGWNRRNNTARSVVK 159  
 Db 70 QWEIFLEHVEQLINQITENARNTALARLOGLGDSFRAYQCSLEDWLENRDADRSTRVLY 129  
 QY 160 SOVIALELMFVKLPSPVSGSEVPLLLPIYAAANLHLLLRDASIFGKWLGSSETST 219  
 Db 130 TQYIALELDLFLNAMPFLAIRNQEVFLMVYAAANLHLLLRDASLGFSEGLTSQETOR 189  
 QY 220 FYNROVERAGDYSYHCVKWYSTGLNNLRTGNAESWVRYNQFRDNTLMLVLDLVALFPSSYD 279  
 Db 190 YVERQVERTEDYDYCVIEWYNTGLNSLRTGNAASWVRYNQFRDNTLGLVLDLVALFPSSYD 249  
 QY 280 TOMYPIKTTAOLTRVYTTDAICTVHPHPSFTSTWYNNNAPSFAIEAAVVENPHLLDFL 339  
 Db 250 TRTYPINTSAQLTREVYTTDAIGAT--GVNMAWMYNNNAPSFAIEAAAIRSPHLLDFL 307  
 QY 340 EQWTIYSLLSRWSNTQYMMNGHKLBFRTTIGTLNISTQSTNTSINPVTLPFTSRDVI 399  
 Db 308 EQLTIFSASSRWSNTRHMTYWRGHTIQSRPIGGGLNTSTHGATNTSINPVTLPASRDVI 367  
 QY 400 RTESLAGNLF--LTQPNV--VPVDFHMKFVTHP-----IASDNFYFPGYAGIGTQLODS 451  
 Db 368 RTESYAGVLLWGIYLEPIHGVPTVRNF--TNPNQISDRGTANYQP--YESPGIQLKDS 423  
 QY 452 ENELPPEATGQPNYSYSHRLSHIGLISASHVKALVSWTHRSADRTNTIFPNSITQIPL 511  
 Db 424 ETELPEETERENYSYSHRLSHIGLILQSRVNVVSVWTHRSADRTNTIGNRIQIPM 483  
 QY 512 VKAFNLSGAAVVRGPGTGGDILRTNTGTGDIRVNNPFPFQRYVRIRYASTTDLQ 571  
 Db 484 VKASELPQGTTVVRGPGTGGDILRTNTGGFGPIRVTVNGPLTQRYRIGFRYASTVDVD 543  
 QY 572 FHTSINGKAINQGNFSAWNRGSDLDYKTEVTGFTTFLSLDQVSTFTICAMNPPSSGNE 631  
 Db 544 FVSRGGTTVNNFRRLTNVSGDELYKGNFVRRAFTTFTTQIQTQDIIRTSIQGLSGNGE 603  
 QY 632 VYIDRIEFVPEVTEYAEYDFEKAQKVYALFTSTNPRGLKTDVKDXXHIDQVSNLVESLS 691  
 Db 604 VYIDKIEIIPVTATFEAEYDLERAQEAVALFTNTNPRRLKTDVTDYHIDQVSNLVACLS 663  
 QY 692 DEFYLDKRELEPEIVKYAKQLHIERNM 718  
 Db 664 DEFCLDKRELEKVKYAKRUSDERNL 690

RESULT 15  
 US-08-459-448A-7  
 ; Sequence 7, Application US/08459448A  
 ; Patent No. 5859336  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Koziel, Michael G.  
 ; APPLICANT: Desai, Nalini M.  
 ; APPLICANT: Lewis, Kelly S.  
 ; APPLICANT: Kramer, Vance C.  
 ; APPLICANT: Warren, Gregory W.  
 ; APPLICANT: Evola, Stephen V.  
 ; APPLICANT: Crossland, Lyle D.  
 ; APPLICANT: Wright, Martha S.  
 ; APPLICANT: Merlin, Ellis J.  
 ; APPLICANT: Launis, Karen L.  
 ; APPLICANT: Rothstein, Steven J.  
 ; APPLICANT: Bowman, Cindy G.  
 ; APPLICANT: Dawson, John L.  
 ; APPLICANT: Dunder, Erik M.  
 ; APPLICANT: Pace, Gary M.  
 ; APPLICANT: Suttie, Janet L.

; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
 ; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE  
 ; NUMBER OF SEQUENCES: 94  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: No. 5859336artis Corporation  
 ; STREET: Patent & Trademark Dept., 520 White Plains  
 ; STREET: Rd., POB 2005  
 ; CITY: Tarrytown  
 ; STATE: New York  
 ; COUNTRY: USA  
 ; ZIP: 10591-9005  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/459,448A  
 ; FILING DATE: 02-JUN-1995  
 ; CLASSIFICATION: 800  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/951,715  
 ; FILING DATE: 25-SEP-1992  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/772,027  
 ; FILING DATE: 04-OCT-1991  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Pace, Gary M.  
 ; REGISTRATION NUMBER: 40403  
 ; REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV4  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (919)541-8582  
 ; TELEFAX: (919)541-8689  
 ; INFORMATION FOR SEQ ID NO: 7:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1207 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-459-448A-7

Query Match 59.6%; Score 2236; DB 2; Length 1207;  
 Best Local Similarity 63.9%; Pred. No. 2.6e-191;  
 Matches 439; Conservative 79; Mismatches 156; Indels 14; Gaps 6;

Qy	40	EDCLKXSEYENVPFVSASTIQTGIGIAGKILGTGVPPAGQVASYSLGELWPKGN	99
Db	10	EDSLCIAEGNNIDPFVSASTVQTGINIAGILGLVGVPPAGQLASYSFLVGLWPKGRD	69
Qy	100	QWEIFMEHVEEINQKISTYARKALTDLKLGDALAVYHDSLESWVGNRNNTRASSVVK	159
Db	70	QWEIFLEHVEQLNQITENARNTALARLQGLGDSFRAYQQSLDLEWLRDARTSVLY	129
Qy	160	SOYIALELMFVKQLPSPFVSGSEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEIST	219
Db	130	QYIALELDPLNAMPFAIRNQEVPLLMVYQAANLHLLLRDASLFGSEFGLTSQEIQR	189
Qy	220	FYNQVERAGDYSVHCVKYKYSTGLNNLRGTNAESWRYNQFRDMLVLDLVALPSPYD	279
Db	190	YVERQVERTRDYSYDCEVWYNTGLNSLRGTNAASWRYNQFRDLTLGLVLDLVALPSPYD	249
Qy	280	QMPYIKTTAQLREVYVTDGIVGHPHPSFTSTWYNNAPSATAEAAVVRNPHLLDEL	339
Db	250	TRYPIINTSALLREVYVTDGAT--GVNNASWYNNAPSATAEAAIRSPHLLDEL	307
Qy	340	EQVTYSLLSRWNTQYNNMWGKLEFRTIGGLTNIQTGSTNTSINPVTLPFTSRDXY	399
Db	308	EQLTIFGASRSEWNTHTYWRGHTIQSRPIGGGLNTSTHGAINTSINPVTLPFASRDYV	367
Qy	400	RTESLAGLNLF--LTQPVN-VPRVDFHWKEVTHP-----IASDNFYYPGAGIGTQLQDS	451
Db	368	RTESYAGVLLWGLYLEPIHGVPVTRFNF---TNPQNISRGTANYSCP-YESPGLQLKDS	423

Qy	452	ENELPPEATGQPNYESYSHRLSHIGLISASHVKALVYSWTHRSADRTNTIEPNSITQIPL	511
Db	424	ETELPPEATTERDNYESYSHRLSHIGIILQSKVNVFVYSWTHRSADRTNTIGNRIQIPM	483
Qy	512	VKAFNLSSGAAVVRGPGTGGDILRRNTGTGDIRVNNINPPFAORYBYRYASTTDLQ	571
Db	484	VKASELPQGTTVVRGPGTGGDILRRNTGTGDIRVNNINPPFAORYBYRYASTVDFD	543
Qy	572	FHTSINGKAINQGNFSAIATNRGEDIYKTFXTVGTTPFTFSLLDVQSTFTIGAWNFSSGNE	631
Db	544	PFVSRGGTTVANNFRFLRTMWSGDELKYGNFVRRAPTFTFTQIQDIIRTSIQGLSGNGE	603
Qy	632	VYIDRIEFVPEVTVYEAEDPEKAEKYTALFTSNRGLKTDYKDYHIDQVSNLVESLS	691
Db	604	VYIDKIEIIPVTATFEAYDILERAQEAVALFTNPRRLKTDVTDYHIDQVSNLVACL	663
Qy	692	DEFYLDKRELFELVYKAKQLHIERNM	718
Db	664	DEFCLDKRELEKVKYAKRLSDERNL	690

Search completed: October 28, 2004, 18:34:11  
 Job time : 26.3033 secs





GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 28, 2004, 17:52:12 ; Search time 98.4365 Seconds  
(without alignments)  
4202.652 Million cell updates/sec

Title: US-10-019-823B-55

Perfect score: 3760

Sequence: 1 MKLKNQDKQSFSSNAKVDK.....KRELPEIVKYAKQLHIERNM 719

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 02.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3760	100.0	719	1 C1IA_BACTK	Q45752 bacillus th
2	3760	100.0	719	2 06X181	Q6x181 bacillus th
3	3760	100.0	719	2 AAP86782	Aap86782 bacillus
4	3755	99.9	719	2 Q93NJ5	Q93nj5 bacillus th
5	3754	99.8	719	2 O85796	O85796 bacillus th
6	3752	99.8	719	2 CAC85964	Cac85964 bacillus
7	3625	96.4	719	2 O8KY61	O8ky61 bacillus th
8	3551	94.4	719	2 Q9F0P8	Q9f0p8 bacillus th
9	3520	93.6	719	1 C1IB_BACTE	Q45709 bacillus th
10	3397	90.3	719	1 C1ID_BACTU	Q9xd11 bacillus th
11	3377	89.8	719	1 C1IC_BACTU	O87404 bacillus th
12	2446.5	65.1	1229	1 C1BB_BACTU	Q45739 bacillus th
13	2446.5	65.1	1233	1 C1BC_BACTM	Q45774 bacillus th
14	2278.5	60.6	1228	2 Q93T75	Q93t75 bacillus th
15	2277.5	60.6	1228	1 C1BA_BACTK	P05317 bacillus th
16	2269.5	60.4	1228	2 Q93NM5	Q93nm5 bacillus th
17	2195.5	58.4	849	2 O6PYW8	O6pyw8 bacillus th
18	2195.5	58.4	849	2 AAS93797	Aas93797 bacillus
19	2195.5	58.4	1227	1 C1BE_BACTU	O85805 bacillus th
20	2112.5	56.2	1231	2 Q8KNV2	Q8kny2 bacillus th
21	2107.5	56.1	1231	1 C1BD_BACTZ	Q92475 bacillus th
22	1988.5	52.9	1215	1 C1K3_BACTM	Q45715 bacillus th
23	1904	50.6	381	2 Q45740	Q45740 bacillus th
24	1670.5	44.4	1157	1 C8AA_BACUK	Q45740 bacillus th
25	1658	44.1	1144	2 O8KZL7	O8kz17 bacillus th
26	1492	39.7	1157	1 C9CA_BACTO	Q45733 bacillus th
27	1486.5	39.5	1169	1 C8BA_BACUK	Q45705 bacillus th
28	1482.5	39.4	1166	1 C1GA_BACTU	Q45746 bacillus th
29	1478	39.3	1167	1 C1UB_BACTU	Q45738 bacillus th
30	1477	39.3	1169	1 C1FB_BACTM	O66377 bacillus th
31	1471	39.1	1174	2 Q45749	Q45749 bacillus th

## RESULT 1

### C1IA\_BACTK

ID C1IA\_BACTK STANDARD; PRT; 719 AA.

AC Q45752; P71092; Q45750; Q45751; Q45756;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DE Pesticidal crystal protein cryIIa (insecticidal delta-endotoxin)

DE CryII(a) (Crystalline entomocidal protoxin) (81 kDa crystal protein).

GN Name=cryIIa; Synonyms=cryII(a), cryV, cryVI, CGCryV;

OS Bacillus thuringiensis (subsp. kurstaki).

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

OX NCBI\_TaxID=29339;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=DSIR732;

RX MEDLINE=92298009; PubMed=8517758;

RA Gleave A.P., Williams R., Hedges R.J.;

RT "Screening by polymerase chain reaction of Bacillus thuringiensis

RT serotypes for the presence of cryV-like insecticidal protein genes and

RT characterization of a cryV gene cloned from B. thuringiensis, subsp.

RT kurstaki.";

RL Appl. Environ. Microbiol. 59:1683-1687(1993).'

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=JHCC4835;

RX MEDLINE=92269582; PubMed=1588820;

RA Taylor R., Tippet J., Gibb G., Pells S., Pike D., Jordan L., Ely S.;

RT "Identification and characterization of a novel Bacillus thuringiensis

RT delta-endotoxin entomocidal to coleopteran and lepidopteran larvae.";

RL Mol. Microbiol. 6:1211-1217(1992).

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=HD-1;

RX MEDLINE=95314293; PubMed=7793960;

RA Shin B.-S., Park S.-H., Choi S.-K., Koo B.T., Lee S.T., Kim J.I.;

RT "Distribution of cryV-type insecticidal protein genes in Bacillus

RT thuringiensis and cloning of cryV-type genes from Bacillus

RT thuringiensis subsp. kurstaki and Bacillus thuringiensis subsp.

RT entomocidus.";

RL Appl. Environ. Microbiol. 61:2402-2407(1995).

RN [4]

RP SEQUENCE FROM N.A.

RC STRAIN=AB88;

RX MEDLINE=96178985; PubMed=8606196;

RA Kostichka K., Warren G.W., Mullins M., Mullins A.D., Palekar N.V.,

RA Craig J.A., Kozel M.G., Estruch J.J.;

RT "Cloning of a cryV-type insecticidal protein gene from Bacillus

RT thuringiensis; the cryV-encoded protein is expressed early in

RT stationary phase.";

RL J. Bacteriol. 178:2141-2144(1996).

RN [5]

RP SEQUENCE FROM N.A.

RC STRAIN=61;

RA Selvapandian A.; Bhatnagar R.K.;  
 RT "Isolation, cloning and expression of cryv gene.";  
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
 CC !- FUNCTION: Promotes colloidomotic lysis by binding to the midgut  
 CC epithelial cells of certain coleopteran and lepidopteran species.  
 CC Active on Plutella xylostella and Bombyx mori.  
 CC !- DEVELOPMENTAL STAGE: The crystal protein is produced during  
 CC sporulation and is accumulated both as an inclusion and as part of  
 CC the spore coat.  
 CC !- MISCELLANEOUS: Toxic segment of the protein is located in the N-  
 CC terminus.  
 CC !- SIMILARITY: Belongs to the delta endotoxin family.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL; M98544; AAA22354.1; -;  
 CC EMBL; X52821; CAA44633.1; -;  
 CC EMBL; L36338; AAC36999.1; -;  
 CC EMBL; L49391; AAB00958.1; -;  
 CC EMBL; Y08920; CAA70124.1; -;  
 CC PIR; I39815; I39815;  
 CC PIR; S25383; S25383.  
 CC HSGP; P02965; ICYI.  
 CC InterPro; IPR001178; Endotoxin.  
 CC InterPro; IPR005638; endotoxin C.  
 CC InterPro; IPR005639; endotoxin N.  
 CC InterPro; IPR008979; Gal bind Like.  
 CC Pfam; PF03944; Endotoxin\_C; 1.  
 CC Pfam; PF00555; Endotoxin\_M; 1.  
 CC Pfam; PF03945; Endotoxin\_N; 1.  
 CC Sporulation; Toxin.  
 KW VARIANT 159 159 K -> R (in strain 61).  
 FT VARIANT 233 233 D -> Y (in strain JHCC4835 and strain HD-  
 FT  
 FT VARIANT 443 443 A -> V (in strain AB88).  
 FT VARIANT 711 712 KQ -> NE (in strain HD-1 and strain 61).  
 FT SEQUENCE 719 AA; 81216 MW; 3627ESA6C25DAFFS CRC64;  
 Query Match 100.0%; Score 3760; DB 1; Length 719;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-253;  
 Matches 719; Conservative -0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MKLNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMSYENVEPVSASTI 60  
 DB 1 MKLNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMSYENVEPVSASTI 60  
 QY 61 QTGIGIAGKILGTGLVPPAGQVASYLSFILGELWPKGNQWEIPEHVEEIIINQKISTYA 120  
 DB 61 QTGIGIAGKILGTGLVPPAGQVASYLSFILGELWPKGNQWEIPEHVEEIIINQKISTYA 120  
 QY 121 RNKALTDLKGLDALAVYHDSLESWGNRNTRARSVVKVQYIALELMFVKQLPSFAVSG 180  
 DB 121 RNKALTDLKGLDALAVYHDSLESWGNRNTRARSVVKVQYIALELMFVKQLPSFAVSG 180  
 QY 191 BEVPLLPPIYAQAANLHLLLDASIFGKEWGLSSSEISTFNQVERAGDYSCHCVKWS 240  
 DB 191 BEVPLLPPIYAQAANLHLLLDASIFGKEWGLSSSEISTFNQVERAGDYSCHCVKWS 240  
 QY 241 TGLNNLRGTNAESWVRYNQFRDMLMVLVDVALPSPSYDTQMPYIKTTAQLTREVYTDI 300  
 DB 241 TGLNNLRGTNAESWVRYNQFRDMLMVLVDVALPSPSYDTQMPYIKTTAQLTREVYTDI 300  
 QY 301 GTVHPHPSFTSTTWNNAFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMW 360  
 DB 301 GTVHPHPSFTSTTWNNAFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMW 360  
 QY 361 GGHKLEFRTIGTLNISTQGSTNTSINPVLPTFSRDVYRTESLAGLNLFLTQPVNGVPR 420

DB 361 GGHKLEFRTIGTLNISTQGSTNTSINPVLPTFSRDVYRTESLAGLNLFLTQPVNGVPR 420  
 QY 421 VDFHWKVFTHPIASDNFYYPYAGIGTQDSENELPEATQPNYSYSHRLSHIGLIS 480  
 DB 421 VDFHWKVFTHPIASDNFYYPYAGIGTQDSENELPEATQPNYSYSHRLSHIGLIS 480  
 QY 481 ASHVKALVYVTHRSADRTNIENSIITQIPLVKAFLNLSGAAVVRGPGFTGGDILRTN 540  
 DB 481 ASHVKALVYVTHRSADRTNIENSIITQIPLVKAFLNLSGAAVVRGPGFTGGDILRTN 540  
 QY 541 TCTFGDIRVNINPPPAQRYRIRYASTDLOFHTSINGKAINQNTSATNWRGDLDYK 600  
 DB 541 TCTFGDIRVNINPPPAQRYRIRYASTDLOFHTSINGKAINQNTSATNWRGDLDYK 600  
 QY 601 TFRTVGFTTPSFILDVQSTFTIGAWNFGSGNEVYIDRIEFVPEVTVYEAEDFKAQEKV 660  
 DB 601 TFRTVGFTTPSFILDVQSTFTIGAWNFGSGNEVYIDRIEFVPEVTVYEAEDFKAQEKV 660  
 QY 661 TALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDEFYLDKEKELFEIVKYAKQLHIERNM 719  
 DB 661 TALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDEFYLDKEKELFEIVKYAKQLHIERNM 719  
 RESULT 2  
 Q6X181 PRELIMINARY; PRT; 719 AA.  
 AC Q6X181;  
 DT 05-JUL-2004 (TREMELrel. 27, Created)  
 DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)  
 DE CryII.  
 OS Name=cryII;  
 OS Bacillus thuringiensis.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1428;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Espindola R., Lemos M.V.F., Lemos E.G.M., Sena J.A.D.;  
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
 DB EMBL; AY262167; AAP86782.1; -;  
 DR InterPro; IPR001178; Endotoxin.  
 DR InterPro; IPR005638; endotoxin C.  
 DR InterPro; IPR005639; endotoxin N.  
 DR InterPro; IPR008979; Gal\_bind\_Like.  
 DR Pfam; PF03944; Endotoxin\_C; 1.  
 DR Pfam; PF00555; Endotoxin\_M; 1.  
 DR Pfam; PF03945; Endotoxin\_N; 1.  
 SQ SEQUENCE 719 AA; 81216 MW; 3627ESA6C25DAFFS CRC64;  
 Query Match 100.0%; Score 3760; DB 2; Length 719;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-253;  
 Matches 719; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MKLNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMSYENVEPVSASTI 60  
 DB 1 MKLNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMSYENVEPVSASTI 60  
 QY 61 QTGIGIAGKILGTGLVPPAGQVASYLSFILGELWPKGNQWEIPEHVEEIIINQKISTYA 120  
 DB 61 QTGIGIAGKILGTGLVPPAGQVASYLSFILGELWPKGNQWEIPEHVEEIIINQKISTYA 120  
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 DB 121 RNKALTDLKGLDALAVYHDSLESWGNRNTRARSVVKVQYIALELMFVKQLPSFAVSG 180  
 QY 181 BEVPLLPPIYAQAANLHLLLDASIFGKEWGLSSSEISTFNQVERAGDYSCHCVKWS 240  
 DB 181 BEVPLLPPIYAQAANLHLLLDASIFGKEWGLSSSEISTFNQVERAGDYSCHCVKWS 240  
 QY 241 TGLNNLRGTNAESWVRYNQFRDMLMVLVDVALPSPSYDTQMPYIKTTAQLTREVYTDI 300  
 DB 241 TGLNNLRGTNAESWVRYNQFRDMLMVLVDVALPSPSYDTQMPYIKTTAQLTREVYTDI 300

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QY 301 GTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDFLEQVITYSLLSRWSNTQYNNMW 360
DB 301 GTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDFLEQVITYSLLSRWSNTQYNNMW 360
QY 361 GGHKLEPRTTGGTLNSTQGSTNTSINPVTLPFTSRDVYRTESLAGLNFLFTOPVNGVPR 420
DB 361 GGHKLEPRTTGGTLNSTQGSTNTSINPVTLPFTSRDVYRTESLAGLNFLFTOPVNGVPR 420
QY 421 VDFHWKFTVTHPIASDNFYPGYAGIGTQLODSNELPPEATGQPNYESYSHRLSHIGLIS 480
DB 421 VDFHWKFTVTHPIASDNFYPGYAGIGTQLODSNELPPEATGQPNYESYSHRLSHIGLIS 480
QY 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
DB 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
QY 541 TGTGFDIRVNNPFFAQRVYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
DB 541 TGTGFDIRVNNPFFAQRVYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
QY 601 TPTVGTFTPTPSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDPEKAQEKV 660
DB 601 TPTVGTFTPTPSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDPEKAQEKV 660
QY 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVESLSDEFYLDKRELFELVYKAKQLHIERNM 719
DB 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVESLSDEFYLDKRELFELVYKAKQLHIERNM 719

RESULT 3
AAP86782
ID AAP86782 PRELIMINARY; PRT; 719 AA.
AC AAP86782;
DT 02-MAR-2004 (T-EMBLrel. 27, Created)
DT 02-MAR-2004 (T-EMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (T-EMBLrel. 27, Last annotation update)
DE Cryli.
GN Cryli.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=T01 328;
RA Espindola R., Lemos M.V.F., Lemos E.G.M., Sena J.A.D.;
RT "Complete sequence of cryII gene of isolate T01 328 from Bacillus
RT thuringiensis from Cubatao (SP - Brazil) soil.";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY262167; AAP86782.1; -.
DR EMBL; AY262167; AAP86782.1; -.
SQ SEQUENCE 719 AA; 81216 MW; 3627E5A6C25DAFF5 CRC64;

Query Match 100.0%; Score 3760; DB 2; Length 719;
Best Local Similarity 100.0%; Pred. No. 2.6e-253;
Matches 719; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLXGSEYENVPFVSASTI 60
DB 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLXGSEYENVPFVSASTI 60
QY 61 QTGIGTAGKILGTLPVFPAGQVASYLFGILGELMPKQKQWEIFMEHVEEIIINOKISTYA 120
DB 61 QTGIGTAGKILGTLPVFPAGQVASYLFGILGELMPKQKQWEIFMEHVEEIIINOKISTYA 120
QY 121 RNKALTDLKGGLDALAYVHDLSLVSGVGNRNNTARSVVKVSKYIALBELMFVKLPFAVSG 180
DB 121 RNKALTDLKGGLDALAYVHDLSLVSGVGNRNNTARSVVKVSKYIALBELMFVKLPFAVSG 180
QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISIFYNQVERAGDYSCHVKWYS 240
DB 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISIFYNQVERAGDYSCHVKWYS 240

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QY 241 TGLNNLRGTNAESVRYNQFRDMDTMLVLDLVALPPSYDVTOMYPIKTTAQLTREYVTDAL 300
DB 241 TGLNNLRGTNAESVRYNQFRDMDTMLVLDLVALPPSYDVTOMYPIKTTAQLTREYVTDAL 300
QY 301 GTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDFLEQVITYSLLSRWSNTQYNNMW 360
DB 301 GTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDFLEQVITYSLLSRWSNTQYNNMW 360
QY 361 GGHKLEPRTTGGTLNSTQGSTNTSINPVTLPFTSRDVYRTESLAGLNFLFTOPVNGVPR 420
DB 361 GGHKLEPRTTGGTLNSTQGSTNTSINPVTLPFTSRDVYRTESLAGLNFLFTOPVNGVPR 420
QY 421 VDFHWKFTVTHPIASDNFYPGYAGIGTQLODSNELPPEATGQPNYESYSHRLSHIGLIS 480
DB 421 VDFHWKFTVTHPIASDNFYPGYAGIGTQLODSNELPPEATGQPNYESYSHRLSHIGLIS 480
QY 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
DB 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
QY 541 TGTGFDIRVNNPFFAQRVYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
DB 541 TGTGFDIRVNNPFFAQRVYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
QY 601 TPTVGTFTPTPSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDPEKAQEKV 660
DB 601 TPTVGTFTPTPSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDPEKAQEKV 660
QY 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVESLSDEFYLDKRELFELVYKAKQLHIERNM 719
DB 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVESLSDEFYLDKRELFELVYKAKQLHIERNM 719

RESULT 4
Q93NJ5
ID Q93NJ5 PRELIMINARY; PRT; 719 AA.
AC Q93NJ5;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Cryli.
GN Name=cryIIa;
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RA Song P., Zhang J., Gu A., Huang D., Li G.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF373207; AAK66742.1; -.
DR HSSP; P02965; IC1Y.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR008979; Gal_bind_like.
DR InterPro; IPR008979; Gal_bind_like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
SQ SEQUENCE 719 AA; 81225 MW; C629DF2C44827241 CRC64;

Query Match 99.9%; Score 3755; DB 2; Length 719;
Best Local Similarity 99.9%; Pred. No. 5.8e-253;
Matches 718; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLXGSEYENVPFVSASTI 60
DB 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLXGSEYENVPFVSASTI 60
QY 61 QTGIGTAGKILGTLPVFPAGQVASYLFGILGELMPKQKQWEIFMEHVEEIIINOKISTYA 120

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Db 61 QTGIGIAGKILGTLGVPFAGQVASYLFIIGELWPKGNQWEIEMHVEBIIINQKISTYA 120  
 QY 121 RNKALTDLKLGDALAVHDSLESWGNRNTRARSVVKSYQIALELMFVQKLPSEAVSG 180  
 Db 121 RNKALTDLKLGDALAVHDSLESWGNRNTRARSVVKSYQIALELMFVQKLPSEAVSG 180  
 QY 181 BEVPLLPPIYAQAANLHLLLDASIFGKRWGLSSSEISTFYNQVERAGDYSDHCVKWYS 240  
 Db 181 BEVPLLPPIYAQAANLHLLLDASIFGKRWGLSSSEISTFYNQVERAGDYSDHCVKWYS 240  
 QY 241 TGLNNLRGTNAESWVRYNQFRDMTLMVLVDLVALFPSTYDQMPYIKTTAQTREVTYDAI 300  
 Db 241 TGLNNLRGTNAESWVRYNQFRDMTLMVLVDLVALFPSTYDQMPYIKTTAQTREVTYDAI 300  
 QY 301 GTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPHLLDLEQVTIYSLLSRWSTQYNNMW 360  
 Db 301 GTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPHLLDLEQVTIYSLLSRWSTQYNNMW 360  
 QY 361 GGHKLEFRTIGTLNISTQGSTNTSINPVTLPFTSRDVRYSLAGLNLFTOPVNGVPR 420  
 Db 361 GGHKLEFRTIGTLNISTQGSTNTSINPVTLPFTSRDVRYSLAGLNLFTOPVNGVPR 420  
 QY 421 VDFHMKFVTHPIASDNFYPGYAGIGTQLODSENELPEATGQPNYESYSHRLSHIGLIS 480  
 Db 421 VDFHMKFVTHPIASDNFYPGYAGIGTQLODSENELPEATGQPNYESYSHRLSHIGLIS 480  
 QY 481 ASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSSCAAVVRGPGTGGDILRRTN 540  
 Db 481 ASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSSCAAVVRGPGTGGDILRRTN 540  
 QY 541 TGTGDIRVNIINPPPAQRYRIRYASTDILQFHTSINGKAINQGNFSATMNRGEDLDYK 600  
 Db 541 TGTGDIRVNIINPPPAQRYRIRYASTDILQFHTSINGKAINQGNFSATMNRGEDLDYK 600  
 QY 601 TFRVVGFTTSPFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660  
 Db 601 TFRVVGFTTSPFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660  
 QY 661 TALFTSTNPRGLKTDVQYHIDQVSNLVESLSDFYLDKRELFEIVKYAKQLHIERNM 719  
 Db 661 TALFTSTNPRGLKTDVQYHIDQVSNLVESLSDFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 5  
 O85796 PRELIMINARY; PRT; 719 AA.  
 AC O85796  
 DT 01-NOV-1998 (TREMBLrel. 08, Created)  
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DE Insecticidal protein.  
 GN Name=crv101;  
 OS Bacillus thuringiensis (subsp. kurstaki).  
 OC Plasmid large plasmid.  
 CC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 RX NCBI\_taxid=29339;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=S101;  
 RA Zhong Q., Deng R., Long Q., Yuan M., Pang Y., Wang X.;  
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF076953; AAC26910.1; -.  
 DR HSSP; P02965; 1CIY.  
 DR GO; GO:0005102; F:receptor binding; IEA.  
 DR GO; GO:0006952; P:defense response; IEA.  
 DR GO; GO:0009405; P:pathogenesis; IEA.  
 DR InterPro; IPR001178; Endotoxin.  
 DR InterPro; IPR005638; endotoxin C.  
 DR InterPro; IPR005639; endotoxin N.  
 DR InterPro; IPR008979; Gal\_bind\_like.  
 DR Pfam; PF03944; Endotoxin C; 1.  
 DR Pfam; PF00555; Endotoxin M; 1.  
 DR Pfam; PF03945; Endotoxin N; 1.

KW Plasmid. 719 AA; 81230 MW; 42746D478359BBA7 CRC64;  
 SQ SEQUENCE  
 Query Match 99.8%; Score 3754; DB 2; Length 719;  
 Best Local Similarity 99.9%; Pred. No. 6.8e-253;  
 Matches 718; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MKLKNDKHQSFSSNAKVDKISTDSLKNETDIELQNTNHEDCLAKSEYENVEPVSASTI 60  
 Db 1 MKLKNDKHQSFSSNAKVDKISTDSLKNETDIELQNTNHEDCLAKSEYENVEPVSASTI 60  
 QY 61 QTGIGIAGKILGTLGVPFAGQVASYLFIIGELWPKGNQWEIEMHVEBIIINQKISTYA 120  
 Db 61 QTGIGIAGKILGTLGVPFAGQVASYLFIIGELWPKGNQWEIEMHVEBIIINQKISTYA 120  
 QY 121 RNKALTDLKLGDALAVHDSLESWGNRNTRARSVVKSYQIALELMFVQKLPSEAVSG 180  
 Db 121 RNKALTDLKLGDALAVHDSLESWGNRNTRARSVVKSYQIALELMFVQKLPSEAVSG 180  
 QY 181 BEVPLLPPIYAQAANLHLLLDASIFGKRWGLSSSEISTFYNQVERAGDYSDHCVKWYS 240  
 Db 181 BEVPLLPPIYAQAANLHLLLDASIFGKRWGLSSSEISTFYNQVERAGDYSDHCVKWYS 240  
 QY 241 TGLNNLRGTNAESWVRYNQFRDMTLMVLVDLVALFPSTYDQMPYIKTTAQTREVTYDAI 300  
 Db 241 TGLNNLRGTNAESWVRYNQFRDMTLMVLVDLVALFPSTYDQMPYIKTTAQTREVTYDAI 300  
 QY 301 GTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPHLLDLEQVTIYSLLSRWSTQYNNMW 360  
 Db 301 GTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPHLLDLEQVTIYSLLSRWSTQYNNMW 360  
 QY 361 GGHKLEFRTIGTLNISTQGSTNTSINPVTLPFTSRDVRYSLAGLNLFTOPVNGVPR 420  
 Db 361 GGHKLEFRTIGTLNISTQGSTNTSINPVTLPFTSRDVRYSLAGLNLFTOPVNGVPR 420  
 QY 421 VDFHMKFVTHPIASDNFYPGYAGIGTQLODSENELPEATGQPNYESYSHRLSHIGLIS 480  
 Db 421 VDFHMKFVTHPIASDNFYPGYAGIGTQLODSENELPEATGQPNYESYSHRLSHIGLIS 480  
 QY 481 ASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSSCAAVVRGPGTGGDILRRTN 540  
 Db 481 ASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSSCAAVVRGPGTGGDILRRTN 540  
 QY 541 TGTGDIRVNIINPPPAQRYRIRYASTDILQFHTSINGKAINQGNFSATMNRGEDLDYK 600  
 Db 541 TGTGDIRVNIINPPPAQRYRIRYASTDILQFHTSINGKAINQGNFSATMNRGEDLDYK 600  
 QY 601 TFRVVGFTTSPFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660  
 Db 601 TFRVVGFTTSPFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660  
 QY 661 TALFTSTNPRGLKTDVQYHIDQVSNLVESLSDFYLDKRELFEIVKYAKQLHIERNM 719  
 Db 661 TALFTSTNPRGLKTDVQYHIDQVSNLVESLSDFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 6  
 CAC85964 PRELIMINARY; PRT; 719 AA.  
 ID CAC85964  
 AC CAC85964;  
 DT 02-MAR-2004 (TREMBLrel. 27, Created)  
 DT 02-MAR-2004 (TREMBLrel. 27, Last sequence update)  
 DT 02-MAR-2004 (TREMBLrel. 27, Last annotation update)  
 DE Delta-endotoxin.  
 GN CylIIA.  
 OS Bacillus thuringiensis (subsp. kurstaki).  
 CC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;  
 CC Bacillus cereus group; Bacillus thuringiensis.  
 OX NCBI\_TaxID=29339;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ENS3;  
 RA Tounsi S., Zouari N., Jacua S.;





Db 1 MKLNKPDKHQSLSSNAKVVDKIATDSLKNETDIELKNNMNEYLRMSSEHSIDPFVSASTI 60  
QY 61 QTGIGIAGKILGTLGVPPFAGQVSLYSFILGELWPKGNQWEIFMHEVVEIINOKISTYA 120  
Db 61 QTGIGIAGKILGTLGVPPFAGQVSLYSFILGELWPKGNQWEIFMHEVVEIINOKILTA 120  
QY 121 RNKALDTLKGDLALAVYHDSLSVGNRNNTARSVVKSOYIALELMFVKQLPSPFVSG 180  
Db 121 RNKALSLRGLDALAVYHDSLSVGNRNNTARSVVKSOYIALELMFVKQLPSPFVSG 180  
QY 181 BEVPLPIYAQAANLHLLLRDASIFGKWLSSSISTFYNQVRAGDYSDHCVKWS 240  
Db 181 BEVPLPIYAQAANLHLLLRDASIFGKWLSSSISTFYNQVRAGDYSDHCVKWS 240  
QY 241 TGLNLRGTHNAESVRYNQFRDMLVLDLVALFSPSYDQVPIKTTAQLTREVTYDAI 300  
Db 241 TGLNLRGTHNAESVRYNQFRDMLVLDLVALFSPSYDQVPIKTTAQLTREVTYDAI 300  
QY 301 GTVHPHPSFTSTWYNNAPSFAIAEAVVRNPHLLDFLEQVTLFVPTKTSQLTREVTYDAI 360  
Db 301 GTVHPHPSFTSTWYNNAPSFAIAEAVVRNPHLLDFLEQVTLFVPTKTSQLTREVTYDAI 360  
QY 361 GTVHPHPSFTSTWYNNAPSFAIAEAVVRNPHLLDFLEQVTLFVPTKTSQLTREVTYDAI 360  
Db 361 GTVHPHPSFTSTWYNNAPSFAIAEAVVRNPHLLDFLEQVTLFVPTKTSQLTREVTYDAI 360  
QY 361 GGHKLEFRITGTLNTSTQSTNTSINPVTLPFTSRDVRVTSAGLNLFVTPVNGVPR 420  
Db 361 GGHKLEFRITGTLNTSTQSTNTSINPVTLPFTSRDVRVTSAGLNLFVTPVNGVPR 420  
QY 421 VDFHWKFTVTHPIASDNFYPGYAGIGTQLODSNELPPEATGPNVYESYHRLSHIGLIS 480  
Db 421 VDFHWKFTVTHPIASDNFYPGYAGIGTQLODSNELPPEATGPNVYESYHRLSHIGLIS 480  
QY 481 ASHVKALVSWTHRSADRTNTIIPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
Db 481 ASHVKALVSWTHRSADRTNTIIPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
QY 541 TGTFGDIRVNNPPFAQVRVIRYASTTDLQFHTSINGKAINQGNFSATMARGEDLDYK 600  
Db 541 TGTFGDIRVNNPPFAQVRVIRYASTTDLQFHTSINGKAINQGNFSATMARGEDLDYK 600  
QY 601 TFRVTGFTTSPFLDQVSTFTIGAWNFSSGNEVYIDRIEFVPEVTVYEAEDFEKAQEKV 660  
Db 601 TFRVTGFTTSPFLDQVSTFTIGAWNFSSGNEVYIDRIEFVPEVTVYEAEDFEKAQEKV 660

## RESULT 10

CLID\_BACTU STANDARD; PRT; 719 AA.  
AC Q9XDL1;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Pesticidal crystal protein cry.II (insecticidal delta-endotoxin  
DE Cry.II(d) (crystalline entomocidal protoxin) (81 kDa crystal protein).  
GN Name=cry.II(d); Synonyms=cry.II(d), NRcryV;  
OS Bacillus thuringiensis.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=1428;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BR30;  
RA MEDLINE=20374042; PubMed=10919402;  
RX Choi S.-K., Shin B.-S., Kong E.-M., Rho H.-M., Park S.-H.;  
RT "Cloning of a new Bacillus thuringiensis cry.II-type crystal protein  
RT gene.";  
RL Curr. Microbiol. 41:65-69(2000).  
CC -|- FUNCTION: Promotes colloid osmotic lysis by binding to the midgut  
CC epithelial cells of many lepidopteran larvae. Active on Plutella  
CC xylostella and on Bombyx mori.  
CC -|- DEVELOPMENTAL STAGE: The crystal protein is produced during  
CC sporulation and is accumulated both as an inclusion and as part of

CC the spore coat.  
CC -|- MISCELLANEOUS: Toxic segment of the protein is located in the N-  
CC terminus.  
CC -|- SIMILARITY: Belongs to the delta endotoxin family.  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; AF047579; AAD44366.1; -;  
CC HSSP; P02965; 1CIY.  
CC InterPro; IPR001178; Endotoxin.  
CC InterPro; IPR005638; endotoxin\_C.  
CC InterPro; IPR005639; endotoxin\_N.  
CC InterPro; IPR008979; Gal\_bind\_Like.  
CC Pfam; PF03944; Endotoxin\_C; 1.  
CC Pfam; PF00555; Endotoxin\_M; 1.  
CC Pfam; PF03945; Endotoxin\_N; 1.  
CC Sporulation; Toxin.  
CC KW  
CC SEQUENCE 719 AA; 81403 MW; F335F5689D3B0C45 CRC64;  
CC  
CC Query Match 90.3%; Score 3397; DB 1; Length 719;  
CC Best Local Similarity 89.8%; Pred. No. 5.3e-228;  
CC Matches 646; Conservative 35; Mismatches 38; Indels 0; Gaps 0;  
CC  
CC QY 1 MKLNKPDKHQSLSSNAKVVDKIATDSLKNETDIELQNNHEDCLKMSYENVEPFFVSASTI 60  
CC Db 1 MKSNQNNMYRFSNNATVVDKSFDPLEHTNMLQNSNHEDECLKMSYEVSEVFPFVSSTI 60  
CC QY 61 QTGIGIAGKILGTLGVPPFAGQVSLYSFILGELWPKGNQWEIFMHEVVEIINOKISTYA 120  
CC Db 61 QTGIGIAGKILGTLGVPPFAGQVSLYSFILGELWPKGNQWEIFMHEVVEIINOKISTYA 120  
CC QY 121 RNKALDTLKGDLALAVYHDSLSVGNRNNTARSVVKSOYIALELMFVKQLPSPFVSG 180  
CC Db 121 RNKALADLKGDLALAVYHDSLSVGNRNNTARSVVKSOYIALELMFVKQLPSPFVSG 180  
CC QY 181 BEVPLPIYAQAANLHLLLRDASIFGKWLSSSISTFYNQVRAGDYSDHCVKWS 240  
CC Db 181 BEVPLPIYAQAANLHLLLRDASIFGKWLSSSISTFYNQVRAGDYSDHCVKWS 240  
CC QY 241 TGLNLRGTHNAESVRYNQFRDMLVLDLVALFSPSYDQVPIKTTAQLTREVTYDAI 300  
CC Db 241 TGLNLRGTHNAESVRYNQFRDMLVLDLVALFSPSYDQVPIKTTAQLTREVTYDAI 300  
CC QY 301 GTVHPHPSFTSTWYNNAPSFAIAEAVVRNPHLLDFLEQVTLFVPTKTSQLTREVTYDAI 360  
CC Db 301 GTVHPHPSFTSTWYNNAPSFAIAEAVVRNPHLLDFLEQVTLFVPTKTSQLTREVTYDAI 360  
CC QY 361 GGHKLEFRITGTLNTSTQSTNTSINPVTLPFTSRDVRVTSAGLNLFVTPVNGVPR 420  
CC Db 361 GGHKLEFRITGTLNTSTQSTNTSINPVTLPFTSRDVRVTSAGLNLFVTPVNGVPR 420  
CC QY 421 VDFHWKFTVTHPIASDNFYPGYAGIGTQLODSNELPPEATGPNVYESYHRLSHIGLIS 480  
CC Db 421 VDFHWKFTVTHPIASDNFYPGYAGIGTQLODSNELPPEATGPNVYESYHRLSHIGLIS 480  
CC QY 481 ASHVKALVSWTHRSADRTNTIIPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
CC Db 481 ASHVKALVSWTHRSADRTNTIIPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
CC QY 541 TGTFGDIRVNNPPFAQVRVIRYASTTDLQFHTSINGKAINQGNFSATMARGEDLDYK 600  
CC Db 541 TGTFGDIRVNNPPFAQVRVIRYASTTDLQFHTSINGKAINQGNFSATMARGEDLDYK 600  
CC QY 601 TFRVTGFTTSPFLDQVSTFTIGAWNFSSGNEVYIDRIEFVPEVTVYEAEDFEKAQEKV 660  
CC Db 601 TFRVTGFTTSPFLDQVSTFTIGAWNFSSGNEVYIDRIEFVPEVTVYEAEDFEKAQEKV 660

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QY 661 TALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDBFYLDKRELFEIVKYAKQLHIERNM 719
DB 661 TAMFTSTNRLKTNVTDCHIDQVSNLVESLSDBFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 11
ID C11C BACTU STANDARD; PRT; 719 AA.
AC 087404.
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pesticidal crystal protein cryIIc (Insecticidal delta-endotoxin
DE CryII(c) (Crystalline entomocidal protoxin) (81 kDa crystal protein).
GN Name=cryIIC; Synonyms=cryII(c);
OS Bacillus thuringiensis.
OG Plasmid.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C18 / Egypt;
RA Osman Y.A., Madkour M.A., Bulla L.A. Jr.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut
CC epithelial cells of insects.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -!- SIMILARITY: Belongs to the delta endotoxin family.
CC
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CC
CC EMBL; AF056933; AAC62933.1; -.
DR HSSP; P02965; 1CIY.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal_bind_like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
KW Plasmid; Sporulation; Toxin.
SQ SEQUENCE 719 AA; 81210 MW; 8370B3F068905DFF CRC64;

Query Match 89.8%; Score 3377; DB 1; Length 719;
Best Local Similarity 89.8%; Pred. No. 1.3e-226;
Matches 646; Conservative 33; Mismatches 40; Indels 0; Gaps 0;

QY 1 MKLNQDKHQSPSSNAKYDKLSLKNETDIELQNIHEDCLQWSSYENVEPVSASTI 60
DB 1 MKLNQDKHQSLSSNAKYDKLATSLSKNETDIELKNWEDYLRMSHESIDPVSASTI 60

QY 61 QTGIGIAGKILGTGVPFAGVASYLSFILGELPKGNQWEIFMEHVHVEIINQKISTYA 120
DB 61 QTGIGIAGKILGTGVPFPGQIASYLSFILGELPKGKQWEIFMEHVHVEIINRQKISTYA 120

QY 121 RNKALTDLKGLDALAVHDSLEWGNRNTRARSVVKQSYIALELMFVKQLPSPAVSG 180
DB 121 RNKALTDLKGLDALAVHDSLEWGNRNTRARSVVKQSYIALELMFVKQLPSPAVSG 180

QY 181 BEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSVHCVKWYS 240
DB 181 BEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSVHCVKWYN 240

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RESULT 12
C11B BACTU
ID C11B BACTU STANDARD; PRT; 1229 AA.
AC Q45739;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pesticidal crystal protein cryIB5 (Insecticidal delta-endotoxin
DE CryIB(b) (Crystalline entomocidal protoxin) (140 kDa crystal protein).
GN Name=cryIB5; Synonyms=cryIB(b), cryET5;
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL B-21110 / BG5847;
RA Donovan W.F., Tan Y., Jany C.S., Gonzalez J.M. Jr.;
RT "Bacillus thuringiensis cryet4 and cryet5 toxin genes and proteins
RT toxic to lepidopteran insects.";
RL Patent number US5322687, 21-JUN-1994.
CC -!- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut
CC epithelial cells of many lepidopteran larvae.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -!- SIMILARITY: Belongs to the delta endotoxin family.
CC
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; L32020; AAA22344.1; -.
DR HSSP; P02965; 1CIY.
DR InterPro; IPR001178; Endotoxin.

```

```

QY 241 TGLNNLRGTNAESWVRVYQFRDMTLMVLDLVALFPSPYDTOMYPIKTTAQLTRVYTDAI 300
DB 241 TGLNNLRATNGQSWVRVYQFRKDIELMVLVLRVPSPYDTLVYPIKTTSQLTRVYTDAI 300

QY 301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDELEOVITYSLLSRNSQYMNW 360
DB 301 GTVDNQALRSTTWYNNNAPSFAIEAAVVRNPHLLDELEKVTIYSLLSRNSQYMNW 360

QY 361 GGHLEPRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTTESLAGLNLFLTQPVNGVPR 420
DB 361 GGHRLSRPIGALNTSTQGSTNTSINPVTLPFTSRDVRTTESWAGLNLFLTQPVNGVPR 420

QY 421 VDFHWKFTVTHPIASNFYYPGAGIGTQLODSENLPEATGQPNYSYSHRLSHIGLIS 480
DB 421 VDFHWKFTPIASDNFYFLGYAGVGTQLODSENLPEETGQPNYESYSHRLSHIGLIS 480

QY 481 ASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
DB 481 GSHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGHILRRTK 540

QY 541 TCTFGDIRVWINPPFAQRYRVRIRYASTDLDQFHTSINGKAINQGNFSATWNRGEDLDYK 600
DB 541 SGTFGHIRVWINPPFAQRYRVRMSYASTDLDQFHTSINGKAINQGNFSATWNRGEDLDYK 600

QY 601 TPTVTGFTTPTSFQVSTFTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEKV 660
DB 601 TPTVTGFTTPTSFQVSTFTIGAWNFSSGNEVYIGRIEFVPEVVEYAEYDFEKAQEKV 660

QY 661 TALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDBFYLDKRELFEIVKYAKQLHIERNM 719
DB 661 TALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDBFYLDKRELFEIVKYAKQLHIERNM 719

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DR	InterPro; IPR005638; endotoxin_C.
DR	InterPro; IPR005639; endotoxin_N.
DR	InterPro; IPR008979; Gal_bind_like.
DR	Pfam; PF03944; Endotoxin_C; 1.
DR	Pfam; PF00555; Endotoxin_M; 1.
DR	Pfam; PF03945; Endotoxin_N; 1.
KW	Sporulation; Toxin.
SQ	SEQUENCE 1229 AA; 139769 MW; A4C949DB675C3269 CRC64;
Query Match 65.1%; Score 2446.5; DB 1; Length 1229;	
Best Local Similarity 65.6%; Pred. No. 2.2e-161;	
Matches 470; Conservative 92; Mismatches 138; Indels 17; Gaps 6;	
QY	13 SSNAKVDKISTSLKN-EFTDIELQ-NINHEDCLKMSEYENVEPVSASTQTGIGIAGKI 70
DB	7 NENEIINALSIPTVSNPSQMNLSPDARIEDSLCAEVNNDPPFVSASTVTGTGINIAGRI 66
QY	71 LGTLGVFPAGQVASLYSFTLGLBPKGNQWEIFMEHVBEIIINOKISTYARNKALTDLKG 130
DB	67 LGVLGVFPAGQLASFYSFLVGELWFSGRDPWEIFLEHVQEILRQQVTENTTAIRLEG 126
QY	131 LGDALAVYHDSLESWGVRNNTARSVKQSYIALELMFVKLPFAVSGEEVPLLPIYA 190
DB	127 LGRGYRSYQALETWLDNRDARSRISILERYVALELDITTAIPLRINEEVPLLMVYA 186
QY	191 QAAHLHLLLRLDASIFGKEWLGSSEISTFYNQVERAGDYSDHCWKYSTGLNNLRGTN 250
DB	187 QAANLHLLLRLDASIFGSEGWASDVNQYIQEQIRYTEESNCHVCQWYNTGLNNLRGTN 246
QY	251 AESWRYNQFRDMTLMVLDLVALFPSYDTQMYPKTAAQTREVVYDAIGTVHPHSFT 310
DB	247 AESWLRYNQFRDLTLGLVDLVALFPSYDTRTPINTSAQLTRBIYTDPIGRTNAPSGFA 306
QY	311 STTWANNAPSATBAAVRNPHLLDFLEQVTIYSLSRMSNTQYMNMGHGKLEPRTI 370
DB	307 STWNFNNAAPSALAEAI FRPPLHLLDFPEQTIYSSASSRWSTQHWNVWGHKLNFRI 366
QY	371 GGTLNISTQGST-NTSINPVTLPTFRDVRVYTESLAGLNLFLOPVNGVPRVDFHWKFVT 429
DB	367 GGTLNTSTQGLTNNTSINPVTLQFTSRDVRVYTESNAGTNILFTTPVNGVFWARENF--- 422
QY	430 HPIASDNFYPG-----YAGIGTOLQDSENELPPEATGPNYVESYSHRLSHIGLISAS 482
DB	423 --INPNQIERGATTYSQPQGGVIQJFDSETSELPPETTERPNYESISHRLSHIGLIIGN 480
QY	483 HVKALVSWTHRSADRNTIENSITQPLVKAFLSSLGAAVRGPGFTGGDILLRNTTG 542
DB	481 TLRAPYVSWTHRSADRNTIENGRIITQPLVKALNLHSGVTVVGGPGFTGGDILLRNTG 540
QY	543 TFGDIRWINPFPAQRVRIRYASTDLOPHTSINGKAINCGNFSATMRGEDLDYKTF 602
DB	541 TFGDIRLNVLSQRYRIRIYASTDLOPFTTRINGTVNIGNFSRMTNRGNLLEYRSF 600
QY	603 RTVGFTTFESLDVOSTFTIGAWNFSSGNEVVIDRIEVPVVEVYEAIDYFEKAQEKVTA 662
DB	601 RTAGFTSTPNFLNAQSTFTLGQSFSN-QEVIDRVEFPVAEIVFEAYDLERAKAVNA 659
QY	663 LFTSTNPRLGKTDVKDHYHDQSVNLVSESDFSFLDEKRELFEIKVYAKQHLIERNM 719
DB	660 LFTSTNPRLKTDVTDYHIDQSVNMVACLSDEFCLDEXRELFEKYVAKRLSDERNL 716
RESULT 13	
CIBC_BACTM	STANDARD; PRT; 1233 AA.
ID	CIBC_BACTM AC Q45774;
DT	30-MAY-2000 (Rel. 39, Created)
DT	30-MAY-2000 (Rel. 39, Last sequence update)
DT	05-JUL-2004 (Rel. 44, Last annotation update)
DE	Pesticidal crystal protein crylBc (Insecticidal delta-endotoxin)
DE	CrylB(c) (Crystalline entomocidal protoxin) (140 kDa crystal protein).
GN	Name=crylBc; Synonyms=cryIB(c), crylBc;
OS	Bacillus thuringiensis (subsp. morrisoni).

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Db 481 TLAPVSWTHRSADRTNIGPNIQTPLVYKALNLSGVTVGPGFTGGDILRRNTG 540
QY 543 TFGDIRVNNPPFAQRVRYRYASTTDLQPHTSINGKAINQGNFSAATMARGEDLDYKTF 602
Db 541 TFGDIRLNNVPSLQRYRYRYASTTDLQPHTSINGKAINQGNFSAATMARGEDLDYKTF 600
QY 603 RTVGTTTFFSLDVOSTFTICAWNFSSGVEYVIRIEVPVVEVYEAEDFKAQEKVTA 662
Db 601 RTAGSTTFNLAAQSTFTLGAQFSN-QEVIIDRVFPVPAEVTFEAYDULERAQKAVNA 659
QY 663 LFTSTNPRGLTKVDKDYHIDQVSNLVESLSEDFYDLKRELFVYKAKOLHIERNM 719
Db 660 LFTSTNPRRLKTDVTDYHIDQVSNVACLSEDFCLDKRELFVYKAKOLHIERNM 716

RESULT 14
Q93T75 PRELIMINARY; PRT; 1228 AA.
AC Q93T75;
DT 01-DEC-2001 (TRENDEL. 19, Created)
DT 01-DEC-2001 (TRENDEL. 19, Last sequence update)
DT 01-MAR-2004 (TRENDEL. 26, Last annotation update)
DE Delta-endotoxin CryIa2.
GN Name=cryIa2;
OS Bacillus thuringiensis (subsp. entomocidus).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1436;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=HD-9;
RA Mat Isa M.N., Abdullah M.A.F., Mahadi N.M.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF363025; AAK51084.1; -
DR HSSP; P07130; 1DLX.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin N.
DR InterPro; IPR005639; endotoxin C.
DR InterPro; IPR008979; Gal bind like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
SQ SEQUENCE 1228 AA; 139620 MW; 3DA2A4DBF59C95C3 CRC64;

Query Match
Best Local Similarity 60.6%; Score 2278.5; DB 2; Length 1228;
Matches 449; Conservative 80; Mismatches 162; Indels 25; Gaps 6;

QY 23 TDSLKNETDIELOINH-----EDCKMSEYENVEPVFSASTTGTGIGAKI 70
Db 2 TSNRKNENIINAVSNHSAQMDLLPDARIEDSLCIAAGNNIDPVFSASTVGTGINIAGRI 61
QY 71 LGLGVPPAGVAGVSYSTIGELWPKGNQWEIEMFHEVEIINOKISTYARNKALTDLKG 130
Db 62 LGVLGVPPAGVAGVSYSTIGELWPKGNQWEIEMFHEVEIINOKISTYARNKALTDLKG 121
QY 131 LGDALVTHDSLESVGNVNNNRARSVVKSYIALEMFVOKLPSFAVSGEEVPLPIYA 190
Db 122 LGDSFRAYQQSLEDWLENRDARTSVLHTQYIALEDFLNAFLFAIRNQVEPFLMVA 181
QY 191 QAANLHLLLDASTFFGKWLGSSETSTFYNNROVERAGDYSCHVKWYSTGLNLRGTN 250
Db 182 QAANLHLLLDASTFFGKWLGSSETSTFYNNROVERAGDYSCHVKWYSTGLNLRGTN 241
QY 251 AESWRYNQFRDMTLMVLDLVALPPSYDQYPIKTAQLTRVYTDATGTVHPHSFT 310
Db 242 AASWRYNQFRDMTLMVLDLVALPPSYDQYPIKTAQLTRVYTDATGTVHPHSFT 299
QY 311 STTWANNAPSPSATEAAVAVNPHLLDPLEQVITYSLLSRWNTQYNNWGGHKLERTI 370

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Db 300 SMWYNNNAPSPSATEAAVAVNPHLLDPLEQVITYSLLSRWNTQYNNWGGHKLERTI 359
QY 371 GGTANISCGSTNTSINPVLPFTSRDYVRYTESLAGLNF--LTQPVNGVPRVDFHMKFV 428
Db 360 GGLNTSTHGATNTSINPVLPFTSRDYVRYTESLAGLNF--LTQPVNGVPRVDFHMKFV 416
QY 429 THP-----IASDNFYPGYAGIGTQDSNELPEPEATQCPNYESYSHRLSHIGILQSR 483
Db 417 TNPQISDRGTANYSCP-YESPLQLKDSLETPEPPERPNYESYSHRLSHIGILQSR 475
QY 484 VVALVYSWTHRSADRTNIEPNSITQIPLVYKALNLSGVTVGPGFTGGDILRRNTG 543
Db 476 VNPVYSWTHRSADRTNIEPNSITQIPLVYKALNLSGVTVGPGFTGGDILRRNTG 535
QY 544 FGDIVNINPPFAQRVRYRYASTTDLQPHTSINGKAINQGNFSAATMARGEDLDYKTF 603
Db 536 FGPVIRVNGPLTQRYRIGFVASTVDFDFVSRGGTTVNNFRFLRTVNSGDELKYGNFV 595
QY 604 TVGTTTFFSLDVOSTFTICAWNFSSGVEYVIRIEVPVVEVYEAEDFKAQEKVTA 663
Db 596 RRAFTTPTFTQIQDIIRTSIQGLSGNGEVYDKIEIIPVTATFEAYDULERAQKAVNA 655
QY 664 FTSTNPRGLTKVDKDYHIDQVSNLVESLSEDFYDLKRELFVYKAKOLHIERNM 719
Db 656 FTNTNPRRLKTDVTDYHIDQVSNVACLSEDFCLDKRELFVYKAKOLHIERNM 711

RESULT 15
C1BA BACTK
ID C1BA BACTK STANDARD; PRT; 1228 AA.
AC 205517; Q45731;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pesticidal crystal protein cryIaB (insecticidal delta-endotoxin
DE CryIaB(a)) (crystalline entomocidal protoxin) (140 kDa crystal protein).
GN Name=cryIaB; Synonyms=cryIaB(a), cryA4;
OS Bacillus thuringiensis (subsp. kurstaki), and
OS Bacillus thuringiensis (subsp. entomocidus).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=29339, 1436;
RN [1]_
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.kurstaki; STRAIN=HD-2;
RC MEDLINE=89203216; PubMed=3362680;
RX Brizzard B.L., Whiteley H.R.;
RA "Nucleotide sequence of an additional crystal protein gene cloned from
RT Bacillus thuringiensis subsp. thuringiensis.";
RL Nucleic Acids Res. 16:2723-2723 (1988).
RN [2]_
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.entomocidus; STRAIN=HD-110;
RC Soccaert P.;
RA Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Promotes colloidomotic lysis by binding to the midgut
CC epithelial cells of insects.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -!- SIMILARITY: Belongs to the delta endotoxin family.
CC
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CC
CC EMBL; X06711; CAA29898.1; -.
CC EMBL; X95704; CAA65003.1; -.

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DR PIR: S00873; S00873.
DR HSP: P07130; DLCL
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal bind like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
KW Sporulation; Toxin.
FT VARIANT 150 150 Y -> H (in strain HD-110).
SQ SEQUENCE 1228 AA; 139647 MW; C8E3A19FB5D98575 CRC64;

Query Match 60.6%; Score 2277.5; DB 1; Length 1228;
Best Local Similarity 62.7%; Pred. No. 1.3e-149;
Matches 449; Conservative 80; Mismatches 162; Indels 25; Gaps 6;

Qy 23 TDSLKNETDIELQNIN-----EDCLKMEYENVEPVFSASTIQTGIGIAGKI 70
Db 2 TSNRKNENETINAVSNHSAQMDLLPDARIEDSLCIAEGNNIDPFVSASTVQTGINIAGRI 61

Qy 71 LGTLGVFPAGVASLYSFIILGELWPKGNOWEIFMEHVEEIIINOKISTYARNKALTDLKG 130
Db 62 LGVLGVFPAGQLASFYSFLVGLWPRGRDQWEIFLEHVEQLINQQITENARN TALARLOG 121

Qy 131 LGDALAVYHDSLESWGNRNRRNSRVKSYIALELMFVQKLPFAVSGEEVPLPIYA 190
Db 122 LGDSFRAYQQSLEDWLENRDDATRSVLYTYQYIALELDFLNAMPLFAIRNQEVPELLMWYA 181

Qy 191 QANLHLLILLRDAISIFKENGSLSSSETSTFYNQVERAGDYSDHCYKWTSTGLNNLRGTN 250
Db 182 QANLHLLILLRDAISLGFSEFGLTSQETQRYERQVERTRDYSYCVIEWYNTGLNSLRGTN 241

Qy 251 AESVRYNQPRRDMTLMVLVALFYSYDTQMPYIKTTAQLTREVTYDAIGTVHPHPSFT 310
Db 242 AASVRYNQPRRDLTLGVLDLVALFYSYDTRTPINTSAQLTREVTYDAIGAT--GVNMA 299

Qy 311 STTWYNNAPFSAIEAENAVRNPHLLDFLEQVTIYLLSRWSNTQNMWGGHKEFRTI 370
Db 300 SMWYNNAPFSAIEAAARSPELLDFLEQLTFSSASSWSNTRHMYWRGHTIQSRPI 359

Qy 371 GGTINISTGTSNTSINPVTLPFTSRDVRTESLAGLNF--LTQPVNGVPRVDVHMKFV 428
Db 360 GGGINTSTHGATNTSINPVTLPASRDVRYTESYAGVLLWGIYLEPIHGVTVRNF--- 416

Qy 429 THP-----IASDNFYPGYAGIGTQLQDSNELPPEATGQPNYESYSHLSHIGLSASH 483
Db 417 TNPQNISDRGTANYSQP-YESPGQLKDSLETLPETTERPNYESYSHLSHIGIILQSR 475

Qy 484 VKALVSWTHRSADRNTNTEPNSITQIPLKAYNLSSGAAYVZPGFTGCDILRRNTGT 543
Db 476 VNPVYSWTHRSADRNTNTEPNSITQIPLMVKASLPQGTTVVRGPGFTGCDILRRNTGG 535

Qy 544 FGBIRVINPFFAQRVRYRIRYASTTDLQPHTSINGKAINQGNFSATMNRGEDLDYKTR 603
Db 536 FGBIRVTNGLPQRYRIGFRYASTVDFDFVSRGGTTVNNFRFLRTMNSGDELKYGNFV 595

Qy 604 TVGPTTFPFLDVQSTTIGAWNFSSGNEVYIDRIEFPVVEVYEAHYDFEKAQKV TAL 663
Db 596 RRAFTTFPTQIQDIIRTSIQGLSGNGEYVIDKIEIIPVTATFEAYDLERAQEAVAL 655

Qy 664 FTSNPRGLKTDVKYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKOLHIERNM 719
Db 656 FTNTNPRLKTVDYHIDQVSNLVACLSDEFCLDEKRELLEKVKAKLSDERNL 711

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Search completed: October 28, 2004, 18:29:51  
Job time : 101.579 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 28, 2004, 17:51:02 ; Search time 86.6903 Seconds  
(without alignments)  
2975.262 Million cell updates/sec

Title: US-10-019-823b-55  
Perfect score: 3760  
Sequence: 1 MKLKNQDKQSPSSNAKVDK.....KRELPEIVYAKQLHIERNM 719

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:\*

- 1: Genesecp1980s:\*
- 2: Genesecp1990s:\*
- 3: Genesecp2000s:\*
- 4: Genesecp2001s:\*
- 5: Genesecp2002s:\*
- 6: Genesecp2003as:\*
- 7: Genesecp2003bs:\*
- 8: Genesecp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3760	100.0	719	4	AAB66908 Insectici
2	3760	100.0	719	6	AAB66908 Insectici
3	3756	99.9	719	4	AAB66910 Insectici
4	3756	99.9	719	6	AAB66910 Insectici
5	3751	99.8	719	4	AAB66910 Insectici
6	3749	99.7	719	4	AAB66911 Insectici
7	3749	99.7	719	6	AAB66911 Insectici
8	3743	99.5	719	4	AAB66909 Insectici
9	3743	99.5	719	6	AAB66909 Insectici
10	3739	99.4	719	2	AAB66907 Insectici
11	3728.5	99.2	718	6	AAB66907 Insectici
12	3722.5	99.0	718	4	AAB66907 Insectici
13	3551	94.4	719	7	ADM74717 B. thurin
14	3520	93.6	719	4	AAB66912 Insectici
15	3520	93.6	719	6	AAB66912 Insectici
16	3476.5	92.5	710	4	AAU02041 B. thurin
17	3397	90.3	719	3	ABB07073 Bacillus
18	3377	89.8	719	2	AAW49089 Bacillus
19	3291	87.5	1217	4	AAU02092 Bacillus
20	2734	72.7	1208	4	AAU02093 Bacillus
21	2448	65.1	1230	8	ADK98484 B thuring
22	2448	65.1	1230	8	ADK98489 B thuring
23	2448	65.1	1230	8	ADK98481 B thuring
24	2448	65.1	1230	8	ADK98491 B thuring
25	2448	65.1	1230	8	ADK98487 B thuring

26 2446.5 65.1 1229 2 AAR54074 CryET5. 2  
27 2446.5 65.1 1229 2 AAW35259 Bacillus  
28 2446.5 65.1 1229 2 AAW17699 CryET5. 3  
29 2446.5 65.1 1229 2 AAW87633 CryET5 pr  
30 2446.5 65.1 1229 2 AAY30923 B. thurin  
31 2446.5 65.1 1229 8 ADK98479 B. thuring  
32 2344.5 62.4 488 2 AAW44322 Bacillus  
33 2344.5 62.4 488 2 AAB19947 Bacillus  
34 2278.5 60.6 1228 4 AAR50955 Bacillus  
35 2273.5 60.5 1209 4 AAU02094 Bacillus  
36 2264.5 60.2 1227 2 AAY31990 Chimeric  
37 2195.5 58.4 1227 2 AAW44321 Bacillus  
38 2195.5 58.4 1227 4 AAB19950 Bacillus  
39 2186.5 58.2 1227 4 AAU02046 B. thurin  
40 2171.5 57.8 1186 2 AAY16796 Amino aci  
41 2156.5 57.4 1221 4 AAU00421 B. thurin  
42 2142.5 57.0 1221 4 AAU00420 B. thurin  
43 2116 56.3 1228 4 AAB84628 Amino aci  
44 2116 56.3 1228 4 AAU02039 B. thurin  
45 1932.5 51.4 543 2 AAY16797 Amino aci

## ALIGNMENTS

RESULT 1  
AAB66908  
ID AAB66908 standard; protein; 719 AA.  
XX AC AAB66908;  
XX AC  
DT 12-APR-2001 (first entry)  
DE Insecticidal protein cryIIa2.  
XX DE  
KW Insecticide; transgenic plant; insect-resistance.  
XX OS Paecilomyces sp.  
XX PN WO200100841-A1.  
PD 04-JAN-2001.  
PF 23-JUN-2000; 2000WO-GB002457.  
PR 29-JUN-1999; 99GB-00015215.  
PR 23-DEC-1999; 99GB-00030536.  
XX (ZENE ) ZENECA LTD.  
PI Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;  
PI Vincent JL, Lee MD;  
XX WPI; 2001-123015/13.  
PT Novel insecticidal protein obtained from species of Paecilomyces for  
PT controlling insects, and for insect-resistant transgenic plant  
PS production.  
XX Claim 14; Page 55-57; 72pp; English.  
XX The present invention relates to novel insecticidal proteins obtained  
CC from Paecilomyces sp. (see AAB66909 to AAB66901 and AAB66913). The  
CC insecticidal proteins can be used to produce transgenic plants, which are  
CC insect-resistant. Also, the insecticidal proteins are useful for  
CC controlling insects by providing them at a locus where insects feed  
SQ Sequence 719 AA;

Query Match 100.0%; Score 3760; DB 4; Length 719;  
Best Local Similarity 100.0%; Pred. No. 1.1e-293;  
Matches 719; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCLKNQKHQSFSSNAKVDKISTDSLKNETDIELQNIHEDCLKMSYENVEPVSASTI 60  
 Db 1 MCLKNQKHQSFSSNAKVDKISTDSLKNETDIELQNIHEDCLKMSYENVEPVSASTI 60  
 QY 61 QTGIGIAGKILGTLGVFPAGQVAVSLYFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
 Db 61 QTGIGIAGKILGTLGVFPAGQVAVSLYFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
 QY 121 RNKALTDLKGGLDALAVYHDSLESWGNRNTRARSVVKQYIALELMFVKQLPSFAVSG 180  
 Db 121 RNKALTDLKGGLDALAVYHDSLESWGNRNTRARSVVKQYIALELMFVKQLPSFAVSG 180  
 QY 181 BEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWYS 240  
 Db 181 BEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWYS 240  
 QY 241 TGLNNLRGTNAESWVRYNQFRDRLMVLVDLVALFPSTQMPYIKTTAQLTREVTDAI 300  
 Db 241 TGLNNLRGTNAESWVRYNQFRDRLMVLVDLVALFPSTQMPYIKTTAQLTREVTDAI 300  
 QY 301 GTVHPHPSFTSTTWNNNAPSFAIEAAVVRNPHLLDLEQVTIYSLSRWSNTQYNNMW 360  
 Db 301 GTVHPHPSFTSTTWNNNAPSFAIEAAVVRNPHLLDLEQVTIYSLSRWSNTQYNNMW 360  
 QY 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGNLFQTQVNGVPR 420  
 Db 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGNLFQTQVNGVPR 420  
 QY 421 VDFHWKFVTHPIASDNFYYPGAGIGTQLODSENELPEATGQPNYESYSHRLSHIGLIS 480  
 Db 421 VDFHWKFVTHPIASDNFYYPGAGIGTQLODSENELPEATGQPNYESYSHRLSHIGLIS 480  
 QY 481 ASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRTN 540  
 Db 481 ASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRTN 540  
 QY 541 TGTGDIRVNNPPPAQRYRIRYASTTDLOFTSINGKAINQGNFSATNNGEDLDYK 600  
 Db 541 TGTGDIRVNNPPPAQRYRIRYASTTDLOFTSINGKAINQGNFSATNNGEDLDYK 600  
 QY 601 TFRVGTFTTSPFLDVQSTFTTIGAWNFSSGNEVIDRIEFVPEVTVYEAEDFEKAQEKV 660  
 Db 601 TFRVGTFTTSPFLDVQSTFTTIGAWNFSSGNEVIDRIEFVPEVTVYEAEDFEKAQEKV 660  
 QY 661 TALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719  
 Db 661 TALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 2

AAE36272  
 ID AAE36272 standard; protein; 719 AA.  
 AC  
 XX AAE36272;  
 DT 26-JUN-2003 (first entry)  
 DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa2.  
 DE Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.  
 KW Bacillus thuringiensis.  
 OS  
 XX WO200298911-A2.  
 PD 12-DEC-2002.  
 XX  
 PF 30-MAY-2002; 2002WO-GB002666.  
 XX  
 PR 07-JUN-2001; 2001GB-00013900.  
 XX  
 PA (SYGN ) SYNGENTA LTD.  
 XX

PI Vincent JL, Viner R;  
 XX WPI; 2003-175137/17.  
 XX  
 PT New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.  
 PT  
 XX  
 PS Claim 12; Page 44-47; 67pp; English.  
 XX  
 CC The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects.  
 CC Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention  
 CC  
 XX  
 SQ Sequence 719 AA;  
 Query Match 100.0%; Score 3760; DB 6; Length 719;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-293;  
 Matches 719; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MCLKNQKHQSFSSNAKVDKISTDSLKNETDIELQNIHEDCLKMSYENVEPVSASTI 60  
 Db 1 MCLKNQKHQSFSSNAKVDKISTDSLKNETDIELQNIHEDCLKMSYENVEPVSASTI 60  
 QY 61 QTGIGIAGKILGTLGVFPAGQVAVSLYFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
 Db 61 QTGIGIAGKILGTLGVFPAGQVAVSLYFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
 QY 121 RNKALTDLKGGLDALAVYHDSLESWGNRNTRARSVVKQYIALELMFVKQLPSFAVSG 180  
 Db 121 RNKALTDLKGGLDALAVYHDSLESWGNRNTRARSVVKQYIALELMFVKQLPSFAVSG 180  
 QY 181 BEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWYS 240  
 Db 181 BEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWYS 240  
 QY 241 TGLNNLRGTNAESWVRYNQFRDRLMVLVDLVALFPSTQMPYIKTTAQLTREVTDAI 300  
 Db 241 TGLNNLRGTNAESWVRYNQFRDRLMVLVDLVALFPSTQMPYIKTTAQLTREVTDAI 300  
 QY 301 GTVHPHPSFTSTTWNNNAPSFAIEAAVVRNPHLLDLEQVTIYSLSRWSNTQYNNMW 360  
 Db 301 GTVHPHPSFTSTTWNNNAPSFAIEAAVVRNPHLLDLEQVTIYSLSRWSNTQYNNMW 360  
 QY 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGNLFQTQVNGVPR 420  
 Db 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGNLFQTQVNGVPR 420  
 QY 421 VDFHWKFVTHPIASDNFYYPGAGIGTQLODSENELPEATGQPNYESYSHRLSHIGLIS 480  
 Db 421 VDFHWKFVTHPIASDNFYYPGAGIGTQLODSENELPEATGQPNYESYSHRLSHIGLIS 480  
 QY 481 ASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRTN 540  
 Db 481 ASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRTN 540  
 QY 541 TGTGDIRVNNPPPAQRYRIRYASTTDLOFTSINGKAINQGNFSATNNGEDLDYK 600  
 Db 541 TGTGDIRVNNPPPAQRYRIRYASTTDLOFTSINGKAINQGNFSATNNGEDLDYK 600  
 QY 601 TFRVGTFTTSPFLDVQSTFTTIGAWNFSSGNEVIDRIEFVPEVTVYEAEDFEKAQEKV 660  
 Db 601 TFRVGTFTTSPFLDVQSTFTTIGAWNFSSGNEVIDRIEFVPEVTVYEAEDFEKAQEKV 660  
 QY 661 TALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719  
 Db 661 TALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719

QY 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFITQPVNGYPR 420  
 DB 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFITQPVNGYPR 420  
 QY 421 VDFHMKFVTHPIASDNFYYPGVAGIGTQLOSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 DB 421 VDFHMKFVTHPIASDNFYYPGVAGIGTQLOSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 QY 481 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 540  
 DB 481 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 540  
 QY 541 TGTGDIRVNIINPPFAQRYRVRIRYASTTDLOFHTSINGKAINQGNFSAATWNRGDDLYK 600  
 DB 541 TGTGDIRVNIINPPFAQRYRVRIRYASTTDLOFHTSINGKAINQGNFSAATWNRGDDLYK 600  
 QY 601 TPTVGTTPFSLDVQSTFTTIGAWNFSSGNEVYDRIEFVFPVEVTEAEYDFEKAQEKV 660  
 DB 601 TPTVGTTPFSLDVQSTFTTIGAWNFSSGNEVYDRIEFVFPVEVTEAEYDFEKAQEKV 660  
 QY 661 TALFTSTNPRGLKTDVVDYHIDQVSNLVESLSDFFYLDEKRELFEIVKAKQLHIERNM 719  
 DB 661 TALFTSTNPRGLKTDVVDYHIDQVSNLVESLSDFFYLDEKRELFEIVKAKQLHIERNM 719

RESULT 4

ID AAE36274 standard; protein; 719 AA.  
 AC AAE36274;  
 DT 26-JUN-2003 (first entry)  
 DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa4.  
 DE Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.  
 OS Bacillus thuringiensis.  
 PN WO200298911-A2.  
 PD 12-DEC-2002.  
 PF 30-MAY-2002; 2002WO-GB002666.  
 PR 07-JUN-2001; 2001GB-00013900.  
 PA (SYGN) SYNGENTA LTD.  
 PI Vincent JL, Viner R;  
 DR WPI; 2003-175137/17.  
 PT New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.  
 PS Claim 12; Page 50-53; 67pp; English.

The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects. Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention  
 Sequence 719 AA;  
 Query Match 99.9%; Score 3756; DB 6; Length 719;  
 Best Local Similarity 99.9%; Pred. No. 2.3e-293;  
 Matches 718; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 3  
 ID AAB66910 standard; protein; 719 AA.  
 AC AAB66910;  
 DT 12-APR-2001 (first entry)  
 DE Insecticidal protein cryIIa4.  
 DE Insecticide; transgenic plant; insect-resistance.  
 OS Paecilomyces sp.  
 PN WO200100841-A1.  
 PD 04-JAN-2001.  
 PF 23-JUN-2000; 2000WO-GB002457.  
 PR 29-JUN-1999; 99GB-00015215.  
 PR 23-DEC-1999; 99GB-00030536.  
 PA (ZENE) ZENECA LTD.  
 PI Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;  
 PI Vincent JL, Lee MD;  
 DR WPI; 2001-123015/13.  
 PT Novel insecticidal protein obtained from species of Paecilomyces for controlling insects, and for insect-resistant transgenic plant production.  
 PS Claim 14; Page 60-62; 72pp; English.

The present invention relates to novel insecticidal proteins obtained from Paecilomyces sp. (see AAB66910 and AAB66913). The insecticidal proteins can be used to produce transgenic plants, which are insect-resistant. Also, the insecticidal proteins are useful for controlling insects by providing them at a locus where insects feed  
 Sequence 719-AA;  
 Query Match 99.9%; Score 3756; DB 4; Length 719;  
 Best Local Similarity 99.9%; Pred. No. 2.3e-293;  
 Matches 718; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 1 MKLKNQDKHOSFSSNAKVDKISTDSLNKNETDIELQINHEDECKMSEYENVEPVSASTI 60  
 1 MKLKNQDKHOSFSSNAKVDKISTDSLNKNETDIELQINHEDECKMSEYENVEPVSASTI 60  
 61 QTGIGIAGKILGTLPVFPAGQVASYLSFILGELWPKGKQWEIFMEHVEEIIINQKISTYA 120  
 61 QTGIGIAGKILGTLPVFPAGQVASYLSFILGELWPKGKQWEIFMEHVEEIIINQKISTYA 120  
 121 RNKALTDLKLGDALAVYHDSLESWGNNRNTARSQYIALMLFVKLPSPFVSG 180  
 121 RNKALTDLKLGDALAVYHDSLESWGNNRNTARSQYIALMLFVKLPSPFVSG 180  
 181 EYVPLPIYAQAANLHLLLRDASIFGKEWGLSSSISFTYNNQVERAGDYSDHCWKYS 240  
 181 EYVPLPIYAQAANLHLLLRDASIFGKEWGLSSSISFTYNNQVERAGDYSDHCWKYS 240  
 241 TGLNLRGTNAESWRYNQPRDMTLMVLVDLVALFPSYDTQMPYIKTTAQLTREYTDI 300  
 241 TGLNLRGTNAESWRYNQPRDMTLMVLVDLVALFPSYDTQMPYIKTTAQLTREYTDI 300  
 301 GTVHPHPSFTSTTWYNNAPSFSAIAAVVRNPHLLDLEQVITYSLISWNSNTQYNNMW 360  
 301 GTVHPHPSFTSTTWYNNAPSFSAIAAVVRNPHLLDLEQVITYSLISWNSNTQYNNMW 360

QY 1 MKLNQDQKQSFSSNAKVDKISTDSLNKNETDIELQININHEDCMKSEYENVEPVSASTI 60  
 DB 1 MKLNQDQKQSFSSNAKVDKISTDSLNKNETDIELQININHEDCMKSEYENVEPVSASTI 60  
 QY 61 QTGIGIAGKILGTGVPPAGQVASYLFIIGELMPKGNQWEIFMEHVEEIIINQKISTYA 120  
 DB 61 QTGIGIAGKILGTGVPPAGQVASYLFIIGELMPKGNQWEIFMEHVEEIIINQKISTYA 120  
 QY 121 RNKALTDLKGIDALAVVHDSLEWVGNNRNNTRARSVVKQYIALELMFVKQLPSFAVSG 180  
 DB 121 RNKALTDLKGIDALAVVHDSLEWVGNNRNNTRARSVVKQYIALELMFVKQLPSFAVSG 180  
 QY 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNRQVERAGDYSCHVKWYS 240  
 DB 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNRQVERAGDYSCHVKWYS 240  
 QY 241 TGLNLRGTNAESWRYNQFRDMLVLDLVALPSPSYDTQMPYPIKTAQLTREVTYDAI 300  
 DB 241 TGLNLRGTNAESWRYNQFRDMLVLDLVALPSPSYDTQMPYPIKTAQLTREVTYDAI 300  
 QY 301 GTVHPHPSFTTWTNNNAPSFSAIEAAVVRNPHLLDFLEQVTTIYSLLSRWSNTQYNNMW 360  
 DB 301 GTVHPHPSFTTWTNNNAPSFSAIEAAVVRNPHLLDFLEQVTTIYSLLSRWSNTQYNNMW 360  
 QY 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFLTQPVNGVPR 420  
 DB 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFLTQPVNGVPR 420  
 QY 421 VDFHWKFVTHPIASDNFYYPGAGICTQDSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 DB 421 VDFHWKFVTHPIASDNFYYPGAGICTQDSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 QY 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRTN 540  
 DB 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRTN 540  
 QY 541 TGTGDIRVNIAPPFAQRYRIRYASTDLOFHTSINGKAINQGNFSAIWMRGEDLDYK 600  
 DB 541 TGTGDIRVNIAPPFAQRYRIRYASTDLOFHTSINGKAINQGNFSAIWMRGEDLDYK 600

RESULT 5  
 ID AAU02095  
 AC AAU02095 standard; protein; 719 AA.  
 XX  
 XX AAU02095;  
 XX  
 XX 07-SEP-2001 (first entry)  
 XX  
 DE Bacillus thuringiensis partial mutant CryIIa.  
 XX  
 XX Crystal protein; CryIIa; CryIIa; moth; butterfly; Colorado potato beetle;  
 XX mutant; mutein.  
 XX  
 OS Bacillus thuringiensis.  
 XX  
 XX Location/Qualifiers  
 FH 1.19  
 FT Peptide  
 FT /label= Signal\_peptide  
 FT 20..719  
 FT Protein  
 FT /label= Mature\_CryIIa  
 XX  
 XX EP1099760-A1.  
 PN  
 XX

PD 16-MAY-2001.  
 XX 09-NOV-1999; 99EP-00203723.  
 XX 09-NOV-1999; 99EP-00203723.  
 PR (CPRO-) CPRO-DLO CENT PLANTENVERDEDELINGS REPROD.  
 XX De Maagd RA, Bosch HJ;  
 PI WPI; 2001-337141/36.  
 DR N-PSDB; AAS04855.  
 XX  
 PT New hybrid Bacillus thuringiensis hybrid toxins comprising structural  
 PT domains derived from at least 2 different crystal proteins, such as  
 PT CryIIa and CryIIb, and having insecticidal activity, useful for combating  
 PT insects.  
 XX  
 PS Example; Page 30-32; 43pp; English.  
 XX  
 CC The sequence is B. thuringiensis (Bt) crystal protein CryIIa, the DNA  
 CC encoding which was mutated to allow cloning of domain III or domains I  
 CC and II, to make the hybrid protoxins of the invention. The hybrid toxins  
 CC of the invention, having structural domains I, II and III in this order  
 CC starting from the N-terminal derived from at least 2 different crystal  
 CC proteins, are useful for protecting plants against pest insects, e.g.  
 CC moths, butterflies and Colorado potato beetle or for combating insects  
 XX  
 SQ Sequence 719 AA;  
 Query Match 99.8%; Score 3751; DB 4; Length 719;  
 Best Local Similarity 99.9%; Pred. No. 5.8e-293;  
 Matches 718; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MKLNQDQKQSFSSNAKVDKISTDSLNKNETDIELQININHEDCMKSEYENVEPVSASTI 60  
 DB 1 MKLNQDQKQSFSSNAKVDKISTDSLNKNETDIELQININHEDCMKSEYENVEPVSASTI 60  
 QY 61 QTGIGIAGKILGTGVPPAGQVASYLFIIGELMPKGNQWEIFMEHVEEIIINQKISTYA 120  
 DB 61 QTGIGIAGKILGTGVPPAGQVASYLFIIGELMPKGNQWEIFMEHVEEIIINQKISTYA 120  
 QY 121 RNKALTDLKGIDALAVVHDSLEWVGNNRNNTRARSVVKQYIALELMFVKQLPSFAVSG 180  
 DB 121 RNKALTDLKGIDALAVVHDSLEWVGNNRNNTRARSVVKQYIALELMFVKQLPSFAVSG 180  
 QY 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNRQVERAGDYSCHVKWYS 240  
 DB 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNRQVERAGDYSCHVKWYS 240  
 QY 241 TGLNLRGTNAESWRYNQFRDMLVLDLVALPSPSYDTQMPYPIKTAQLTREVTYDAI 300  
 DB 241 TGLNLRGTNAESWRYNQFRDMLVLDLVALPSPSYDTQMPYPIKTAQLTREVTYDAI 300  
 QY 301 GTVHPHPSFTTWTNNNAPSFSAIEAAVVRNPHLLDFLEQVTTIYSLLSRWSNTQYNNMW 360  
 DB 301 GTVHPHPSFTTWTNNNAPSFSAIEAAVVRNPHLLDFLEQVTTIYSLLSRWSNTQYNNMW 360  
 QY 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFLTQPVNGVPR 420  
 DB 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFLTQPVNGVPR 420  
 QY 421 VDFHWKFVTHPIASDNFYYPGAGICTQDSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 DB 421 VDFHWKFVTHPIASDNFYYPGAGICTQDSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 QY 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRTN 540  
 DB 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRTN 540  
 QY 541 TGTGDIRVNIAPPFAQRYRIRYASTDLOFHTSINGKAINQGNFSAIWMRGEDLDYK 600  
 DB 541 TGTGDIRVNIAPPFAQRYRIRYASTDLOFHTSINGKAINQGNFSAIWMRGEDLDYK 600



QY 601 TFRVTGTTTSPFLDVQSTTTIGAWNFSSGNEVYIDRIEFVPEVVEVYAEYDFEKAQEKV 660  
 DB 601 TFRVTGTTTSPFLDVQSTTTIGAWNFSSGNEVYIDRIEFVPEVVEVYAEYDFEKAQEKV 660  
 QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719  
 DB 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 6  
 AAB66911  
 ID AAB66911 standard; protein; 719 AA.  
 XX AC AAB66911;  
 XX DT 12-APR-2001 (first entry)  
 XX DE Insecticidal protein cryIIa5.  
 XX KW Insecticide; transgenic plant; insect-resistance.  
 XX OS Paecilomyces sp.  
 XX PN WO200100841-A1.  
 XX PD 04-JAN-2001.  
 XX PF 23-JUN-2000; 2000WO-GB002457.  
 XX PR 29-JUN-1999; 99GB-00015215.  
 XX PR 23-DEC-1999; 99GB-00030536.  
 XX PA (ZENE ) ZENECA LTD.  
 XX PI Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;  
 XX PI Vincent JL, Lee MD;  
 XX WPI; 2001-123015/13.  
 XX Novel insecticidal protein obtained from species of Paecilomyces for  
 PT controlling insects, and for insect-resistant transgenic plant  
 PT production.  
 PS Claim 14; Page 62-64; 72pp; English.  
 XX The present invention relates to novel insecticidal proteins obtained  
 CC from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The  
 CC insecticidal proteins can be used to produce transgenic plants, which are  
 CC insect-resistant. Also, the insecticidal proteins are useful for  
 CC controlling insects by providing them at a locus where insects feed  
 XX Sequence 719 AA;  
 SQ Query Match 99.7%; Score 3749; DB 4; Length 719;  
 Best Local Similarity 99.6%; Pred.No. 8.4e-293;  
 Matches 716; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MCLKNQDKHQSFSNAKVXDISTSLKNETDIELQINNHEDCLKMGEYENVEPVFVSGASTI 60  
 DB 1 MCLKNQDKHQSFSNAKVXDISTSLKNETDIELQINNHEDCLKMGEYENVEPVFVSGASTI 60  
 QY 61 QTGIGIAGKILGTGVFPAGQVSLYSFIIIGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
 DB 61 QTGIGIAGKILGTGVFPAGQVSLYSFIIIGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
 QY 121 RNKALTDLKLGLDALAYVHDSLESVGNRRNNTARSVYKVSQYIALELMFVQKLPSPAVSG 180  
 DB 121 RNKALTDLKLGLDALAYVHDSLESVGNRRNNTARSVYKVSQYIALELMFVQKLPSPAVSG 180  
 QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFTYNQVERAGDYSCHCKWVWS 240  
 DB 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFTYNQVERAGDYSCHCKWVWS 240

RESULT 7

AAB36275  
 ID AAB36275 standard; protein; 719 AA.  
 XX AC AAB36275;  
 XX DT 26-JUN-2003 (first entry)  
 XX DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa5.  
 XX KW Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.  
 XX OS Bacillus thuringiensis.  
 XX PN WO200298911-A2.  
 XX PD 12-DEC-2002.  
 XX PF 30-MAY-2002; 2002WO-GB002666.  
 XX PR 07-JUN-2001; 2001GB-00013900.  
 XX PA (SYGN ) SYNGENTA LTD.  
 XX PI Vincent JL, Viner R;  
 XX WPI; 2003-175137/17.  
 PT New insecticidal protein comprising an X-glycine motif at the amino-  
 PT terminus, useful as an active ingredient of a pesticide.  
 XX Claim 12; Page 53-56; 67pp; English.  
 XX The invention relates to insecticidal protein comprising an X-glycine  
 CC motif at the amino-terminus. Polynucleotide or DNA constructs of the  
 CC invention are useful for producing plants or plant parts that are  
 CC resistant to insects. The protein or synergistic combination is useful as  
 CC an active ingredient of a pesticide or for controlling insects.  
 CC Antibodies raised to the insecticidal proteins can be used to identify

CC other proteins with insecticidal activity. The present sequence is  
 CC *Bacillus thuringiensis* insecticidal crystal endotoxin (Cry) protein. This  
 CC sequence is used in the invention  
 XX  
 SQ Sequence 719 AA;

Query Match 99.7%; Score 3749; DB 6; Length 719;  
 Best Local Similarity 99.6%; Pred. No. 8.4e-293;  
 Matches 716; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKLNQDKHQSFSSNAKVDKISTDSLNKNETDIELQINHEDCLOKSEYENVEPVSASTI 60  
 DB 1 MKLNQDKHQSFSSNAKVDKISTDSLNKNETDIELQINHEDCLOKSEYENVEPVSASTI 60

QY 61 QTGIGIAGKILGTGVPAGQVASYLSFILGELMPKGNQWEIFMEHVEEIIINQKISTYA 120  
 DB 61 QTGIGIAGKILGTGVPAGQVASYLSFILGELMPKGNQWEIFMEHVEEIIINQKISTYA 120

QY 121 RNKALTDLKLGDALAVYHDSLESWGNRNTRARSVVSQYIALELMFVQKLPSPFAVSG 180  
 DB 121 RNKALTDLKLGDALAVYHDSLESWGNRNTRARSVVSQYIALELMFVQKLPSPFAVSG 180

QY 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNQVERAGDYSYHCVKWS 240  
 DB 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNQVERAGDYSYHCVKWS 240

QY 241 TGLNNLRGTNAESWVRNQFRDMLVLDLVALFPSTQYPIKTAQITREVVYTDAL 300  
 DB 241 TGLNNLRGTNAESWVRNQFRDMLVLDLVALFPSTQYPIKTAQITREVVYTDAL 300

QY 301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVITYSLSRWSNTQYNNMW 360  
 DB 301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVITYSLSRWSNTQYNNMW 360

QY 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGNLFLTPQVNGVPR 420  
 DB 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGNLFLTPQVNGVPR 420

QY 421 VDFHMKFVTHPIASDNFYYPGAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 DB 421 VDFHMKFVTHPIASDNFYYPGAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLIS 480

QY 481 ASHVKALVSWTHRSADRTNIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRTN 540  
 DB 481 ASHVKALVSWTHRSADRTNIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRTN 540

QY 541 TGTFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600  
 DB 541 TGTFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600

RESULT 8  
 AAB66909  
 ID AAB66909 standard; protein; 719 AA.  
 XX  
 AC AAB66909;  
 XX  
 DT 12-APR-2001 (first entry)  
 XX  
 DE Insecticidal protein cryIIa3.  
 XX  
 KW Insecticide; transgenic plant; insect-resistance.  
 XX  
 OS *Paecilomyces* sp.  
 XX

PN WO200100841-A1.  
 XX 04-JAN-2001.  
 XX 23-JUN-2000; 2000WO-GB002457.  
 XX 29-JUN-1999; 99GB-00015215.  
 PR 23-DEC-1999; 99GB-00030536.  
 XX (ZENE ) ZENECA LTD.  
 PA Griffin J, Carlisle AJ, Cayley PJ, Mackay EA, Warner SAJ;  
 PI Vincent JL, Lee MD;  
 XX WPI; 2001-123015/13.  
 DR Novel insecticidal protein obtained from species of *Paecilomyces* for  
 XX controlling insects, and for insect-resistant transgenic plant  
 PT production.  
 PT Claim 14; Page 57-59; 72pp; English.  
 XX The present invention relates to novel insecticidal proteins obtained  
 CC from *Paecilomyces* sp. (see AAB66909 to AAB66901 and AAB66913). The  
 CC insecticidal proteins can be used to produce transgenic plants, which are  
 CC insect-resistant. Also, the insecticidal proteins are useful for  
 CC controlling insects by providing them at a locus where insects feed  
 XX  
 SQ Sequence 719 AA;

Query Match 99.5%; Score 3743; DB 4; Length 719;  
 Best Local Similarity 99.6%; Pred. No. 2.5e-292;  
 Matches 716; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MKLNQDKHQSFSSNAKVDKISTDSLNKNETDIELQINHEDCLOKSEYENVEPVSASTI 60  
 DB 1 MKLNQDKHQSFSSNAKVDKISTDSLNKNETDIELQINHEDCLOKSEYENVEPVSASTI 60

QY 61 QTGIGIAGKILGTGVPAGQVASYLSFILGELMPKGNQWEIFMEHVEEIIINQKISTYA 120  
 DB 61 QTGIGIAGKILGTGVPAGQVASYLSFILGELMPKGNQWEIFMEHVEEIIINQKISTYA 120

QY 121 RNKALTDLKLGDALAVYHDSLESWGNRNTRARSVVSQYIALELMFVQKLPSPFAVSG 180  
 DB 121 RNKALTDLKLGDALAVYHDSLESWGNRNTRARSVVSQYIALELMFVQKLPSPFAVSG 180

QY 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNQVERAGDYSYHCVKWS 240  
 DB 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNQVERAGDYSYHCVKWS 240

QY 241 TGLNNLRGTNAESWVRNQFRDMLVLDLVALFPSTQYPIKTAQITREVVYTDAL 300  
 DB 241 TGLNNLRGTNAESWVRNQFRDMLVLDLVALFPSTQYPIKTAQITREVVYTDAL 300

QY 301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVITYSLSRWSNTQYNNMW 360  
 DB 301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVITYSLSRWSNTQYNNMW 360

QY 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGNLFLTPQVNGVPR 420  
 DB 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGNLFLTPQVNGVPR 420

QY 421 VDFHMKFVTHPIASDNFYYPGAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 DB 421 VDFHMKFVTHPIASDNFYYPGAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLIS 480

QY 481 ASHVKALVSWTHRSADRTNIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRTN 540  
 DB 481 ASHVKALVSWTHRSADRTNIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRTN 540

QY 541 TGTFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600  
 DB 541 TGTFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600

QY 601 TPTVGTTPFSLDVQSTFTICAMNFSSGNEVYIDRIEFPVPEVTEAEYDFEKAQKV 660  
 Db 601 TPTVGTTPFSLDVQSTFTICAMNFSSGNEVYIDRIEFPVPEVTEAEYDFEKAQKV 660  
 QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVSLSDSEFYLDKRELFVIVKAKQLHIERNM 719  
 Db 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVSLSDSEFYLDKRELFVIVKAKQLHIERNM 719

RESULT 9  
 AAE36273  
 ID AAE36273 standard; protein; 719 AA.  
 AC AAE36273;  
 XX  
 DT 26-JUN-2003 (first entry)  
 DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa3.  
 XX  
 KW Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.  
 OS Bacillus thuringiensis.  
 XX  
 PN WO200298911-A2.  
 XX  
 PD 12-DEC-2002.  
 XX  
 PF 30-MAY-2002; 2002WO-GB002666.  
 XX  
 PR 07-JUN-2001; 2001GB-00013900.  
 XX  
 PA (SYGN ) SYNGENTA LTD.  
 XX  
 PI Vincent JL, Viner R;  
 XX  
 DR WPI; 2003-175137/17.  
 XX  
 PT New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.  
 PT  
 PS Claim 12; Page 47-50; 67pp; English.  
 XX  
 CC The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects.  
 CC Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention  
 CC  
 SQ Sequence 719 AA;  
 Query Match 99.5%; Score 3743; DB 6; Length 719;  
 Best Local Similarity 99.6%; Pred. No. 2-5e-292;  
 Matches 716; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MKLKNQKHQSFSNNAKVYKISTDSLKNETDIELQINHEHDCIKMSEYENVEFVSASTI 60  
 Db 1 MKLKNQKHQSFSNNAKVYKISTDSLKNETDIELQINHEHDCIKMSEYENVEFVSASTI 60  
 QY 61 QTGIGIAGKILGTLGVFPAGQVSLYSLFGLGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
 Db 61 QTGIGIAGKILGTLGVFPAGQVSLYSLFGLGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
 QY 121 RNKALTDLKGLDALAVYHDSLSWGVRNNTARSVVKSQYIALELMFVKLPSPFAVSG 180  
 Db 121 RNKALTDLKGLDALAVYHDSLSWGVRNNTARSVVKSQYIALELMFVKLPSPFAVSG 180  
 QY 181 EEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWS 240

Db 181 EEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWS 240  
 QY 241 TGLNLRGTNAESVRYNQFRDMLVLDVALVFPSTYDQMYPIKTAQLTRVYTDAL 300  
 Db 241 TGLNLRGTNAESVRYNQFRDMLVLDVALVFPSTYDQMYPIKTAQLTRVYTDAL 300  
 QY 301 GTVHPHPSFTTWTNNNAPSFAIEAAVAVNPHLLDFLEQVTTYSLSRWSNTQYMMW 360  
 Db 301 GTVHPHPSFTTWTNNNAPSFAIEAAVAVNPHLLDFLEQVTTYSLSRWSNTQYMMW 360  
 QY 361 GGHKLEPRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGNLFLTPQVNGVPR 420  
 Db 361 GGHKLEPRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGNLFLTPQVNGVPR 420  
 QY 421 VDFHMKFVTHPIASDNFYPCYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 Db 421 VDFHMKFVTHPIASDNFYPCYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 QY 481 ASHVKALVYSWTHRSADRTNIEPNSITQPLVKAFNLSSCAAUVRGFGFTGGDILARTN 540  
 Db 481 ASHVKALVYSWTHRSADRTNIEPNSITQPLVKAFNLSSCAAUVRGFGFTGGDILARTN 540  
 QY 541 TGTGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATNRGDEDLYK 600  
 Db 541 TGTGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATNRGDEDLYK 600  
 QY 601 TPTVGTTPFSLDVQSTFTICAMNFSSGNEVYIDRIEFPVPEVTEAEYDFEKAQKV 660  
 Db 601 TPTVGTTPFSLDVQSTFTICAMNFSSGNEVYIDRIEFPVPEVTEAEYDFEKAQKV 660  
 QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVSLSDSEFYLDKRELFVIVKAKQLHIERNM 719  
 Db 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVSLSDSEFYLDKRELFVIVKAKQLHIERNM 719

RESULT 10  
 AAR08041  
 ID AAR08041 standard; protein; 719 AA.  
 XX  
 AC AAR08041;  
 XX  
 DT 24-OCT-2003 (revised)  
 DT 25-MAR-2003 (revised)  
 DT 27-FEB-1991 (first entry)  
 XX  
 DE 81 kD endotoxin deduced from DNA carried on pJH12.  
 XX  
 KW Crystal; insecticide; toxin; delta endotoxin.  
 XX  
 OS Bacillus thuringiensis; JHCC 4353 and 4835.  
 XX  
 PN WO9013651-A.  
 XX  
 PD 15-NOV-1990.  
 XX  
 PF 09-MAY-1989; 89GB-00010624.  
 XX  
 PR 09-MAY-1989; 89GB-00010624.  
 XX  
 PA (ICIL ) IMPERIAL CHEM IND PLC.  
 XX  
 PI Blenk RG, Ely S, Tailor RH, Tippet JM;  
 XX  
 DR WPI; 1990-361486/48.  
 XX  
 DR N-PSDB; AAQ06636.  
 XX  
 PT Bacillus thuringiensis strains - used for producing an endotoxin for protecting plants against insects, partic. Lepidoptera and Coleoptera.  
 PS Claim 5; Fig 5-10; 66pp; English.  
 CC The sequence carried on pJH12 which was isolated from B. thuringiensis strains JHCC4835 and JHCC 4353 (NCIB 40091 and 40090 resp.). The DNA can

CC be used to produce transformants E.coli strain MC12022/pJH12 (NCIB 40278,  
 CC or bacteriophage EMBL4 vector (NCIB 40279) or E.coli strain B21/pJH11  
 CC (NCIB 40275). The delta-endo- toxin produced by the transformants can be  
 CC used in formulations for combatting Lepidoptera and Coleoptera pests.  
 CC (Updated on 25-MAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to  
 CC standardise OS field)  
 XX  
 SQ

Query Match	99.4%;	Score 3739;	DB 2;	Length 719;
Best Local Similarity	99.6%;	Pred. No. 5.3e-292;		
Matches 716;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;

  

QY	1	MKLKNDKQHSFSSNAKVDKISTDSLKNETDIELQINNHEDCLKMSYENVEPVSASTI	60
DB	1	MKLKNDKQHSFSSNAKVDKISTDSLKNETDIELQINNHEDCLKMSYENVEPVSASTI	60
QY	61	QTGIGIACKILGTGVPAGQVASYLSFILGELPKGNQWEIPEHVEEILNOKISTYA	120
DB	61	QTGIGIACKILGTGVPAGQVASYLSFILGELPKGNQWEIPEHVEEILNOKISTYA	120
QY	121	RNKALTDLKLGDALAVYHDSLESVGNRNTRARSVVKSQYIALELMFVKLPSPAVSG	180
DB	121	RNKALTDLKLGDALAVYHDSLESVGNRNTRARSVVKSQYIALELMFVKLPSPAVSG	180
QY	181	BEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNRQVERAGDYSHCVKWYS	240
DB	181	BEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNRQVERAGDYSHCVKWYS	240
QY	241	TGLNLRGTNAESWRYNQFRDMTLMVLDLVALFPYSYDTQYPIKTTAQLTREYVTDAL	300
DB	241	TGLNLRGTNAESWRYNQFRDMTLMVLDLVALFPYSYDTQYPIKTTAQLTREYVTDAL	300
QY	301	GTVPHPSPFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTTIYSLLSRWSNTQYNNMW	360
DB	301	GTVPHPSPFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTTIYSLLSRWSNTQYNNMW	360
QY	361	GGHKLFEFTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGNLFLTQPVNGVPR	420
DB	361	GGHKLFEFTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGNLFLTQPVNGVPR	420
QY	421	VDHFKFVTHPIASDNFYYPGAGIGTQDSENELPPEATQGNYESYSHRSLHIGLIS	480
DB	421	VDHFKFVTHPIASDNFYYPGAGIGTQDSENELPPEATQGNYESYSHRSLHIGLIS	480
QY	481	ASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRTN	540
DB	481	ASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRTN	540
QY	541	TGTFGDIRVNPFPFAQRYRIRYASTDLOQFTSINGKAINQGNFSATMNRGEDLDYK	600
DB	541	TGTFGDIRVNPFPFAQRYRIRYASTDLOQFTSINGKAINQGNFSATMNRGEDLDYK	600
QY	601	TPRVGFTPTSPFLDVQSTFTTIGAWNPSGNEVYIDRIEFPVPEVTVYEAEDYDEKAEKV	660
DB	601	TPRVGFTPTSPFLDVQSTFTTIGAWNPSGNEVYIDRIEFPVPEVTVYEAEDYDEKAEKV	660
QY	661	TALFTSTNPRGLKTDVXDYHIDQVSNLVESSDSEFYLDKRELPEIIVKYAKQLHIERNM	719
DB	661	TALFTSTNPRGLKTDVXDYHIDQVSNLVESSDSEFYLDKRELPEIIVKYAKQLHIERNM	719

RESULT 11  
 AAEE36271  
 ID AAEE36271 standard; protein; 718 AA.  
 XX  
 AC AAEE36271;  
 XX  
 DT 26-JUN-2003 (first entry)  
 XX  
 DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, crystall.  
 XX  
 KW Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.

XX	Bacillus thuringiensis.
OS	WO200298911-A2.
PN	12-DEC-2002.
XX	30-MAY-2002; 2002WO-CB002666.
PF	07-JUN-2001; 2001GB-00013900.
XX	(SYGN ) SYNGENTA LTD.
PA	Vincent JL, Viner R;
XX	WPI; 2003-175137/17.
PI	New insecticidal protein comprising an X-glycine motif at the amino-
XX	terminus, useful as an active ingredient of a pesticide.
PT	Claim 12; Page 42-44; 67pp; English.
PS	The invention relates to insecticidal protein comprising an X-glycine
XX	motif at the amino-terminus. Polynucleotide or DNA constructs of the
CC	invention are useful for producing plants or plant parts that are
CC	resistant to insects. The protein or synergistic combination is useful as
CC	an active ingredient of a pesticide or for controlling insects.
CC	Antibodies raised to the insecticidal proteins can be used to identify
CC	other proteins with insecticidal activity. The present sequence is
CC	Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This
CC	sequence is used in the invention
XX	Sequence 718 AA;
SQ	

Query Match	99.2%;	Score 3728.5;	DB 6;	Length 718;
Best Local Similarity	99.6%;	Pred. No. 3.7e-291;		
Matches 716;	Conservative 0;	Mismatches 2;	Indels 1;	Gaps 1;

  

QY	1	MKLKNDKQHSFSSNAKVDKISTDSLKNETDIELQINNHEDCLKMSYENVEPVSASTI	60
DB	1	MKLKNDKQHSFSSNAKVDKISTDSLKNETDIELQINNHEDCLKMSYENVEPVSASTI	60
QY	61	QTGIGIACKILGTGVPAGQVASYLSFILGELPKGNQWEIPEHVEEILNOKISTYA	120
DB	61	QTGIGIACKILGTGVPAGQVASYLSFILGELPKGNQWEIPEHVEEILNOKISTYA	120
QY	121	RNKALTDLKLGDALAVYHDSLESVGNRNTRARSVVKSOYIALELMFVKLPSPAVSG	180
DB	121	RNKALTDLKLGDALAVYHDSLESVGNRNTRARSVVKSOYIALELMFVKLPSPAVSG	180
QY	181	BEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNRQVERAGDYSHCVKWYS	240
DB	181	BEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNRQVERAGDYSHCVKWYS	240
QY	241	TGLNLRGTNAESWRYNQFRDMTLMVLDLVALFPYSYDTQYPIKTTAQLTREYVTDAL	300
DB	241	TGLNLRGTNAESWRYNQFRDMTLMVLDLVALFPYSYDTQYPIKTTAQLTREYVTDAL	300
QY	301	GTVPHPSPFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTTIYSLLSRWSNTQYNNMW	360
DB	301	GTVPHPSPFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTTIYSLLSRWSNTQYNNMW	360
QY	361	GGHKLFEFTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGNLFLTQPVNGVPR	420
DB	361	GGHKLFEFTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGNLFLTQPVNGVPR	420
QY	421	VDHFKFVTHPIASDNFYYPGAGIGTQDSENELPPEATQGNYESYSHRSLHIGLIS	480
DB	421	VDHFKFVTHPIASDNFYYPGAGIGTQDSENELPPEATQGNYESYSHRSLHIGLIS	480
QY	481	ASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRTN	540
DB	481	ASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRTN	540

QY 541 TGTGDIRVNINPPFAQRVVRIRYASTTDLPHTSINGKAINQGNFSAATMNRGEDLDYK 600  
 DB 540 TGTGDIRVNINPPFAQRVVRIRYASTTDLPHTSINGKAINQGNFSAATMNRGEDLDYK 599  
 QY 601 TFRVGTFTPFSLDVQSTFTIGAMNFSNGEYVIDRIEFVPEVTEYAEYDFEKAQEKV 660  
 DB 600 TFRVGTFTPFSLDVQSTFTIGAMNFSNGEYVIDRIEFVPEVTEYAEYDFEKAQEKV 659  
 QY 661 TALFTSTNPRGLTKDVKDHYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719  
 DB 660 TALFTSTNPRGLTKDVKDHYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 718

RESULT 12  
 AAB66907  
 ID AAB66907 standard; protein; 718 AA.

XX AC AAB66907;  
 XX DT 12-APR-2001 (first entry)  
 XX DE Insecticidal protein cryIIa1.  
 XX DE Insecticide; transgenic plant; insect-resistance.  
 XX KW Paecilomyces, sp.  
 XX OS WO200100841-A1.  
 XX PN 04-JAN-2001.  
 XX PD 23-JUN-2000; 2000WO-GB002457.  
 XX PF 29-JUN-1999; 99GB-00015215.  
 XX PR 23-DEC-1999; 99GB-00030536.  
 XX XX (ZENE ) ZENECA LTD.  
 XX X Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;  
 XX X Vincent JL, Lee ND;  
 XX X WPI; 2001-123015/13.  
 XX PT Novel insecticidal protein obtained from species of Paecilomyces for  
 XX PT controlling insects, and for insect-resistant transgenic plant  
 XX PT production.  
 XX PS Claim 14; Page 53-55; 72pp; English.  
 XX CC The present invention relates to novel insecticidal proteins obtained  
 XX CC from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The  
 XX CC insecticidal proteins can be used to produce transgenic plants, which are  
 XX CC insect-resistant. Also, the insecticidal proteins are useful for  
 XX CC controlling insects by providing them at a locus where insects feed  
 XX SQ Sequence 718 AA;

Query Match 99.08; Score 3722.5; DB 4; Length 718;  
 Best Local Similarity 99.4%; Pred. No. 1.1e-290;  
 Matches 715; Conservative 0; Mismatches 3; Indels 1; Gaps 1;  
 QY 1 MCLKNQDKHQSFSNAKVDKISTDSLKNETDIELQININHEDECLKMSEYENVEPFVSASTI 60  
 DB 1 MCLKNQDKHQSFSNAKVDKISTDSLKNETDIELQININHEDECLKMSEYENVEPFVSASTI 60  
 QY 61 QTGIGIAGKILGTGVFPAGQASLSFILGELWPKGNQWEIFMHEVEIINQKISTYA 120  
 DB 61 QTGIGIAGKILGTGVFPAGQASLSFILGELWPKGNQWEIFMHEVEIINQKISTYA 120  
 QY 121 RNKALTDLKLGDALAYVHDSLSWGVRNNTARSVVKSQYIALMLFVKQLPSFAVSG 180  
 DB 121 RNKALTDLKLGDALAYVHDSLSWGVRNNTARSVVKSQYIALMLFVKQLPSFAVSG 180

QY 181 EEVPLLPYAAQANLHLLLRDASIFGKEWGLSSSEISTFYNROVERAGDYSHCVKWYS 240  
 DB 181 EEVPLLPYAAQANLHLLLRDASIFGKEWGLSSSEISTFYNROVERAGDYSHCVKWYS 240  
 QY 241 TGLNNLRGTNAESWVRVNCQFRDMTLMVLDLVALPSPYDTOMYPIKTTAQITREYITDAI 300  
 DB 241 TGLNNLRGTNAESWVRVNCQFRDMTLMVLDLVALPSPYDTOMYPIKTTAQITREYITDAI 300  
 QY 301 GTVHPHPFSTTWTWNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRNSNTQYMMNW 360  
 DB 301 GTVHPHPFSTTWTWNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRNSNTQYMMNW 360  
 QY 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGNLFLTQPVN-VPR 420  
 DB 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGNLFLTQPVN-VPR 419  
 QY 421 VDFHWKFTVTHPIASDNFYVPGVAGIGTQLOQSENELPEATGQPNYESYSHRLSHIGLIS 480  
 DB 420 VDFHWKFTVTHPIASDNFYVPGVAGIGTQLOQSENELPEATGQPNYESYSHRLSHIGLIS 479  
 QY 481 ASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
 DB 480 ASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 539  
 QY 541 TGTGDIRVNINPPFAQRVVRIRYASTTDLPHTSINGKAINQGNFSAATMNRGEDLDYK 600  
 DB 540 TGTGDIRVNINPPFAQRVVRIRYASTTDLPHTSINGKAINQGNFSAATMNRGEDLDYK 599  
 QY 601 TFRVGTFTPFSLDVQSTFTIGAMNFSNGEYVIDRIEFVPEVTEYAEYDFEKAQEKV 660  
 DB 600 TFRVGTFTPFSLDVQSTFTIGAMNFSNGEYVIDRIEFVPEVTEYAEYDFEKAQEKV 659  
 QY 661 TALFTSTNPRGLTKDVKDHYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719  
 DB 660 TALFTSTNPRGLTKDVKDHYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 718

RESULT 13  
 ADM74717  
 ID ADM74717 standard; protein; 719 AA.

XX AC ADM74717;  
 XX DT 03-JUN-2004 (first entry)  
 XX DE B. thuringiensis cryIIel SEQ ID NO:2.  
 XX KW cryI; toxicity; lepidoptera; cryIIab; cryIIa; coleoptera; diptera;  
 XX KW cryIIel.  
 XX OS Bacillus thuringiensis.  
 XX PN CN1401772-A.  
 XX PD 12-MAR-2003.  
 XX PF 20-AUG-2001; 2001CN-00124163.  
 XX PR 20-AUG-2001; 2001CN-00124163.  
 XX PA (PLAN-) PLANT PROTECTION INST CHINESE ACAD AGRIC.  
 XX PI Song F, Zhang J, Huang D;  
 XX PI WPI; 2003-442339/42.  
 XX DR N-PSDB; ADM74716.  
 XX PT Bacillus thuringiensis cryI gene, expression vector, nucleoside sequence  
 XX PT with high-toxicity to lepidoptera pests, encoded protein, primer  
 XX PT sequences and the shuttle vector pSXV422b, useful as a pesticide.  
 XX PS Example 3; SEQ ID NO 2; 29pp; Chinese.

XX The invention relates to a novel Bacillus thuringiensis cryII gene, gene  
 CC combination, expression vector, nucleotide sequence of the B  
 CC thuringiensis cryII gene with high-toxicity to lepidoptera pests and the  
 CC amino acid sequence of the protein encoded by it, cooperative use of the  
 CC cryII gene with the expression product of cryIAb or cryIAb, primer  
 CC sequences for expressing the genes, and the constructed shuttle vector  
 CC pSV422b. The gene in combination with the cryIAb or cryIAb genes  
 CC displays high toxicity to the lepidoptera, coleoptera and diptera pests.  
 CC The present sequence represents the cryII gene protein.  
 XX Sequence 719 AA;  
 SQ  
 Query Match 94.4%; Score 3551; DB 7; Length 719;  
 Best Local Similarity 93.6%; Pred. No. 7.5e-277;  
 Matches 673; Conservative 26; Mismatches 20; Indels 0; Gaps 0;  
 QY 1 MKLNQDKHQSPSSNAKVDKISTDSLNKNETDIELQNHEDCLAKSEVENVEPVSASTI 60  
 DB 1 MKLNQDKHQSPSSNAKVDKISTDSLNKNETDIELQNHEDCLAKSEVENVEPVSASTI 60  
 QY 61 QTGIGIAGKILGTGVPFAGQVAVSYFILGELMPKGNQWEIFMEHVEEIIINQKISTYA 120  
 DB 61 QTGIGIAGKILGTGVPFAGQVAVSYFILGELMPKGNQWEIFMEHVEEIIINQKISTYA 120  
 QY 121 RNKALTDLKLGDALAVYHDSLESWGNRNTRARSVVKSOYIALELMFVQKLPFAVSG 180  
 DB 121 RNKALTDLKLGDALAVYHDSLESWGNRNTRARSVVKSOYIALELMFVQKLPFAVSG 180  
 QY 181 BEVPLLPYIAQAANLHLLLDASIFGKEWGLSSSEISTFYNNROVERAGDYSCHCVKWS 240  
 DB 181 BEVPLLPYIAQAANLHLLLDASIFGKEWGLSSSEISTFYNNROVERAGDYSCHCVKWS 240  
 QY 241 TGLNLRGTNAESWVRYNQFRRDMLVLDLVALPSPYDTQMPYIKTTAQLTREVTYDAI 300  
 DB 241 TGLNLRGTNAESWVRYNQFRRDMLVLDLVALPSPYDTQMPYIKTTAQLTREVTYDAI 300  
 QY 301 GTVHPHPSFTSTWYNNNAPSFAIEAAVNPVHLLDFLEQVTIYSLLSWSNTQYNNMW 360  
 DB 301 GTVHPHPSFTSTWYNNNAPSFAIEAAVNPVHLLDFLEQVTIYSLLSWSNTQYNNMW 360  
 QY 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDYRTESLAGNLFITQPVNGVPR 420  
 DB 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDYRTESLAGNLFITQPVNGVPR 420  
 QY 421 VDFHWKFVTHPIASDNFYYPGAGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 DB 421 VDFHWKFVTHPIASDNFYYPGAGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 QY 481 ASHVKALVYSWTHRSADRNTIEPNSITQIPLVKAFLNLSGAAVVRPGFTGGDILARTN 540  
 DB 481 ASHVKALVYSWTHRSADRNTIEPNSITQIPLVKAFLNLSGAAVVRPGFTGGDILARTN 540  
 QY 541 TGTGDIRVNIINPPAQRYRIRYASTDLOFTSNGKALNCGNFSATNMGEDLDYK 600  
 DB 541 TGTGDIRVNIINPPAQRYRIRYASTDLOFTSNGKALNCGNFSATNMGEDLDYK 600  
 QY 601 TFRVTGFTPTPSFDVQSTFTIGAWNFSSGNEVDIIEFVFPVETVYEAEDFEKAQEKV 660  
 DB 601 TFRVTGFTPTPSFDVQSTFTIGAWNFSSGNEVDIIEFVFPVETVYEAEDFEKAQEKV 660  
 QY 661 TALFTSTNPRGKTDVQKDYHDQVNLVESLSDSFYLDKRELBEIVKYAKQLHIERNM 719  
 DB 661 TALFTSTNPRGKTDVQKDYHDQVNLVESLSDSFYLDKRELBEIVKYAKQLHIERNM 719

RESULT 14

AAB66912

ID AAB66912 standard; protein; 719 AA.

XX AAB66912;

AC AAB66912;

DT 12-APR-2001 (first entry)

XX Insecticidal protein cryIIb1.  
 XX Insecticide; transgenic plant; insect-resistance.  
 XX Paecilomyces sp.  
 PN WO200100841-A1.  
 XX 04-JAN-2001.  
 XX 23-JUN-2000; 2000WO-CB002457.  
 XX 29-JUN-1999; 99GB-00015215.  
 PR 23-DEC-1999; 99GB-00030536.  
 XX (ZENE ) ZENECA LTD.  
 XX Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;  
 PI Vincent JL, Lee MD;  
 PI WPI; 2001-123015/13.  
 DR Novel insecticidal protein obtained from species of Paecilomyces for  
 PT controlling insects, and for insect-resistant transgenic plant  
 PT production.  
 XX Claim 14; Page 64-66; 72pp; English.  
 XX The present invention relates to novel insecticidal proteins obtained  
 CC from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The  
 CC insecticidal proteins can be used to produce transgenic plants, which are  
 CC insect-resistant. Also, the insecticidal proteins are useful for  
 CC controlling insects by providing them at a locus where insects feed  
 XX Sequence 719 AA;  
 SQ  
 Query Match 93.6%; Score 3520; DB 4; Length 719;  
 Best Local Similarity 92.9%; Pred. No. 2.4e-274;  
 Matches 668; Conservative 31; Mismatches 20; Indels 0; Gaps 0;  
 QY 1 MKLNQDKHQSPSSNAKVDKISTDSLNKNETDIELQNHEDCLAKSEVENVEPVSASTI 60  
 DB 1 MKLNQDKHQSPSSNAKVDKISTDSLNKNETDIELQNHEDCLAKSEVENVEPVSASTI 60  
 QY 61 QTGIGIAGKILGTGVPFAGQVAVSYFILGELMPKGNQWEIFMEHVEEIIINQKISTYA 120  
 DB 61 QTGIGIAGKILGTGVPFAGQVAVSYFILGELMPKGNQWEIFMEHVEEIIINQKISTYA 120  
 QY 121 RNKALTDLKLGDALAVYHDSLESWGNRNTRARSVVKSOYIALELMFVQKLPFAVSG 180  
 DB 121 RNKALTDLKLGDALAVYHDSLESWGNRNTRARSVVKSOYIALELMFVQKLPFAVSG 180  
 QY 181 BEVPLLPYIAQAANLHLLLDASIFGKEWGLSSSEISTFYNNROVERAGDYSCHCVKWS 240  
 DB 181 BEVPLLPYIAQAANLHLLLDASIFGKEWGLSSSEISTFYNNROVERAGDYSCHCVKWS 240  
 QY 241 TGLNLRGTNAESWVRYNQFRRDMLVLDLVALPSPYDTQMPYIKTTAQLTREVTYDAI 300  
 DB 241 TGLNLRGTNAESWVRYNQFRRDMLVLDLVALPSPYDTQMPYIKTTAQLTREVTYDAI 300  
 QY 301 GTVHPHPSFTSTWYNNNAPSFAIEAAVNPVHLLDFLEQVTIYSLLSWSNTQYNNMW 360  
 DB 301 GTVHPHPSFTSTWYNNNAPSFAIEAAVNPVHLLDFLEQVTIYSLLSWSNTQYNNMW 360  
 QY 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDYRTESLAGNLFITQPVNGVPR 420  
 DB 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDYRTESLAGNLFITQPVNGVPR 420  
 QY 421 VDFHWKFVTHPIASDNFYYPGAGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 DB 421 VDFHWKFVTHPIASDNFYYPGAGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480

QY 481 ASHVKALVYSWTHRSADRNTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
 DB 481 ASHVKALVYSWTHRSADRNTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
 QY 541 TGTFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDDLYK 600  
 DB 541 TGTFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDDLYK 600  
 QY 601 TTRTVGFTTPFSGFLDVQSTFTTGAMNFFSSGNEVYIDRIEFVPEVYEAEDYFEKAQEKV 660  
 DB 601 TTRTVGFTTPFSGFLDVQSTFTTGAMNFFSSGNEVYIDRIEFVPEVYEAEDYFEKAQEKV 660  
 QY 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQIHIERNM 719  
 DB 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQIHIERNM 719  
 RESULT 15  
 AAE36276  
 ID AAE36276 standard; protein; 719 AA.  
 AC AAE36276;  
 DT 26-JUN-2003 (first entry)  
 DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIb1.  
 KW Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.  
 OS Bacillus thuringiensis.  
 XX WO200298911-A2.  
 PD 12-DEC-2002.  
 PF 30-MAY-2002; 2002WO-GB002666.  
 PR 07-JUN-2001; 2001GB-00013900.  
 PA (SYGN ) SYNGENTA LTD.  
 PI Vincent JL, Viner R;  
 DR WPI; 2003-175137/17.  
 XX New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.  
 PS Claim 12; Page 56-58; 67pp; English.  
 CC The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects.  
 CC Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention  
 XX Sequence 719 AA;

Query Match 93.6%; Score 3520; DB 6; Length 719;  
 Best Local Similarity 92.9%; Pred. No. 2.4e-274;  
 Matches 668; Conservative 31; Mismatches 20; Indels 0; Gaps 0;  
 QY 1 MKLKNQDKHQSFSNAKVDKIATDSLKNETDIELQNIHEDCLKMSEYENVEPVSASTI 60  
 DB 1 MKLKNPDKHQSLSNAKVDKIATDSLKNETDIELKNMKNEDYLRVSEHSIDPFSASTI 60  
 QY 61 QTGIGIAGKILGTGVFPAGQIASLSYFILGELWPKGKQWEIFMEHVEIINOKISTYA 120  
 DB 61 QTGIGIAGKILGTGVFPAGQIASLSYFILGELWPKGKQWEIFMEHVEIINOKILTVA 120

QY 121 RNKALTDLKGIDALAVYHDSLESWVGNRNNTNRRS VVKSQYIALELMFVKLPSPFVSG 180  
 DB 121 RNKALSDLRGIDALAVYHDSLESWVENRNTNRRS VVKQYIALELMFVKLPSPFVSG 180  
 QY 181 BEVPLLIYQAANLHLLILDASI FKGKGLSSSEISTEFNRCVBERAGDYS DHCVKWYS 240  
 DB 181 BEVPLLIYQAANLHLLILDASI FKGKGLSSSEISTEFNRCVBERAGDYS DHCVKWYS 240  
 QY 241 TGLNLRGTNAESVRYNQFRDMTLMVLDLVALFPSYDTQMPYIKTTAQTREVVYDAI 300  
 DB 241 TGLNLRGTNAESVRYNQFRDMTLMVLDLVALFPSYDTQMPYIKTTAQTREVVYDAI 300  
 QY 301 GTVHPHPSFTSTWYNNNAFSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYNNMW 360  
 DB 301 GTVHPHPSFTSTWYNNNAFSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYNNMW 360  
 QY 361 GGHLEPRTIGTGLNISTOGSTNTSINPVTLPFTSRDVRVYTESLAGLNLFLTPVNGVPR 420  
 DB 361 GGHLEPRTIGTGLNISTOGSTNTSINPVTLPFTSRDVRVYTESLAGLNLFLTPVNGVPR 420  
 QY 421 VDFHWKFTVTHPIASDNFYYPGYAGIGTQLQDSSENELPPEATGQPNYESYSHRISHIGLIS 480  
 DB 421 VDFHWKFTVTHPIASDNFYYPGYAGIGTQLQDSSENELPPEATGQPNYESYSHRISHIGLIS 480  
 QY 481 ASHVKALVYSWTHRSADRNTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
 DB 481 ASHVKALVYSWTHRSADRNTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
 QY 541 TGTFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDDLYK 600  
 DB 541 TGTFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDDLYK 600  
 QY 601 TTRTVGFTTPFSGFLDVQSTFTTGAMNFFSSGNEVYIDRIEFVPEVYEAEDYFEKAQEKV 660  
 DB 601 TTRTVGFTTPFSGFLDVQSTFTTGAMNFFSSGNEVYIDRIEFVPEVYEAEDYFEKAQEKV 660  
 QY 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQIHIERNM 719  
 DB 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQIHIERNM 719

Search completed: October 28, 2004, 18:19:54  
 Job time : 95.6903 secs





GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 28, 2004, 18:06:07 ; Search time 22.3343 Seconds  
(without alignments)  
2134.948 Million cell updates/sec

Title: US-10-019-823B-55  
Perfect score: 3760  
Sequence: 1 MKLKNQKHQSFSNAKVDK.....KRELFEIVKAYQLHIERNM 719

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*  
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2: /cgn2\_6/prodata/1/iaa/5B COMB.pep.\*  
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6: /cgn2\_6/prodata/1/iaa/backfiles.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3755	99.9	719	3	US-08-286-870A-8
2	3476.5	92.5	710	4	US-09-661-322A-42
3	3398	90.4	648	3	US-08-286-870A-4
4	3377	89.8	719	2	US-09-003-217-2
5	3372	89.7	719	3	US-09-218-942-2
6	2804	74.6	535	3	US-08-286-870A-6
7	2446.5	65.1	1229	1	US-08-100-709-4
8	2446.5	65.1	1229	1	US-08-176-865-4
9	2446.5	65.1	1229	1	US-08-474-038-4
10	2446.5	65.1	1229	2	US-08-779-046-4
11	2446.5	65.1	1229	1	US-08-881-340-4
12	2344.5	62.4	488	1	US-08-448-170-10
13	2344.5	62.4	488	3	US-08-961-803-10
14	2265.5	60.3	1207	1	US-07-951-715A-7
15	2265.5	60.3	1207	2	US-08-459-448A-7
16	2265.5	60.3	1207	3	US-08-459-595A-7
17	2265.5	60.3	1207	3	US-08-459-504B-7
18	2265.5	60.3	1207	3	US-08-459-444-7
19	2265.5	60.3	1207	3	US-09-053-549-8
20	2265.5	60.3	1207	3	US-09-547-422-7
21	2265.5	60.3	1207	3	US-09-988-462-7
22	2264.5	60.2	1227	3	US-09-053-549-2
23	2195.5	58.4	1227	1	US-08-448-170-8
24	2195.5	58.4	1227	3	US-08-961-803-9
25	2186.5	58.2	1227	4	US-09-661-322A-63
26	2171.5	57.8	1186	3	US-09-178-252-23
27	2171.5	57.8	1186	4	US-09-826-660-23

28	2116	56.3	1228	4	US-09-661-322A-38
29	1932.5	51.4	643	3	US-09-178-252-25
30	1932.5	51.4	643	4	US-09-826-660-25
31	1900	50.5	380	5	PCT-US91-02560-4
32	1681.5	44.7	653	4	US-09-661-322A-6
33	1670.5	44.4	1157	1	US-07-876-280-30
34	1670.5	44.4	1157	1	US-07-812-180A-2
35	1670.5	44.4	1157	1	US-08-315-468-2
36	1670.5	44.4	1157	3	US-07-941-650A-2
37	1507.5	40.1	1176	1	US-08-257-999-2
38	1492	39.7	1157	2	US-08-532-547-5
39	1492	39.7	1157	2	US-08-379-656B-5
40	1492	39.7	1157	3	US-08-455-838-5
41	1492	39.7	1157	3	US-09-019-809-5
42	1492	39.7	1157	4	US-09-471-177-5
43	1492	39.7	1157	4	US-09-220-806-5
44	1486.5	39.5	1169	1	US-08-315-468-4
45	1485.5	39.5	1156	3	US-09-002-285-72

#### ALIGNMENTS

#### RESULT 1

US-08-286-870A-8  
; Sequence 8, Application US/08286870A  
; Patent No. 6063605  
; GENERAL INFORMATION:  
; APPLICANT: ELY, S  
; APPLICANT: TAILOR, RH  
; APPLICANT: TIPPETT, JM  
; APPLICANT: BLENN, RG  
; TITLE OF INVENTION: BACTERIAL GENES.  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CUSHMAN DAREY & CUSHMAN  
; ADDRESSEE: Intellectual Property Group of  
; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP  
; STREET: 1100 New York Avenue, N.W.  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3918  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/286,870A  
; FILING DATE: 05-AUG-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/520228  
; FILING DATE: 09-MAY-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 8910624.9  
; FILING DATE: 09-MAY-1989  
; ATTORNEY/AGENT INFORMATION:  
; NAME: PAUL N. KOKULIS  
; REGISTRATION NUMBER: 16,773  
; REFERENCE/DOCKET NUMBER: 70608/220720  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 861-3000  
; TELEFAX: (202) 822-0944  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 719 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-286-870A-8

Sequence 38, Appl  
Sequence 25, Appl  
Sequence 25, Appl  
Sequence 4, Appl  
Sequence 6, Appl  
Sequence 30, Appl  
Sequence 2, Appl  
Sequence 2, Appl  
Sequence 2, Appl  
Sequence 2, Appl  
Sequence 5, Appl  
Sequence 5, Appl  
Sequence 5, Appl  
Sequence 5, Appl  
Sequence 4, Appl  
Sequence 2, Appl  
Sequence 72, Appl

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Query Match      99.9%; Score 3756; DB 3; Length 719;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 718; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MKLKNQDKHQSSNAKVDKISTDSLKNETDIEIQNHEDCLKMSYENVEPVSASTI 60

61 QTGIGIAGKILGTLGVPAGQVASYLSFILGELWPKGNQWEI FMEHVEEII NOKISTYA 120
QY 61 QTGIGIAGKILGTLGVPAGQVASYLSFILGELWPKGNQWEI FMEHVEEII NOKISTYA 120
Db 61 QTGIGIAGKILGTLGVPAGQVASYLSFILGELWPKGNQWEI FMEHVEEII NOKISTYA 120

121 RNKALTDLKGDLAVYHDSLEWGNRNTRRSVVKSOYIALELMFVKLPSPAVSG 180
QY 121 RNKALTDLKGDLAVYHDSLEWGNRNTRRSVVKSOYIALELMFVKLPSPAVSG 180
Db 121 RNKALTDLKGDLAVYHDSLEWGNRNTRRSVVKSOYIALELMFVKLPSPAVSG 180

181 BEVPLLPITYAQAANLHLLLRDASIFGKEMGLSSSEISTFYNROVERAGDYS DHCVKWYS 240
QY 181 BEVPLLPITYAQAANLHLLLRDASIFGKEMGLSSSEISTFYNROVERAGDYS DHCVKWYS 240
Db 181 BEVPLLPITYAQAANLHLLLRDASIFGKEMGLSSSEISTFYNROVERAGDYS DHCVKWYS 240

241 TGLNNLRGTNAESWRYNQFRDMLVLDLVALFPSTQMPYIKTTAQLTREVTDAI 300
QY 241 TGLNNLRGTNAESWRYNQFRDMLVLDLVALFPSTQMPYIKTTAQLTREVTDAI 300
Db 241 TGLNNLRGTNAESWRYNQFRDMLVLDLVALFPSTQMPYIKTTAQLTREVTDAI 300

301 GTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMW 360
QY 301 GTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMW 360
Db 301 GTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMW 360

361 GGHKLEFRTIGTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFTQPVNGVPR 420
QY 361 GGHKLEFRTIGTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFTQPVNGVPR 420
Db 361 GGHKLEFRTIGTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFTQPVNGVPR 420

421 VDFHWKFVTHPIASDNFYYPGAGIGTQDSENELPPEATGQPNYESYSHRSLSHIGLIS 480
QY 421 VDFHWKFVTHPIASDNFYYPGAGIGTQDSENELPPEATGQPNYESYSHRSLSHIGLIS 480
Db 421 VDFHWKFVTHPIASDNFYYPGAGIGTQDSENELPPEATGQPNYESYSHRSLSHIGLIS 480

481 ASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSGAAVVRGPGTGGDILRRTN 540
QY 481 ASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSGAAVVRGPGTGGDILRRTN 540
Db 481 ASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSGAAVVRGPGTGGDILRRTN 540

541 TGTFGDIRVNIAPPQARYRVRIRYASTTDLOFHTSINGKAINOCNFSATWNRGEDLDYK 600
QY 541 TGTFGDIRVNIAPPQARYRVRIRYASTTDLOFHTSINGKAINOCNFSATWNRGEDLDYK 600
Db 541 TGTFGDIRVNIAPPQARYRVRIRYASTTDLOFHTSINGKAINOCNFSATWNRGEDLDYK 600

601 TPTVTGFTTTPSFDFDVQSTFTIGAWNFSSGNEVIDRIEFVPEVVTYEAEDFEKAQEKV 660
QY 601 TPTVTGFTTTPSFDFDVQSTFTIGAWNFSSGNEVIDRIEFVPEVVTYEAEDFEKAQEKV 660
Db 601 TPTVTGFTTTPSFDFDVQSTFTIGAWNFSSGNEVIDRIEFVPEVVTYEAEDFEKAQEKV 660

661 TALFTSTNPRGLKTDVQDHYHDQVNLVSLSDSEFYLDKRELFEI VKYAKQLHIERNM 719
QY 661 TALFTSTNPRGLKTDVQDHYHDQVNLVSLSDSEFYLDKRELFEI VKYAKQLHIERNM 719
Db 661 TALFTSTNPRGLKTDVQDHYHDQVNLVSLSDSEFYLDKRELFEI VKYAKQLHIERNM 719

RESULT 2
US-09-661-322A-42
; Sequence 42, Application US/09661322A
; Patent No. 6593293
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Chu, Chih-Rei
; APPLICANT: Donovan, William P.
; APPLICANT: Gilmer, Amy J.
; APPLICANT: Rugar, Mark J.
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin Compo
; FILE REFERENCE: MECO201
; CURRENT APPLICATION NUMBER: US/09/661.322A
; CURRENT FILING DATE: 2000-09-13
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 42
; LENGTH: 710
; TYPE: PRT

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; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (200)..(200)
; OTHER INFORMATION: No. 6593293-Coding
US-09-661-322A-42

Query Match      92.5%; Score 3476.5; DB 4; Length 710;
Best Local Similarity 92.5%; Pred. No. 5 2e-303;
Matches 665; Conservative 15; Mismatches 30; Indels 9; Gaps 1;

1 MKLKNQDKHQSSNAKVDKISTDSLKNETDIEIQNHEDCLKMSYENVEPVSASTI 60
Db 1 MKLKNQDKHQSSNAKVDKISTDSLKNETDIEIQNHEDCLKMSYENVEPVSASTI 51

61 QTGIGIAGKILGTLGVPAGQVASYLSFILGELWPKGNQWEI FMEHVEEII NOKISTYA 120
QY 61 QTGIGIAGKILGTLGVPAGQVASYLSFILGELWPKGNQWEI FMEHVEEII NOKISTYA 120
Db 61 QTGIGIAGKILGTLGVPAGQVASYLSFILGELWPKGNQWEI FMEHVEEII NOKISTYA 111

121 RNKALTDLKGDLAVYHDSLEWGNRNTRRSVVKSOYIALELMFVKLPSPAVSG 180
QY 121 RNKALTDLKGDLAVYHDSLEWGNRNTRRSVVKSOYIALELMFVKLPSPAVSG 180
Db 121 RNKALTDLKGDLAVYHDSLEWGNRNTRRSVVKSOYIALELMFVKLPSPAVSG 171

181 BEVPLLPITYAQAANLHLLLRDASIFGKEMGLSSSEISTFYNROVERAGDYS DHCVKWYS 240
QY 181 BEVPLLPITYAQAANLHLLLRDASIFGKEMGLSSSEISTFYNROVERAGDYS DHCVKWYS 240
Db 181 BEVPLLPITYAQAANLHLLLRDASIFGKEMGLSSSEISTFYNROVERAGDYS DHCVKWYS 231

241 TGLNNLRGTNAESWRYNQFRDMLVLDLVALFPSTQMPYIKTTAQLTREVTDAI 300
QY 241 TGLNNLRGTNAESWRYNQFRDMLVLDLVALFPSTQMPYIKTTAQLTREVTDAI 300
Db 241 TGLNNLRGTNAESWRYNQFRDMLVLDLVALFPSTQMPYIKTTAQLTREVTDAI 291

301 GTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMW 360
QY 301 GTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMW 351
Db 301 GTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMW 351

361 GGHKLEFRTIGTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFTQPVNGVPR 420
QY 361 GGHKLEFRTIGTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFTQPVNGVPR 420
Db 361 GGHKLEFRTIGTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFTQPVNGVPR 411

421 VDFHWKFVTHPIASDNFYYPGAGIGTQDSENELPPEATGQPNYESYSHRSLSHIGLIS 480
QY 421 VDFHWKFVTHPIASDNFYYPGAGIGTQDSENELPPEATGQPNYESYSHRSLSHIGLIS 471
Db 421 VDFHWKFVTHPIASDNFYYPGAGIGTQDSENELPPEATGQPNYESYSHRSLSHIGLIS 471

481 ASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSGAAVVRGPGTGGDILRRTN 540
QY 481 ASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSGAAVVRGPGTGGDILRRTN 540
Db 481 ASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSGAAVVRGPGTGGDILRRTN 531

541 TGTFGDIRVNIAPPQARYRVRIRYASTTDLOFHTSINGKAINOCNFSATWNRGEDLDYK 600
QY 541 TGTFGDIRVNIAPPQARYRVRIRYASTTDLOFHTSINGKAINOCNFSATWNRGEDLDYK 591
Db 541 TGTFGDIRVNIAPPQARYRVRIRYASTTDLOFHTSINGKAINOCNFSATWNRGEDLDYK 591

601 TPTVTGFTTTPSFDFDVQSTFTIGAWNFSSGNEVIDRIEFVPEVVTYEAEDFEKAQEKV 660
QY 601 TPTVTGFTTTPSFDFDVQSTFTIGAWNFSSGNEVIDRIEFVPEVVTYEAEDFEKAQEKV 660
Db 601 TPTVTGFTTTPSFDFDVQSTFTIGAWNFSSGNEVIDRIEFVPEVVTYEAEDFEKAQEKV 651

661 TALFTSTNPRGLKTDVQDHYHDQVNLVSLSDSEFYLDKRELFEI VKYAKQLHIERNM 719
QY 661 TALFTSTNPRGLKTDVQDHYHDQVNLVSLSDSEFYLDKRELFEI VKYAKQLHIERNM 719
Db 661 TALFTSTNPRGLKTDVQDHYHDQVNLVSLSDSEFYLDKRELFEI VKYAKQLHIERNM 710

RESULT 3
US-08-286-870A-4
; Sequence 4, Application US/08286870A
; Patent No. 6063605
; GENERAL INFORMATION:
; APPLICANT: ELY, S
; APPLICANT: TAILOR, RH
; APPLICANT: TIPPETT, JM
; APPLICANT: BLENK, RG
; TITLE OF INVENTION: BACTERIAL GENES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DABBY & CUSHMAN

```

ADDRESSEE: Intellectual Property Group of  
 ADDRESSEE: PILLSBURY, WADISON & SUTRO LLP  
 STREET: 1100 New York Avenue, N.W.  
 CITY: Washington  
 STATE: DC  
 COUNTRY: USA  
 ZIP: 20005-3918  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/286,870A  
 FILING DATE: 05-AUG-1994  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/520228  
 FILING DATE: 09-MAY-1990  
 APPLICATION NUMBER: GB 8910624.9  
 FILING DATE: 09-MAY-1989  
 ATTORNEY/AGENT INFORMATION:  
 NAME: PAUL N. KOKULIS  
 REGISTRATION NUMBER: 16,773  
 REFERENCE/DOCKET NUMBER: 70608/220720  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 861-3000  
 TELEFAX: (202) 822-0944  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 648 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-286-870A-4

Query Match 90.4%; Score 3398; DB 3; Length 648;  
 Best Local Similarity 100.0%; Pred. No. 5e-295;  
 Matches 648; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 M L K N Q D K H S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y N V E P F V S A S T I 60  
 Db 1 M L K N Q D K H S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y N V E P F V S A S T I 60

QY 61 Q T G I G I A G K I L G T L G V P F A G Q V A S L Y S F I L G E L M P K G N Q W E I F M E H V E E I I N K I S T Y A 120  
 Db 61 Q T G I G I A G K I L G T L G V P F A G Q V A S L Y S F I L G E L M P K G N Q W E I F M E H V E E I I N K I S T Y A 120

QY 121 R N K A L T D L K G L D A L A V Y H D S L E S W G N R N N T R A S V V K S Q Y I A L E M F V Q K L P S F A V S G 180  
 Db 121 R N K A L T D L K G L D A L A V Y H D S L E S W G N R N N T R A S V V K S Q Y I A L E M F V Q K L P S F A V S G 180

QY 181 E V P L L P I Y A Q A N L H L L R D A S I F K E W G L S S E I S T F Y N Q V E R A G D Y S D H C V K W Y S 240  
 Db 181 E V P L L P I Y A Q A N L H L L R D A S I F K E W G L S S E I S T F Y N Q V E R A G D Y S D H C V K W Y S 240

QY 241 T G L N N L R G T N A E S W R Y N Q F R R D M T L M V L D L V A L F P S Y D T Q M Y P I K T T A O L T R E V Y T D A I 300  
 Db 241 T G L N N L R G T N A E S W R Y N Q F R R D M T L M V L D L V A L F P S Y D T Q M Y P I K T T A O L T R E V Y T D A I 300

QY 301 G T V H P H S F S T T T W Y N N A P S F S A I E A A V V R N P H L D F L E Q V T I Y S L L S W S N T Q Y N M W 360  
 Db 301 G T V H P H S F S T T T W Y N N A P S F S A I E A A V V R N P H L D F L E Q V T I Y S L L S W S N T Q Y N M W 360

QY 361 G G H K L E R T I G G T L N I S T Q G S T N T S I N P V L P T S R D V Y T E S I A G L N L F L T O P V N G V P R 420  
 Db 361 G G H K L E R T I G G T L N I S T Q G S T N T S I N P V L P T S R D V Y T E S I A G L N L F L T O P V N G V P R 420

QY 421 V D F H W K V T H P I A S D N F Y P C Y A G I G T Q L O D S E N E L P P E A T G O P N Y E S Y G H R L S H I G L I S 480  
 Db 421 V D F H W K V T H P I A S D N F Y P C Y A G I G T Q L O D S E N E L P P E A T G O P N Y E S Y G H R L S H I G L I S 480

QY 481 A S H V K A L V Y S W T H R S A D R T N I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G D I L R T N 540  
 Db 481 A S H V K A L V Y S W T H R S A D R T N I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G D I L R T N 540

QY 541 T C T F G D I R V N I N P P F A Q R Y R V R I A S T T D L O F H T S I N G K A I N Q N F S A T M N R G S D L D Y K 600  
 Db 541 T C T F G D I R V N I N P P F A Q R Y R V R I A S T T D L O F H T S I N G K A I N Q N F S A T M N R G S D L D Y K 600

QY 601 T R T V G F T T P F S F L D V Q S T F I G A W N F S S G N E V Y I D R I E F V P E V T Y E 648  
 Db 601 T R T V G F T T P F S F L D V Q S T F I G A W N F S S G N E V Y I D R I E F V P E V T Y E 648

RESULT 4  
 US-09-003-217-2  
 ; Sequence 2, Application US/09003217  
 ; Patent No. 5986177  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Osman, Yehia A.  
 ; APPLICANT: Madkour, Magdy A.  
 ; APPLICANT: Bulla, Lee A.  
 ; TITLE OF INVENTION: BACILLUS THURINGIENSIS ISOLATES WITH  
 ; TITLE OF INVENTION: BROAD SPECTRUM ACTIVITY  
 ; NUMBER OF SEQUENCES: 2  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSES: W. Murray Spruill (Alston & Bird, LLP)  
 ; STREET: 3605 Glenwood Ave. Suite 310  
 ; CITY: Raleigh  
 ; STATE: NC  
 ; COUNTRY: US  
 ; ZIP: 27622  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/003,217  
 ; FILING DATE:  
 ; CLASSIFICATION: 800  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Spruill, W. Murray  
 ; REGISTRATION NUMBER: 32,943  
 ; REFERENCE/DOCKET NUMBER: 5718-3  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 919 420 2202  
 ; TELEFAX: 919 881 3175  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 719 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-09-003-217-2

Query Match 89.8%; Score 3377; DB 2; Length 719;  
 Best Local Similarity 89.8%; Pred. No. 4.6e-294;  
 Matches 646; Conservative 33; Mismatches 40; Indels 0; Gaps 0;

QY 1 M L K N Q D K H S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y N V E P F V S A S T I 60  
 Db 1 M L K N P D R H Q T L U S S N A K V D K I A T D S L K N E T D I E L K M N N E D Y L R M S E H S I D P F V S A S T I 60

QY 61 Q T G I G I A G K I L G T L G V P F A G Q V A S L Y S F I L G E L M P K G N Q W E I F M E H V E E I I N K I S T Y A 120  
 Db 61 Q T G I G I A G K I L G T L G V P F G Q I A S L Y S F I L G E L M P K G S Q W E I F M E H V E A I I N R K I S T Y A 120

QY 121 R N K A L T D L K G L D A L A V Y H D S L E S W G N R N N T R A S V V K S Q Y I A L E M F V Q K L P S F A V S G 180  
 Db 121 R N K A L T D L K G L D A L A V Y H S L E S W G N R N N T R A S V V K N Q Y I A L E M F V Q K L P S F A V S G 180

QY 181 E V P L L P I Y A Q A N L H L L R D A S I F K E W G L S S E I S T F Y N Q V E R A G D Y S D H C V K W Y S 240  
 Db 181 E V P L L P I Y A Q A N L H L L R D A S I F K E W G L S S E I S T F Y N Q V E R A G D Y S D H C V K W Y S 240

Db 181 BEVPLPIYAQAANLHLLLRDASIFKNGGLSASEISTFYNNQVERTRDYSYHCVKWN 240  
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 Db 241 TGLNLRGTNAESWRYNQFRDMLVLDLVALPSPYDTOMYPIKTTAQLTREVVYDAI 300  
 QY 301 GTVHPHPSFTSTWYNNAPSAEAAVVRNPHLLDLEQVTIYSLSRMSNTQYNNMW 360  
 Db 301 GTVDPNQALRSTWYNNAPSAEAAVVRNPHLLDLEQVTIYSLSRMSNTQYNNMW 360  
 QY 361 GGHLEPFTIGTINISOGSTNTSINPVTLPTSRDYRTESLAGNLFLTQPVNGVPR 420  
 Db 361 GGHLEPFTIGTINISOGSTNTSINPVTLPTSRDYRTESLAGNLFLTQPVNGVPR 420  
 QY 421 VDFHMKFVTHPIASDNFYYPGAGTQLODSENELPPEATGQPNYESYSHRSLSHIGLIS 480  
 Db 421 VDFHMKFVTHPIASDNFYYPGAGTQLODSENELPPEATGQPNYESYSHRSLSHIGLIS 480  
 QY 481 ASHVKALVSWTHRSADRTNIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDIILRTN 540  
 Db 481 GSHVKALVSWTHRSADRTNIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDIILRTN 540  
 QY 541 TGTGDIRVNIWNPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATWNRGDDLKY 600  
 Db 541 SGTGDIRVNIWNPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATWNRGDDLKY 600  
 QY 601 TTRTVGFTTFFSFLDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 660  
 Db 601 TTRTVGFTTFFSFLDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 660  
 QY 661 TALFTSTNPRGLTKDVKYHIDQVSNLVSDELYLDEKRELFEIVKAKQIHIERNM 719  
 Db 661 TALFTSTNPRGLTKDVKYHIDQVSNLVSDELYLDEKRELFEIVKAKQIHIERNM 719

## RESULT 5

US-09-218-942-2  
 ; Sequence 2, Application US/09218942  
 ; Patent No. 6232439  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Osman, Yehia  
 ; TITLE OF INVENTION: Bacillus Thuringiensis Isolates with Broad Spectrum  
 ; TITLE OF INVENTION: Activity  
 ; FILE REFERENCE: Crv11  
 ; CURRENT APPLICATION NUMBER: US/09/218,942  
 ; CURRENT FILING DATE: 1998-12-22  
 ; EARLIER APPLICATION NUMBER: 60/035,361  
 ; EARLIER FILING DATE: 1997-01-10  
 ; EARLIER APPLICATION NUMBER: 09/003,217  
 ; EARLIER FILING DATE: 1998-01-06  
 ; NUMBER OF SEQ ID NOS: 2  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 2  
 ; LENGTH: 719  
 ; TYPE: PRT  
 ; ORGANISM: Bacillus thuringiensis  
 US-09-218-942-2

Query Match 89.7%; Score 3372; DB 3; Length 719;  
 Best Local Similarity 89.8%; Pred. No. 1.3e-293;  
 Matches 646; Conservative 33; Mismatches 40; Indels 0; Gaps 0;  
 QY 1 MKLNQDKHQFSSNAKYDKISTDLKNETDIELQNHEDCLKMSYENVFPVSASTI 60  
 Db 1 MKLNQDKHQFSSNAKYDKISTDLKNETDIELQNHEDCLKMSYENVFPVSASTI 60  
 QY 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGLPKGNQWEIPEHVEEINOKISTYA 120  
 Db 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGLPKGNQWEIPEHVEEINOKISTYA 120  
 QY 121 RNKALTDLKGLDALAVYHDSLESWGNRNTRARSVVKSYIALELMFVQKLPSPAVSG 180  
 Db 121 RNKALTDLKGLDALAVYHDSLESWGNRNTRARSVVKSYIALELMFVQKLPSPAVSG 180

QY 181 BEVPLPIYAQAANLHLLLRDASIFKNGGLSASEISTFYNNQVERAGDYSCHCVKWS 240  
 Db 181 BEVPLPIYAQAANLHLLLRDASIFKNGGLSASEISTFYNNQVERTRDYSYHCVKWN 240  
 QY 241 TGLNLRGTNAESWRYNQFRDMLVLDLVALPSPYDTOMYPIKTTAQLTREVVYDAI 300  
 Db 241 TGLNLRGTNAESWRYNQFRDMLVLDLVALPSPYDTOMYPIKTTAQLTREVVYDAI 300  
 QY 301 GTVHPHPSFTSTWYNNAPSAEAAVVRNPHLLDLEQVTIYSLSRMSNTQYNNMW 360  
 Db 301 GTVDPNQALRSTWYNNAPSAEAAVVRNPHLLDLEQVTIYSLSRMSNTQYNNMW 360  
 QY 361 GGHLEPFTIGTINISOGSTNTSINPVTLPTSRDYRTESLAGNLFLTQPVNGVPR 420  
 Db 361 GGHLEPFTIGTINISOGSTNTSINPVTLPTSRDYRTESLAGNLFLTQPVNGVPR 420  
 QY 421 VDFHMKFVTHPIASDNFYYPGAGTQLODSENELPPEATGQPNYESYSHRSLSHIGLIS 480  
 Db 421 VDFHMKFVTHPIASDNFYYPGAGTQLODSENELPPEATGQPNYESYSHRSLSHIGLIS 480  
 QY 481 ASHVKALVSWTHRSADRTNIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDIILRTN 540  
 Db 481 ASHVKALVSWTHRSADRTNIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDIILRTN 540  
 QY 541 TGTGDIRVNIWNPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATWNRGDDLKY 600  
 Db 541 SGTGDIRVNIWNPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATWNRGDDLKY 600  
 QY 601 TTRTVGFTTFFSFLDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 660  
 Db 601 TTRTVGFTTFFSFLDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 660  
 QY 661 TALFTSTNPRGLTKDVKYHIDQVSNLVSDELYLDEKRELFEIVKAKQIHIERNM 719  
 Db 661 TALFTSTNPRGLTKDVKYHIDQVSNLVSDELYLDEKRELFEIVKAKQIHIERNM 719

## RESULT 6

US-08-286-870A-6  
 ; Sequence 6, Application US/08286870A  
 ; Patent No. 6063605  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ELY, S  
 ; APPLICANT: TAILOR, RH  
 ; APPLICANT: TIPPETT, JM  
 ; APPLICANT: BLENK, RG  
 ; TITLE OF INVENTION: BACTERIAL GENES  
 ; NUMBER OF SEQUENCES: 10  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: CUSHMAN DARBY & CUSHMAN  
 ; ADDRESSEE: Intellectual Property Group of  
 ; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP  
 ; STREET: 1100 New York Avenue, N.W.  
 ; CITY: Washington  
 ; STATE: DC  
 ; COUNTRY: USA  
 ; ZIP: 20005-3918  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/286,870A  
 ; FILING DATE: 05-AUG-1994  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/520228  
 ; FILING DATE: 09-MAY-1990  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: GB 8910624.9  
 ; FILING DATE: 09-MAY-1989

ATTORNEY/AGENT INFORMATION:  
NAME: PAUL N. KOKULIS  
REGISTRATION NUMBER: 16,773  
REFERENCE/DOCKET NUMBER: 70608/220720  
TELEPHONE: (202) 861-3000  
TELEFAX: (202) 822-0944  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 535 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-286-870A-6

Query Match 74.6%; Score 2804; DB 3; Length 535;  
Best Local Similarity 100.0%; Pred. No. 7.7e-243;  
Matches 535; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLKNQDKQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKSEYENVPFVSASTI 60  
DB 1 MKLKNQDKQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKSEYENVPFVSASTI 60  
QY 61 QTGIGIAGKILGTLGVPFAGQVASYLXSFILGELWPKGKQWEIFMEHVEEIIQKISTYA 120  
DB 61 QTGIGIAGKILGTLGVPFAGQVASYLXSFILGELWPKGKQWEIFMEHVEEIIQKISTYA 120  
QY 121 RNKALTDLKGDLALAVYHDSLESWGNRNTRARSVVKSQYIALBLMFVQKLPSPAVSG 180  
DB 121 RNKALTDLKGDLALAVYHDSLESWGNRNTRARSVVKSQYIALBLMFVQKLPSPAVSG 180  
QY 181 EYVPLPIYAQAANLHLLLRDASIFGKEWGLSSSISFTYRQVERAGDYSDHCVKWS 240  
DB 181 EYVPLPIYAQAANLHLLLRDASIFGKEWGLSSSISFTYRQVERAGDYSDHCVKWS 240  
QY 241 TGLNLRGNTNAESWRYNQRRDMLVLDLVALFSPYDTQMPYIKTTAQLTREYVTDI 300  
DB 241 TGLNLRGNTNAESWRYNQRRDMLVLDLVALFSPYDTQMPYIKTTAQLTREYVTDI 300  
QY 301 GTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLDLEQVITYLLSRWSNTQYMMNW 360  
DB 301 GTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLDLEQVITYLLSRWSNTQYMMNW 360  
QY 361 GGHKLEFRITGTLNISTQGSTNTSINPVLPTSRDVRTESLAGNLFLTPQVNGVPR 420  
DB 361 GGHKLEFRITGTLNISTQGSTNTSINPVLPTSRDVRTESLAGNLFLTPQVNGVPR 420  
QY 421 VDFHWKFTVPIASDNFYPGYAGIGTQLODSENEPPEATGQPNYESYSHRLSHIGLIS 480  
DB 421 VDFHWKFTVPIASDNFYPGYAGIGTQLODSENEPPEATGQPNYESYSHRLSHIGLIS 480  
QY 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLYKAFNLSSGAAVVRGPGFTGGDI 535  
DB 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLYKAFNLSSGAAVVRGPGFTGGDI 535

RESULT 7  
US-08-100-709-4  
Sequence 4, Application US/08100709  
Patent No. 5322687  
GENERAL INFORMATION:  
APPLICANT: Donovan, William P.  
APPLICANT: Tan, Yuping  
APPLICANT: Jany, Christine S.  
APPLICANT: Gonzalez Jr., Jose M.  
TITLE OF INVENTION: BACILLUS THURINGIENSIS CRYET4 AND CRYETS  
TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.  
ADDRESSEE: Nadel  
STREET: 1601 Market Street, 36th Floor  
CITY: Philadelphia

STATE: Pennsylvania  
COUNTRY: U.S.A.  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/100,709  
FILING DATE: 19930729  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Egolf, Christopher  
REGISTRATION NUMBER: 27633  
REFERENCE/DOCKET NUMBER: 7205-49  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-757-1590  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1229 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-100-709-4

Query Match 65.1%; Score 2446.5; DB 1; Length 1229;  
Best Local Similarity 65.6%; Pred. No. 3.7e-210;  
Matches 470; Conservative 92; Mismatches 138; Indels 17; Gaps 6;

QY 13 SSNAKVDKISTDSLKN-ETDIELQ-NINHEDECLKSEYENVPFVSASTIQTGIGIAGKI 70  
DB 7 NENEIINALSIPTVSNPSTOMNLSPDARIEDSLCAEVNNDIPFVSASTVQTGINIAGRI 66  
QY 71 LGTGVPPAGQVASYLXSFILGELWPKGKQWEIFMEHVEEIIQKISTYARKALTDLKG 130  
DB 67 LGVGVPPAGQVASYLXSFILGELWPKGKQWEIFMEHVEEIIQKISTYARKALTDLKG 126  
QY 131 LGDALAVYHDSLESWGNRNTRARSVVKSQYIALBLMFVQKLPSPAVSGEVEPLPIYA 190  
DB 127 LGRGVSQQALETWLDNRNDARSIIERYVALELDITTAIFLRINESEVLLMUYA 186  
QY 191 QAANLHLLLRDASIFGKEWGLSSSISFTYRQVERAGDYSDHCVKWSYGLNLRGNT 250  
DB 187 QAANLHLLLRDASIFGSEWGMASDVNQQYQEQIRYEEYSNHCVOYNTGLNLRGNT 246  
QY 251 AESWRYNQRRDMLVLDLVALFSPYDTQMPYIKTTAQLTREYVTDIATGVHPHPSFT 310  
DB 247 AESWRYNQRRDMLVLDLVALFSPYDTQMPYIKTTAQLTREYVTDIATGVHPHPSFT 306  
QY 311 STTWYNNAPSFSAIEAAVVRNPHLDLEQVITYLLSRWSNTQYMMNWGGHKLLEPRTI 370  
DB 307 STTWYNNAPSFSAIEAAVVRNPHLDLEQVITYLLSRWSNTQYMMNWGGHKLLEPRTI 366  
QY 371 GGTNLNISTQGST-NTSINPVLPTSRDVRTESLAGNLFLTPQVNGVPRVDFHWKFTV 429  
DB 367 GGTNLNISTQGST-NTSINPVLPTSRDVRTESLAGNLFLTPQVNGVPRVDFHWKFTV 422  
QY 430 HPIASDNFYPG------YAGIGTQLODSENEPPEATGQPNYESYSHRLSHIGLISAS 482  
DB 423 --INPNIYERGATTYSQYQGVGLFDFSETLPETTERPNYESYSHRLSHIGLIS 480  
QY 483 HVKALVYSWTHRSADRTNTIEPNSITQIPLYKAFNLSSGAAVVRGPGFTGGDIARRNTG 542  
DB 481 TLRAFYVSWTHRSADRTNTIEPNSITQIPLYKAFNLSSGAAVVRGPGFTGGDIARRNTG 540  
QY 543 TFGDIRVNINPPFAQRYVRIRYASTTDLOPHTSINGKAINQGNFSAATMNRGEDIQKTF 602  
DB 541 TFGDIRVNINPPFAQRYVRIRYASTTDLOPHTSINGKAINQGNFSAATMNRGEDIQKTF 600  
QY 603 RTVGFTTFFSFLDVQSTETIGAMNPFSSGNEVYIDRIEFPVPEVVEYEAEDPEKQKVTYA 662  
DB 601 RTAGFSTPFFNLNAQSTFTLGAQFSN-QEYVIDRVEFPVPAEVTFEAYDILERAQKAVNA 659





QY 543 TFGDIRVNINPPFAQRYVRIRYASTTDLQFHTSINGKAINCQNFSAATMRGDLVYKTP 602  
 DB 541 TFGDIRVNINPLSQRYVRIRYASTTDLQFHTSINGKAINCQNFSAATMRGDLVYKTP 600  
 QY 603 RTVGFTTTPFSDQSTFTIGAMFSSGNEVYIDRIEFVFPVEVYEAEDFEKAQKAVTA 662  
 DB 601 RTAGSTPFPNLAQSTFTLGAQSFN-QEYVIDRVEFVPAEYFEAYDLERAQKAVNA 659  
 QY 663 LFTSTNPRGLTKDVKYHIDQVSNVACLSDEFCLDEKRELFEVYKAKQLHIERNM 719  
 DB 660 LFTSTNPRGLTKDVKYHIDQVSNVACLSDEFCLDEKRELFEVYKAKQLHIERNM 716

RESULT 11  
 US-08-881-340-4  
 ; Sequence 4, Application US/08881340  
 ; Patent No. 5942658  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Donovan, William P.  
 ; APPLICANT: Tan, Yiping  
 ; APPLICANT: Jany, Christine S.  
 ; APPLICANT: Gonzalez Jk, Jose M.  
 ; TITLE OF INVENTION: Bacillus thuringiensis cryET4 and cryET5  
 ; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS  
 ; NUMBER OF SEQUENCES: 5  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.  
 ; ADDRESS: Nadel  
 ; STREET: 1601 Market Street, 36th Floor  
 ; CITY: Philadelphia  
 ; STATE: Pennsylvania  
 ; COUNTRY: U.S.A.  
 ; ZIP: 19103  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/881.340  
 ; FILING DATE: 24-JUN-1997  
 ; CLASSIFICATION: 424  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/100,709  
 ; FILING DATE: 29-JUL-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Egolf, Christopher  
 ; REGISTRATION NUMBER: 27633  
 ; REFERENCE/DOCKET NUMBER: 7205-49  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 215-757-1590  
 ; INFORMATION FOR SEQ ID NO: 4:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1229 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-881-340-4

Query Match 65.1%; Score 2446.5; DB 2; Length 1229;  
 Best Local Similarity 65.6%; Pred. No. 3.7e-210;  
 Matches 470; Conservative 92; Mismatches 138; Indels 17; Gaps 6;

QY 13 SSNAKVDKISTDLQK-ETDTELQ-NINHECLKMSYENVEPVFVASTIOTGIGIAGKI 70  
 DB 7 NENEIINALSPTVNSPTQNLSPDRIEDSLCVAEVNNDPFPVASTVOTGINIAGRI 66  
 QY 71 LGTLGVFPAGVASYSPILGELPKGNQNEIFPWEHVEEIIINQKISTYAKNALTDLKG 130  
 DB 67 LGVLGVFPAGLASYSFLVGLWPSGRDPWEIFLEHVEQLIRQOVVTEINTAARLEG 126  
 QY 131 LGDALAVYHDSLESVGVGNRNTBRSVYKSYIALELMFVQKLPSPFVSGVEVLLPIYA 190

DB 127 LGGYRSYQQALETWLDNRNDARSIIILERYVALELDITTAIFLIRINEEVLMMVYA 186  
 QY 191 QAANLHILLRLDASIFGKEMGLSSSEISTFYNRQVERAGDYSDHCVKWYSTGLNLRGTN 250  
 DB 187 QAANLHILLRLDASIFGSEWGNASSDVNOYQOEQRIRYTEESNHCVCQWYNLGLNLRGTN 246  
 QY 251 AESSWRYNQFRDMLTMLDLVALFPSTYDTQWPIKTTAQLTREYVYDTAIGTVHPHSFT 310  
 DB 247 AESSWRYNQFRDMLTMLDLVALFPSTYDTQWPIKTTAQLTREYVYDTAIGTVHPHSFT 306  
 QY 311 STWNNNAPSFAIAEAAVVRNPHLLDFLEQVYIYSLSRNSNTQYMNMGHGLERTI 370  
 DB 307 STWNNNAPSFAIAEAAVVRNPHLLDFLEQVYIYSLSRNSNTQYMNMGHGLERTI 366  
 QY 371 GGTLANISQGST-NTSINPVTLPFTSRDVRTESLAGLNLFLTQPVNGVPRVDFHWKEVT 429  
 DB 367 GGTLANISQGST-NTSINPVTLPFTSRDVRTESLAGLNLFLTQPVNGVPRVDFHWKEVT 422  
 QY 430 HPIASDNFYPG-----YAGIGTQLODSNELPPEATGQPNYESYSHRLSHGLISAS 482  
 DB 423 --INPQNIYERGATTYQPYQGVIGLFDSELTPELTPETTERPNYESYSHRLSHGLIIGN 480  
 QY 483 HVKALVSWTHRSADRTNTIBNSITQPLVKAFLSSGAAVVRGPGTGGDILARTNTG 542  
 DB 481 TRAPVYSWTHRSADRTNTIGPNRITQPLVKAFLSSGAAVVRGPGTGGDILARTNTG 540  
 QY 543 TFGDIRVNINPPFAQRYVRIRYASTTDLQFHTSINGKAINCQNFSAATMRGDLVYKTP 602  
 DB 541 TFGDIRVNINPLSQRYVRIRYASTTDLQFHTSINGKAINCQNFSAATMRGDLVYKTP 600  
 QY 603 RTVGFTTTPFSDQSTFTIGAMFSSGNEVYIDRIEFVFPVEVYEAEDFEKAQKAVTA 662  
 DB 601 RTAGSTPFPNLAQSTFTLGAQSFN-QEYVIDRVEFVPAEYFEAYDLERAQKAVNA 659  
 QY 663 LFTSTNPRGLTKDVKYHIDQVSNVACLSDEFCLDEKRELFEVYKAKQLHIERNM 719  
 DB 660 LFTSTNPRGLTKDVKYHIDQVSNVACLSDEFCLDEKRELFEVYKAKQLHIERNM 716

RESULT 12  
 US-08-448-170-10  
 ; Sequence 10, Application US/08448170  
 ; Patent No. 5723758  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Payne, Jewel  
 ; APPLICANT: Cummings, David A.  
 ; APPLICANT: Cannon, Raymond J.C.  
 ; APPLICANT: Narva, Kenneth E.  
 ; APPLICANT: Stelman, Steve  
 ; TITLE OF INVENTION: No. 5723758el Bacillus thuringiensis Isolate Denoted  
 ; TITLE OF INVENTION: B.t. PS158C2, Active Against Lepidopteran Pests, and Genes  
 ; TITLE OF INVENTION: Encoding Lepidopteran-Active Toxins  
 ; NUMBER OF SEQUENCES: 10  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: David R. Saliwanchik  
 ; STREET: 2421 N.W. 41st Street, Suite A-1  
 ; CITY: Gainesville  
 ; STATE: Florida  
 ; COUNTRY: USA  
 ; ZIP: 32606  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/448,170  
 ; FILING DATE:  
 ; CLASSIFICATION: 424  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/069,902  
 ; FILING DATE: 01-JUNE-1993  
 ; CLASSIFICATION: 424



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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/759,247
; FILING DATE: 13-SEPT-1991
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: M/S 102D.C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 488 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-448-170-10

Query Match 62.4%; Score 2344.5; DB 1; Length 488;
Best Local Similarity 89.7%; Pred. No. 1.2e-201;
Matches 446; Conservative 13; Mismatches 29; Indels 9; Gaps 1;

Qy 1 MKLNQDKHQSFSNAKVDKISTDSLKNETDIELQINNHEDCLKMSYENVEPVSASTI 60
Db 1 MKSKQNNHQSLSNNATVDKNTGSLNNTNTELQNFH-----EGIEPPFVSSTI 51

Qy 61 QTGIGIAGKILGTLGVPPAGQVASYLSYFILGELWPKGKQWEIFMEHVVEEIIINQISTYA 120
Db 52 QTGIGIVGKILGNLGVPPAGQVASYLSYFILGELWPKGKQWEIFMEHVVEELINQISTYA 111

Qy 121 RNKALTDKGLDALAVYHDSLESWGNRNTRARSVVKSOYIALBELMFVKLPSFAVSG 180
Db 112 RNKALADKGLDALAVYHDSLESWGNRNTRARSVVKSOYITLLEMFVQSLPSFAVSG 171

Qy 181 BEVPLPIYAQAANLHLLLRDASIFGKWLGSSEISTFYNROVERAGDYSCHCKWYS 240
Db 172 BEVPLPIYAQAANLHLLLRDASIFGKWLGSSEISTFYNROSGKSKESYDCHCKWYN 231

Qy 241 TGLNLRGTNAESWYRNYQFRDMLVLDLVALPSPYDTQWPIKTTAQLTREYVTDI 300
Db 232 TGLNLRMGNAESWYRNYQFRDMLVLDLVALPSPYDTQWPIKTTAQLTREYVTDI 291

Qy 301 GTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYNNMW 360
Db 292 GTVHPHPSFTSTWYNNAPSFSTIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYNNMW 351

Qy 361 GGHKLEBRTIGTLNISTQSTNTSINPVLPTSRDVRTESLAGLNLFLOPVGNGVPR 420
Db 352 GGHKLEBRTIGTLNISTQSTNTSINPVLPTSRDVRTESLAGLNLFLOPVGNGVPR 411

Qy 421 VDPHFKVTHPIASDNFYPYAGIGTQLODSNELPPEATGQPNYESYSHRLSHIGLIS 480
Db 412 VDPHFKVTHPIASDNFYPYAGIGTQLODSNELPPEATGQPNYESYSHRLSHIGLIS 471

Qy 481 ASHVKAIVSWTHRSAD 497
Db 472 ASHVKAIVSWTHRSAD 488

RESULT 13
US-08-961-803-10
; Sequence 10, Application US/08961803
; Patent No. 6150589
; GENERAL INFORMATION:
; APPLICANT: Payne, Jewel
; APPLICANT: Cummings, David A.
; APPLICANT: Cannon, Raymond J.C.
; APPLICANT: Narva, Kenneth E.
; APPLICANT: Stelman, Steve
; TITLE OF INVENTION: No. 6150589e1 Bacillus thuringiensis Isolate Denoted
; ; TITLE OF INVENTION: B.t. PS158C2, Active Against Lepidopteran Pests, and Genes

```

```

; TITLE OF INVENTION: Encoding Lepidopteran-Active Toxins
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jay M. Sanders
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,803
; FILING DATE: 31-OCT-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/069,902
; FILING DATE: 01-JUNE-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/759,247
; FILING DATE: 13-SEPT-1991
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/448,170
; FILING DATE: 23-MAY-1995
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Sanders, Jay M.
; REGISTRATION NUMBER: 39,355
; REFERENCE/DOCKET NUMBER: M/S 102D.C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 488 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-961-803-10

Query Match 62.4%; Score 2344.5; DB 3; Length 488;
Best Local Similarity 89.7%; Pred. No. 1.2e-201;
Matches 446; Conservative 13; Mismatches 29; Indels 9; Gaps 1;

Qy 1 MKLNQDKHQSFSNAKVDKISTDSLKNETDIELQINNHEDCLKMSYENVEPVSASTI 60
Db 1 MKSKQNNHQSLSNNATVDKNTGSLNNTNTELQNFH-----EGIEPPFVSSTI 51

Qy 61 QTGIGIAGKILGTLGVPPAGQVASYLSYFILGELWPKGKQWEIFMEHVVEEIIINQISTYA 120
Db 52 QTGIGIVGKILGNLGVPPAGQVASYLSYFILGELWPKGKQWEIFMEHVVEELINQISTYA 111

Qy 121 RNKALTDKGLDALAVYHDSLESWGNRNTRARSVVKSOYIALBELMFVKLPSFAVSG 180
Db 112 RNKALADKGLDALAVYHDSLESWGNRNTRARSVVKSOYITLLEMFVQSLPSFAVSG 171

Qy 181 BEVPLPIYAQAANLHLLLRDASIFGKWLGSSEISTFYNROVERAGDYSCHCKWYS 240
Db 172 BEVPLPIYAQAANLHLLLRDASIFGKWLGSSEISTFYNROSGKSKESYDCHCKWYN 231

Qy 241 TGLNLRGTNAESWYRNYQFRDMLVLDLVALPSPYDTQWPIKTTAQLTREYVTDI 300
Db 232 TGLNLRMGNAESWYRNYQFRDMLVLDLVALPSPYDTQWPIKTTAQLTREYVTDI 291

Qy 301 GTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYNNMW 360
Db 292 GTVHPHPSFTSTWYNNAPSFSTIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYNNMW 351

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361 GGHKLEFRTIGTNTSTQSTNTSINPVTLPFTSRDVRFTESLAGLNLFQTQPVNGVPR 420  
 Db 352 GGHKLEFRTIGTNTSTQSTNTSINPVTLPFTSRDVRFTESLAGLNLFQTQPVNGVPR 411  
 Qy 421 VDFHKKFVTHPTASDNFYVPGVAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 Db 412 VDFHKKFVTHPTASDNFYVPGVAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 471  
 Qy 481 ASHVKALVYSWTHRSAD 497  
 Db 472 ASHVKALVYSWTHRSAD 488

RESULT 14  
 US-07-951-715A-7  
 ; Sequence 7, Application US/07951715A  
 ; Patent No. 5625136  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Koziel, Michael G.  
 ; APPLICANT: Desai, Nalini M.  
 ; APPLICANT: Lewis, Kelly S.  
 ; APPLICANT: Kramer, Vance C.  
 ; APPLICANT: Warren, Gregory W.  
 ; APPLICANT: Evola, Stephen V.  
 ; APPLICANT: Crossland, Lyle D.  
 ; APPLICANT: Wright, Martha S.  
 ; APPLICANT: Merlin, Ellis J.  
 ; APPLICANT: Launis, Karen L.  
 ; APPLICANT: Rothstein, Steven J.  
 ; APPLICANT: Bowman, Cindy G.  
 ; APPLICANT: Dawson, John L.  
 ; APPLICANT: Dunder, Erik M.  
 ; APPLICANT: Pace, Gary M.  
 ; APPLICANT: Suttie, Janet L.  
 ; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
 ; NUMBER OF SEQUENCES: 94  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESS: CIBA-GEIGY Corporation  
 ; STREET: 7 Skyline Drive  
 ; CITY: Hawthorne  
 ; STATE: New York  
 ; COUNTRY: USA  
 ; ZIP: 10532  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.30B  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/07/951.715A  
 ; FILING DATE: 25-SEP-1992  
 ; CLASSIFICATION: 800  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/772,027  
 ; FILING DATE: 04-OCT-1991  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Spruill, W. Murray  
 ; REGISTRATION NUMBER: 32,943  
 ; REFERENCE/DOCKET NUMBER: S-18805/A/CGC 1577/CIP  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (919)541-8615  
 ; TELEFAX: (919)541-8689  
 ; INFORMATION FOR SEQ ID NO: 7:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1207 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-07-951-715A-7

Query Match 60.3%; Score 2265.5; DB 1; Length 1207;

Best Local Similarity 64.3%; Pred No. 6.3e-194;  
 Matches 442; Conservative 78; Mismatches 154; Indels 13; Gaps 5;  
 Qy 40 EPLCKMSEYENVEPFPVASTIQTGTIGIAGKILGTGVFPAGQVASYFLIGELMHPKGN 99  
 Db 10 EDSLCTIAEGNNIDPFSASTVQTGINIAGRIILGVLPAGQVASYFLIGELMHPKGN 69  
 Qy 100 QWEIFMEHVEEILNOKISTYARNKALTDLKGIGDALAVYHDSLESWGVNRRNTRARSVVK 159  
 Db 70 QWEIFMEHVEEILNOKISTYARNKALTDLKGIGDALAVYHDSLESWGVNRRNTRARSVVK 129  
 Qy 160 SQVIALELMFVQKLPFSFVSGEEVPLPIYAQAANLHLLLRDASIFPKWGLSSSEIST 219  
 Db 130 TOYIALELDLFLNAMPFLAIRNQEVPFLMYAQAANLHLLLRDASIFPKWGLSSSEIST 189  
 Qy 220 FYNQVERAGDYSCHVKWYSGTGLNLRGTNAESVYRNQFRRDMTAVLDLVALFPSYD 279  
 Db 190 YVERQVTRDYSYCVEMWYNTGLNSLRGTNAASVYRNQFRRDLTLGLVLDLVALFPSYD 249  
 Qy 280 TOMYPIKTTAQLTREVTYDAIGTVHPHPSFTSTTWNNNAPSFAIEAAVVRNPHLLDFL 339  
 Db 250 TETYPINTSAQLTREVTYDAIGAT--GVNMAWMWYNNAPSFAIEAAVVRNPHLLDFL 307  
 Qy 340 EQVTYLSLRWSNTQYNNMGHKLFPRTTGTGTLNISTQSTNTSINPVTLPFTSRDVI 399  
 Db 308 EQLTIFSSASSRWSNTRHMTYWRGHTIQSRPIGGGLNTSTHGATNTSINPVTLPFTSRDVI 367  
 Qy 400 RTESLAGLNL--LTQPVNGVPRVDFHMKVTHP-----IASDNFVYPGYAGIGTQLODS 452  
 Db 368 RTESVAGVLLNGIYLEPIHGVTVEFNF--TNPNQISDRGTANYSQP-YESPGIQLKDS 423  
 Qy 453 ENELPPEATGQPNYESYSHRLSHIGLISASHVKALVYSWTHRSADRTNTPNSITQIPL 512  
 Db 424 ETELPPETTERPNYESYSHRLSHIGLISASHVKALVYSWTHRSADRTNTPNSITQIPL 483  
 Qy 513 VKAFNLSCAAVVRGPGFTGGDILARTNTGTGDIRVNVINPFAQRYVRIRYASTTDLQ 572  
 Db 484 VKASELPQGTTVVRGPGFTGGDILARTNTGTGDIRVNVINPFAQRYVRIRYASTTDLQ 543  
 Qy 573 FHTSINGKAINQGNFSATNMGEDLDYKTFRTVGTFTTFFSLDVSQSTTTICAMNPFSSGNE 632  
 Db 544 FFSVSGTIVVNNFRFLRTMNSGDELKYGNFVRRATFTTFTQIQTQIIRTSIQGLSGNGE 603  
 Qy 633 VYIDRIEFVPEVTVYEAEDFEKAQKVTALFTSTNPRGLKTDVYHIDQVSNLVSLS 692  
 Db 604 VYIDKIEIIPVATFEAEYDLERAQEAVALFNTNPRRLKTDVYHIDQVSNLVSLS 663  
 Qy 693 DEFYLDKRELFPEIVKYAKQLHIERNM 719  
 Db 664 DEFCLDEKRELFPEIVKYAKQLHIERNM 690

RESULT 15  
 US-08-459-448A-7  
 ; Sequence 7, Application US/08459448A  
 ; Patent No. 5859336  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Koziel, Michael G.  
 ; APPLICANT: Desai, Nalini M.  
 ; APPLICANT: Lewis, Kelly S.  
 ; APPLICANT: Kramer, Vance C.  
 ; APPLICANT: Warren, Gregory W.  
 ; APPLICANT: Evola, Stephen V.  
 ; APPLICANT: Crossland, Lyle D.  
 ; APPLICANT: Wright, Martha S.  
 ; APPLICANT: Merlin, Ellis J.  
 ; APPLICANT: Launis, Karen L.  
 ; APPLICANT: Rothstein, Steven J.  
 ; APPLICANT: Bowman, Cindy G.  
 ; APPLICANT: Dawson, John L.  
 ; APPLICANT: Dunder, Erik M.  
 ; APPLICANT: Pace, Gary M.  
 ; APPLICANT: Suttie, Janet L.

TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
 TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE  
 NUMBER OF SEQUENCES: 94  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: No. 5859336artis Corporation  
 STREET: Patent & Trademark Dept., 520 White Plains  
 STREET: Rd, POB 2005  
 CITY: Tarrytown  
 STATE: New York  
 COUNTRY: USA  
 ZIP: 10591-9005  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/459,448A  
 FILING DATE: 02-JUN-1995  
 CLASSIFICATION: 800  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/951,715  
 FILING DATE: 25-SEP-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/772,027  
 FILING DATE: 04-OCT-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Pace, Gary M.  
 REGISTRATION NUMBER: 40403  
 REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV4  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (919)541-8582  
 TELEFAX: (919)541-8669  
 INFORMATION FOR SEQ ID NO: 7:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1207 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-459-448A-7

Query Match	60.3%;	Score	2265.5;	DB 2;	Length	1207;			
Best Local Similarity	64.3%;	Fred.	No. 6.3e-194;						
Matches	442;	Conservative	78;	Mismatches	154;	Indels	13;	Gaps	5;
QY	40	EDCLKMSVENVEPVFSASTIQTGIGTAGIKILGTGVPPAGOVASSYSFIIGELWPKGN	99						
DB	10	EDSLCIAGNMIDPFVSASTVQTGINAGILGVLPVPPAGLASFSFLVCELWPRGD	69						
QY	100	QWEIFMEHVBEIINQKISTYARNKALTDLKGDLALAVYHDSLESWGVNRRNTRARSVVK	159						
DB	70	QWEIFLEHVEQLINQITENARNLTALRQGLGDSFRAYQOSLEDWLENRRDARTESVLY	129						
QY	160	SOYIALELMEFVQKLPSFAVSGEEVPLPIYQAQANLHLLLRDASTFGKEMGLSSSEIST	219						
DB	130	TYIALELDLFNAPLFAIRNQEVPLLMVYQAQANLHLLLRDASLFGSEFGLTSEQEQR	189						
QY	220	FYNROVERAGDYSRHCVKWYGTGLNNRGTNABSWRYNQFRDMTLMVLVDLVALFPSSY	279						
DB	190	YYERQVTRDYSYCVMEYNTGLNSLRGINAASWRYNQFRDRLTLGVLDLVALFPSSYD	249						
QY	280	TOYPIKTTAQLTREVVYDAIGTVHPHPSTSTWYNNAPSESATEAAVWRNPHLLDPL	339						
DB	250	TRTYPTNSAQLTREVVYDAIGAT - GVNWASMNWYNNAPSESATEAAAIRESPHLLDPL	307						
QY	340	EOVTVYSLLSRWSNTQYNNMGHGKLFRRYIGGTLINISTOGSTNTSINPVTLPFFSRDYY	399						
DB	308	EQLITFSASSRWSNTRHMTYRWGHTIQSRPIGGGLNTSHGATNTSINPVTLPFASRDYY	367						
QY	400	RTESLAGLNLFP - LTQPVNGVRPDRFWKVFTHP - ----IASDNFYYPGAGIGTQLODS	452						
DB	368	RTESYAGVLLMGVLEPHIEHGVEYTVRFNF - --TNPONISDRGTANYSOP - YESFGHQLXDS	423						

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453 QY 453 ENELPREATGQPNYESYSHRISHGLTISASHVKALVYSWTHRSADRNNTTSPNSITQIPL 512
424 Db 424 ETELPPETTERNYESYSHRISHGIILQSRVNVVPVYSWTHRSADRNNTTIGPARIITQIEM 483
513 QY 513 VKAFNLSGAAVVRGFGTGGDIILRRNTGTGDIRVININPPFAQRYVRIRYASTTDLQ 572
484 Db 484 VKASELPGQTTVVRGFGTGGDIILRRNTGTGFGIRVTVANGPLTQRYRIGFRYASTVDDE 543
573 QY 573 FHTSINGKALINGPFSATMNGEOLDYKTPRTVGFTTTFPSFLDVQSPFTTIGAMNFFSGNE 632
544 Db 544 FVVRGGTIVNNFRFLRTMNSGDELKTYGNFVRRAFTTTPFTTQIIDIIRTSIOGLSGNGE 603
633 QY 633 VVIDRIEFPVPEVTYAEYDPEKAQEKVLTFTSTNPNRGKTDVKDHYHDQVSNLVESLS 692
604 Db 604 VVIDKIEIIPVTATPEAYDIERAQEAVNALFTNPNRLKTDVTDHYHDQVSNLVACLS 663
693 QY 693 DEFYLDKRELEFIVKVAQLHIERNM 719
664 Db 664 DEFCDKRELELLEKVKYAKRLSDERNL 690

search completed: October 28, 2004, 18:34:13
Job time : 24.3343 secs

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Search completed: October 28, 2004, 18:34:13  
Job time : 24.3343 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 28, 2004, 18:05:43 ; Search time 19.191 Seconds  
(without alignments)  
3604.811 Million cell updates/sec

Title: US-10-019-823B-55  
Perfect score: 3760  
Sequence: 1 MKLNQDKHQSFSSNAKVDK.....KRELFEIVKYAKOLHIERNM 719

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 791:\*  
1: Pir1.\*  
2: Pir2.\*  
3: Pir3.\*  
4: Pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	3760	100.0	719	2 I39815	insecticidal prote
2	3751	99.8	719	2 S25383	parasporal crystal
3	3743	99.5	719	2 I39814	insecticidal prote
4	3520	93.6	719	2 I40530	crv465 protein -
5	2277.5	60.6	1228	2 S00873	parasporal crystal
6	1900	50.5	380	2 B42459	hypothetical prote
7	1492	39.7	1157	1 S49247	parasporal crystal
8	1482.5	39.4	1166	2 S32645	parasporal crystal
9	1474	39.2	1155	2 A26513	parasporal crystal
10	1471	39.1	1174	2 S32649	parasporal crystal
11	1467	39.0	1155	2 JD0002	parasporal crystal
12	1467	39.0	1156	2 A29125	parasporal crystal
13	1454.5	38.7	934	2 A22798	parasporal crystal
14	1453.5	38.7	1176	2 JT0241	parasporal crystal
15	1450	38.6	1155	2 S02134	parasporal crystal
16	1449.5	38.6	1181	2 A41052	parasporal crystal
17	1447.5	38.5	1176	2 UC2219	parasporal crystal
18	1446	38.5	1155	2 I39838	parasporal crystal
19	1443.5	38.4	1176	2 A22617	parasporal crystal
20	1443.5	38.4	1176	2 S02215	parasporal crystal
21	1360	36.2	1174	2 A42459	parasporal crystal
22	1353	36.0	1138	2 A48944	parasporal crystal
23	1339.5	35.6	1156	2 A29838	parasporal crystal
24	1331.5	35.4	823	2 S04181	parasporal crystal
25	1322.5	35.2	1189	2 S00944	parasporal crystal
26	1310	34.8	1154	2 S39536	parasporal crystal
27	1272	33.8	1171	2 I40572	parasporal crystal
28	1272	33.8	1171	2 A37829	parasporal crystal
29	1263	33.6	1176	2 A48970	parasporal crystal

30	1234	32.8	1160	2 S32647	parasporal crystal
31	1219.5	32.4	1165	2 S11446	parasporal crystal
32	1209.5	32.2	655	2 JC7140	protoxin - Bacilli
33	1196	31.8	1172	2 S32689	parasporal crystal
34	1186	31.5	1160	2 I40589	parasporal crystal
35	1163.5	30.9	1178	1 USBSXH	parasporal crystal
36	1163	30.9	1177	2 A49785	parasporal crystal
37	1156	30.7	652	2 A27323	parasporal crystal
38	1133	30.1	659	2 S10228	parasporal crystal
39	1100.5	29.3	652	2 I39811	parasporal crystal
40	986	26.2	649	1 JH0261	parasporal crystal
41	935	24.9	618	2 S11445	parasporal crystal
42	886	23.6	1156	2 S19306	parasporal crystal
43	828	22.0	1136	1 USES81	parasporal crystal
44	694.5	18.5	934	2 B29838	parasporal crystal
45	667	17.7	1180	2 I39870	parasporal crystal

ALIGNMENTS

RESULT 1

I39815  
insecticidal protein cryV - Bacillus thuringiensis  
C:Species: Bacillus thuringiensis  
C:Date: 19-Jul-1996 #sequence\_revision 19-Jul-1996 #text\_change 09-Jul-2004  
C:Accession: I39815  
R:Gleave, A.P.; Williams, R.; Hedges, R.J.  
Appl. Environ. Microbiol. 59, 1681-1687, 1993  
A:Title: Screening by polymerase chain reaction of Bacillus thuringiensis serotypes for iensis subsp. kurstaki.  
A:Reference number: I39815; MUID:93298009; PMID:8517758  
A:Accession: I39815  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-719 <RES>  
A:Cross-references: UNIPROT:Q45752; GB:M98544; NID:G142767; PIDN:AAA22354.1; PID:G142768  
C:Gene: cryV  
C:Superfamily: parasporal crystal protein

Query Match 100.0%, Score 3760; DB 2; Length 719;  
Best Local Similarity 100.0%; Pred. No. 2.9e-256;  
Matches 719; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MKLKQDKHQSFSSNAKVDKISTDSLKNETDIELQNIHEDCLKMSYENVEPFFVSASTI	60
DB	1	MKLKQDKHQSFSSNAKVDKISTDSLKNETDIELQNIHEDCLKMSYENVEPFFVSASTI	60
QY	61	QTGIGIAGKILGTGVPPAGQVASYLSYFILGELWPKGNQWEIFMEHVEEIIINQKISTYA	120
DB	61	QTGIGIAGKILGTGVPPAGQVASYLSYFILGELWPKGNQWEIFMEHVEEIIINQKISTYA	120
QY	121	RKALTDLKLGDALAVYHDSLESWVGNNRNNTRASVVKSQYIALELMFVKLPSPAVSG	180
DB	121	RKALTDLKLGDALAVYHDSLESWVGNNRNNTRASVVKSQYIALELMFVKLPSPAVSG	180
QY	181	EEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFFYNNRQVERAGDYSCHCVKWS	240
DB	181	EEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFFYNNRQVERAGDYSCHCVKWS	240
QY	241	TGNNLRGNABSWRYNQFRDMLVLDLVALPSPYDTQWYPIKTTAQLTREYVTTAI	300
DB	241	TGNNLRGNABSWRYNQFRDMLVLDLVALPSPYDTQWYPIKTTAQLTREYVTTAI	300
QY	301	GTVHPHPSFTSTWNNNAPSFAEAAVVRNPHLLDLEQVTIYSLLSRNSNTQYMNW	360
DB	301	GTVHPHPSFTSTWNNNAPSFAEAAVVRNPHLLDLEQVTIYSLLSRNSNTQYMNW	360
QY	361	GGHKLFEFTTGTLNISTQGSNTNINPVTLPFTSRDVRTESLAGLNLFTQPVNGVPR	420
DB	361	GGHKLFEFTTGTLNISTQGSNTNINPVTLPFTSRDVRTESLAGLNLFTQPVNGVPR	420

QY 421 VDFHMKFVTHPIASDNFYYPGVAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 DB 421 VDFHMKFVTHPIASDNFYYPGVAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 QY 481 ASHVKALVYSWTHRSADRTNITIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 540  
 DB 481 ASHVKALVYSWTHRSADRTNITIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 540  
 QY 541 TGTGDIRVNIINPPPAQRYRVRIRYASTDLOFHTSINGKAINQGNFSATNWRGDDLYK 600  
 DB 541 TGTGDIRVNIINPPPAQRYRVRIRYASTDLOFHTSINGKAINQGNFSATNWRGDDLYK 600  
 QY 601 TERTVGFTTPPSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEKV 660  
 DB 601 TERTVGFTTPPSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEKV 660  
 QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDBFYLDKRELFVVKYAKQLHIERNM 719  
 DB 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDBFYLDKRELFVVKYAKQLHIERNM 719

## RESULT 2

S25383  
 parasporal crystal protein cryIIal - Bacillus thuringiensis  
 N:Alternate names: delta-endotoxin; parasporal crystal protein cryV  
 C:Species: Bacillus thuringiensis  
 C:Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 09-Jul-2004  
 C:Accession: S25383  
 R:Tailor, R.; Tippett, J.; Gibb, G.; Pells, S.; Pike, D.; Jordan, L.; Ely, S.  
 Mol. Microbiol. 6, 1211-1217, 1992  
 A:Title: Identification and characterization of a novel Bacillus thuringiensis delta-endotoxin  
 A:Reference number: S25383; PMID:92269582; PMID:1588820  
 A:Accession: S25383  
 A:Molecule type: DNA  
 A:Residues: 1-719 <TA>  
 A:Cross-references: UNIPROT:Q45752; EMBL:X62821; NID:G40289; PIDN:CAA44633.1; PID:G40290  
 C:Genetics:  
 A:Gene: cryV  
 C:Superfamily: parasporal crystal protein  
 C:Keywords: delta-endotoxin

Query Match 99.8%; Score 3751; DB 2; Length 719;  
 Best Local Similarity 99.9%; Pred. No. 1.3e-255;  
 Matches 718; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNIHEDCLKMSYENVEPVSASTI 60  
 DB 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNIHEDCLKMSYENVEPVSASTI 60  
 QY 61 QTGIGIAGKILGTGVPPAGQVASYLSPILGELWPKGNQWEIFMEHVEEIIINOKISTYA 120  
 DB 61 QTGIGIAGKILGTGVPPAGQVASYLSPILGELWPKGNQWEIFMEHVEEIIINOKISTYA 120  
 QY 121 RNKALTDLKGDLALAVYHDSLESWVGNNRNRARSVVKSQYIALELMFVQKLSFAVSG 180  
 DB 121 RNKALTDLKGDLALAVYHDSLESWVGNNRNRARSVVKSQYIALELMFVQKLSFAVSG 180  
 QY 181 EEPVLLPIYAQANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSCHVKWYS 240  
 DB 181 EEPVLLPIYAQANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSCHVKWYS 240  
 QY 241 TGLNLRGTNAESWRYNQFRDMLTLMVLDLVALFPSYDTQWPIKTTAQLTREYITDAI 300  
 DB 241 TGLNLRGTNAESWRYNQFRDMLTLMVLDLVALFPSYDTQWPIKTTAQLTREYITDAI 300  
 QY 301 GTVHPHPSFTSTWYNNNAPSFAEAAVVRNPHLLDPLEQVTIYSLSRWSNTQYNNMW 360  
 DB 301 GTVHPHPSFTSTWYNNNAPSFAEAAVVRNPHLLDPLEQVTIYSLSRWSNTQYNNMW 360  
 QY 361 GGHKLEFRITIGTGLNISTQGSTNTSINPVTLPFTSRDVRVRESLAGNLFLTQPVNGVPR 420  
 DB 361 GGHKLEFRITIGTGLNISTQGSTNTSINPVTLPFTSRDVRVRESLAGNLFLTQPVNGVPR 420

QY 421 VDFHMKFVTHPIASDNFYYPGVAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 DB 421 VDFHMKFVTHPIASDNFYYPGVAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 QY 481 ASHVKALVYSWTHRSADRTNITIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 540  
 DB 481 ASHVKALVYSWTHRSADRTNITIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 540  
 QY 541 TGTGDIRVNIINPPPAQRYRVRIRYASTDLOFHTSINGKAINQGNFSATNWRGDDLYK 600  
 DB 541 TGTGDIRVNIINPPPAQRYRVRIRYASTDLOFHTSINGKAINQGNFSATNWRGDDLYK 600  
 QY 601 TERTVGFTTPPSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEKV 660  
 DB 601 TERTVGFTTPPSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEKV 660  
 QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDBFYLDKRELFVVKYAKQLHIERNM 719  
 DB 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDBFYLDKRELFVVKYAKQLHIERNM 719

## RESULT 3

I39814  
 insecticidal protein cryVI - Bacillus thuringiensis  
 C:Species: Bacillus thuringiensis  
 C:Date: 19-Jul-1996 #sequence\_revision 19-Jul-1996 #text\_change 26-Aug-1999  
 C:Accession: I39814  
 R:Shin, B.S.; Choi, S.H.; Koo, B.T.; Lee, S.T.; Kim, J.I.  
 Appl. Environ. Microbiol. 61, 2402-2407, 1995  
 A:Title: Distribution of cryV-type insecticidal protein genes in Bacillus thuringiensis tomocidus.  
 A:Reference number: I39814; MUID:95314293; PMID:7793960  
 A:Accession: I39814  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-719 <RES>  
 A:Cross-references: GB:L36338; NID:G540281; PIDN:AAC36999.1; PID:G540282  
 C:Genetics:  
 A:Gene: cryVI  
 C:Superfamily: parasporal crystal protein

Query Match 99.5%; Score 3743; DB 2; Length 719;  
 Best Local Similarity 99.6%; Pred. No. 4.6e-255;  
 Matches 716; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNIHEDCLKMSYENVEPVSASTI 60  
 DB 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNIHEDCLKMSYENVEPVSASTI 60  
 QY 61 QTGIGIAGKILGTGVPPAGQVASYLSPILGELWPKGNQWEIFMEHVEEIIINOKISTYA 120  
 DB 61 QTGIGIAGKILGTGVPPAGQVASYLSPILGELWPKGNQWEIFMEHVEEIIINOKISTYA 120  
 QY 121 RNKALTDLKGDLALAVYHDSLESWVGNNRNRARSVVKSQYIALELMFVQKLSFAVSG 180  
 DB 121 RNKALTDLKGDLALAVYHDSLESWVGNNRNRARSVVKSQYIALELMFVQKLSFAVSG 180  
 QY 181 EEPVLLPIYAQANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSCHVKWYS 240  
 DB 181 EEPVLLPIYAQANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSCHVKWYS 240  
 QY 241 TGLNLRGTNAESWRYNQFRDMLTLMVLDLVALFPSYDTQWPIKTTAQLTREYITDAI 300  
 DB 241 TGLNLRGTNAESWRYNQFRDMLTLMVLDLVALFPSYDTQWPIKTTAQLTREYITDAI 300  
 QY 301 GTVHPHPSFTSTWYNNNAPSFAEAAVVRNPHLLDPLEQVTIYSLSRWSNTQYNNMW 360  
 DB 301 GTVHPHPSFTSTWYNNNAPSFAEAAVVRNPHLLDPLEQVTIYSLSRWSNTQYNNMW 360  
 QY 361 GGHKLEFRITIGTGLNISTQGSTNTSINPVTLPFTSRDVRVRESLAGNLFLTQPVNGVPR 420  
 DB 361 GGHKLEFRITIGTGLNISTQGSTNTSINPVTLPFTSRDVRVRESLAGNLFLTQPVNGVPR 420

QY 421 VDFHMKVTHPIASDNFYPCYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
DB 421 VDFHMKVTHPIASDNFYPCYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
QY 481 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540  
DB 481 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540  
QY 541 TGTGFGDIRVNNPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAFMNREGDLDYK 600  
DB 541 TGTGFGDIRVNNPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAFMNREGDLDYK 600  
QY 601 TERTVGTFTTFFSFLDVQSTTTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDEFEKAQEKV 660  
DB 601 TERTVGTFTTFFSFLDVQSTTTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDEFEKAQEKV 660  
QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719  
DB 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 4  
I40590  
cryV465 protein - Bacillus thuringiensis  
C/Species: Bacillus thuringiensis  
C/Date: 12-Aug-1996 #sequence\_revision 12-Aug-1996 #text\_change 09-Jul-2004  
C/Accession: I40590  
R/Shin, B.S.; Park, S.H.; Choi, S.K.; Koo, B.T.; Lee, S.T.; Kim, J.I.  
Appl. Environ. Microbiol. 61, 2402-2407, 1995  
A/Title: Distribution of cryV-type insecticidal protein genes in Bacillus thuringiensis  
tomocidus.  
A/Reference number: I39814; MUID: 95314293; PMID: 7793960  
A/Accession: I40590  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-719 <RES>  
A/Cross-references: UNIPROT:Q45709; EMBL:U07642; NID:9467234; PIDN:AAA82114.1; PID:94672  
C/Genetics:  
A/Gene: cryV465  
C/Superfamily: parasporal crystal protein

Query Match 93.6%; Score 3520; DB 2; Length 719;  
Best Local Similarity 92.9%; Pred. No. 2.2e-239;  
Matches 668; Conservative 31; Mismatches 20; Indels 0; Gaps 0;

QY 1 MCLKNQKHQFSNAKVKI2TSLKNETDIELQNNHEDCLKMSYENVEPFSASTI 60  
DB 1 MCLKNPKHQSSLNNAKVKIATDSLKNETDIELKNNNEDYLRMSHESIDPFSASTI 60  
QY 61 QTGIGIAGKILGTGVPAGQVASYLSFILGELMPKGNQWEIFMEHVVEIINQKISTYA 120  
DB 61 QTGIGIAGKILGTGVPAGQVASYLSFILGELMPKGSQWEIFMEHVVEIINQKILTYA 120  
QY 121 RNKALTDLKGLDALAVYHDSLESWVGNNRNNTRARSVVKVQYIALELMFVKLPSPFVSG 180  
DB 121 RNKALSRLGLGDALAVYHDSLESWVENNTRARSVVKVQYIALELMFVKLPSPFVSG 180  
QY 181 EEPVLLPIYQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSCHVKWYS 240  
DB 181 EEPVLLPIYQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERTRDYSCHKWN 240  
QY 241 TGLNLRAGTNAESWVRVYNQFRDMLVLDLVALFPSSYDTQWPIKTTAQLTREVTYDAI 300  
DB 241 TGLNLRAGTNAESWVRVYNQFRDMLVLDLVALFPSSYDTLVVPIKTTSLQTLREVTYDAI 300  
QY 301 GTVPHPSFTSTTWNNAAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYNNMW 360  
DB 301 GTVHNOAFASTTWNNAAPSFAIEAAVVRNPHLLDFLEKVTIYSLLSRWSTQYNNMW 360  
QY 361 GGHKLEFRTGGTGLNISTQSTNTSINPVTLPFTSRDVRVYTESLAGLNLFLTOPVNGVPR 420  
DB 361 GGHLESRPGGALNTSQSTNTSINPVTLPFTSRDVRVYTESLAGLNLFLTOPVNGVPR 420

QY 421 VDFHMKVTHPIASDNFYPCYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
DB 421 VDFHMKVTHPIASDNFYPCYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
QY 481 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540  
DB 481 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540  
QY 541 TGTGFGDIRVNNPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAFMNREGDLDYK 600  
DB 541 TGTGFGDIRVNNPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAFMNREGDLDYK 600  
QY 601 TERTVGTFTTFFSFLDVQSTTTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDEFEKAQEKV 660  
DB 601 TERTVGTFTTFFSFLDVQSTTTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDEFEKAQEKV 660  
QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719  
DB 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 5  
S00873  
parasporal crystal protein cryBa1 - Bacillus thuringiensis subsp. thuringiensis  
N/Alternate names: parasporal crystal protein cryA4  
C/Species: Bacillus thuringiensis subsp. thuringiensis  
C/Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 09-Jul-2004  
C/Accession: S00873  
R/Brizzard, B.L.; Whiteley, H.R.  
Nucleic Acids Res. 16, 2723-2724, 1988  
A/Title: Nucleotide sequence of an additional crystal protein gene cloned from Bacillus t  
A/Reference number: S00873; MUID: 88203216; PMID: 3362680  
A/Accession: S00873  
A/Molecule type: DNA  
A/Residues: 1-1228 <BRI>  
A/Cross-references: UNIPROT:P05517; EMBL:X06711; NID:940264; PIDN:CAA29898.1; PID:g580945  
C/Genetics:  
A/Gene: cryA4  
A/Start codon: TTG  
C/Superfamily: parasporal crystal protein  
C/Keywords: delta-endotoxin

Query Match 60.6%; Score 2277.5; DB 2; Length 1228;  
Best Local Similarity 62.7%; Pred. No. 1.2e-151;  
Matches 449; Conservative 80; Mismatches 16; Indels 25; Gaps 6;

QY 23 TDSLKNETDIELQNNH-----EDCLKMSYENVEPFSASTIQTGIGIAGKI 70  
DB 2 TSNRKNENEIINAVSNHSAQMDLLPDARIEDSLCAEGNNIDPFVSASTVQTGINIAGRI 61  
QY 71 LGTLGVPPAGQVASYLSFILGELMPKGNQWEIFMEHVVEIINQKISTYARNKALTDLKG 130  
DB 62 LGVLGVPPAGQVASYLSFILGELMPKGRDQWEIFLEHVVEIINQKISTYARNKALTDLKG 121  
QY 131 LGDALAVYHDSLESWVGNNRNNTRARSVVKVQYIALELMFVKLPSPFVSGEVPPLPIYA 190  
DB 122 LGDSFRAVQSSLEDNLENDARTSVLYQVIALELDFLNA MPLFAIRNQSVPLMVA 181  
QY 191 QAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSCHVKWYSGLNLRGTN 250  
DB 182 QAANLHLLLRDASIFGSEFGLTSQEIQRXYERQVTRDYSYCVENYNTGLNSLRGTN 241  
QY 251 ASSWVRVYNQFRDMLVLDLVALFPSSYDTQWPIKTTAQLTREVTYDAIGTVPHPSFT 310  
DB 242 ASWVRVYNQFRDMLVLDLVALFPSSYDTQWPIKTTAQLTREVTYDAIGAT--GVNMA 299  
QY 311 STTWNNAAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYNNMWGSHKLEFTTI 370  
DB 300 SMWYNNNAAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYNNMWGSHKLEFTTI 359  
QY 371 GGTNLNISTQSTNTSINPVTLPFTSRDVRVYTESLAGLNLFLTOPVNGVPR 428  
DB 360 GGGLNTSTHGALNTSQSTNTSINPVTLPFTSRDVRVYTESLAGLNLFLTOPVNGVPR 416





D6 YGDKKMLLEAVRAAKLSRNL 732

RESULT 8  
S32645  
parasporeal crystal protein cryoGal - Bacillus thuringiensis  
C:Species: Bacillus thuringiensis  
C>Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
C:Accession: S32645  
R:Lambert, B.  
submitted to the EMBL Data Library, April 1993  
A:Reference number: S32645  
A:Accession: S32645  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1166 <LAM>  
A:Cross-references: UNIPROT\_Q45746; EMBL\_Z22510; NID:Q295861; PIDN\_CAA80233.1; PID:Q295861  
C:Superfamily: parasporeal crystal protein  
C:Keywords: delta-endotoxin

Query Match 39.4%; Score 1482.5; DB 2; Length 1166;  
Best Local Similarity 46.1%; Pred. No. 8.9e-96;  
Matches 325; Conservative 101; Mismatches 204; Indels 75; Gaps 17;

Qy 41 DCLKMSYE-----NVPEFVSASTQTGTAGTKLTGLGVFPAGQVASYSLFGELWPX 96  
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:  
D6 13 NCLNNPSEIFNARNSFGLVQSUGL---TRELLEAPPEAFGLGLDIIWGA!--- 66  
Qy 97 GKNOEIFMEHVEBIIINQISTYARNKALTDKLGDALAYYHDSLESWYGNRNTRAS 156  
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:  
D6 67 GVDQWSLFRLQIEQLIRQEITELEERNATAITLGLSSSYNLYEALREWEENDPNPASQE 126  
Qy 157 VVKSQYALELMFMFKLPSPFAVSGEEVPLPIYAQRANLHLILLRDASI FGKEWG--SSSE 216  
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:  
D6 127 RVRFRFLTDDAI VTGLPTLAIRNLEVVNUSVITYQAANLHLLURDAVYGEKWLUTQAN 186  
Qy 217 ISTFYNRQVERAGYSCHVCWKVYSTGLNNLRGTNAESWRYNQPRRDMTLMLDLVALFP 276  
Db IEDLYRTLSTNIQEYSDHCARWYNQGLNEIGGISR----RYLDFQROLTTISVLIDLVALFP 242  
Qy 277 SYDTQMYPKIKTALTREVYTDAI--GTVHPHPFTSTTWYNNAPSFAIAEAIVRNPH 334  
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:  
D6 243 NYDIRTPVPQSOQLTREITYSPVVAGNI-----NFGLSIANVLRAFH 285  
Qy 335 LLDELEQVTYYSLSRWSNTQYMMWGHKLFPETIG-GTLN-----ISTQGSTNTS 385  
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:  
D6 286 LMDPIDRIVITNSVR--STEY---WAGEVISRTGGOGNEIRFFPLYGVANAEPVPT 340  
Qy 386 INPYTLPTSDDVRYTES-----LAGNLFLTQPVNGVRPDHFHKVFHTPTASDNFY 439  
Db IRPTGFDEQRQWRANSRVVPSRSSQDPFLSDAVG-----FLT-IFSAVISYR 389  
Qy 440 PGYAGICTQLQDSNELPPEATQPNYESYSHRLSHIGLISAS-----HYKALYSWTHR 494  
Db NGF-GPNT---DTIDEPIEGTDP--FTGYSHRLCHVGFLASSPFISQYARAPIFSWTHR 443  
Qy 495 SADRTNTIEPNSITCI PLVKA FNLSGAAVVRGPFGTGCDILRRTN GTGDRLRVNIPP 554  
Db SATUNTIAPOVI TCI PLVKA FNLUHS GATI VKGFGTGGDILRRIN VSGFGMRVNTAP 503  
Qy 555 PAQRYRVRIRYASTTDLOFHTSINGKALNQCQNFSATMNRGEDDYKTRTVTGFTTPSF 614  
Db LSQRYRVRIRYASTTDLOFTYTNINGTINI GNPSSTMDSGDDLQYGRFRVAGFTTPTFS 563  
Qy 615 DVQSTFTTGANNFSGSNEVYIDRIEFVPVEVYTYAEYDFPKAQEKVATLFTSTNPRLGKT 674  
Db DANSTFTLGAGFGFPNNEVYIDRIEFVPAEVTFAEDVLEKQAKVNAVLTFTSSNQIGLKT 623  
Qy 675 DVKYHDHQVSNLVESLDES FYLD EKRLFE IFVIYK AQLHIERNM 719  
D6 DWTDYHDIKVSNLVESLDES FYLD EKRLSESKVHKALSERNL 668

RESULT 9

A26513  
parasporal crystal protein - *Bacillus thuringiensis* (strain aizawai)  
C:Species: *Bacillus thuringiensis*  
C:Date: 11-Mar-1988 #sequence\_revision 11-Mar-1988 #text\_change 09-Jul-2004  
C:Accession: A26513  
R:Oeda, K.; Oshie, K.; Shimizu, M.; Nakamura, K.; Yamamoto, H.; Nakayama, H.; Ohkawa, H.  
Gene 53, 113-119, 1987  
A:Title: Nucleotide sequence of the insecticidal protein gene of *Bacillus thuringiensis*  
A:Reference number: A26513; MUID:87248103; PMID:3297927  
A:Accession: A26513  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1155 <ORD>  
A:Cross-references: UNIPROT:P06578; GB:M16463; NID:g143098; PIDN:AAA22551.1; PID:g143099  
C:Superfamily: parasporal crystal protein  
C:Keywords: delta-endotoxin

Query Match 39.2%; Score 1474; DB 2; Length 1155;  
Best Local Similarity 44.4%; Pred. No. 3.5e-95;  
Matches 315; Conservative 113; Mismatches 227; Indels 54; Gaps 12;

QY 36 NINHEBCLKMSYENVE-PFVSASTIQG-----IGIAGKILGTGLVPFAGQVASIYS 87  
DB 4 NPNINECPYNCLSNPEVEVLGERIEGYTPIDISLSLTQTLSEF-VFCAGFVLGLVD 62  
QY 88 FILGLWPKGNQWEIEMHVEEINQKISTYARNKALTDLKLGLDALAYHDSLESWVG 147  
DB 63 IIWGIF--GPSQWDAFLVQIEQLNQRIEEFARNQAISEGLSNLYQIYAESFREWEA 119  
QY 148 NNNNTFRASVVKSVQIALELMEPVQKLPSPAVSGEEVPLPIYQAANLHLLLLDASIFG 207  
DB 120 DPTNPALBEEWRIQNDNMNSALTALPFAVQNVQVPLLSVYQAANLHLSVLEDVSVFG 179  
QY 208 KEWGLSSEISTFYNRQVERAGYSDHCVKXWSTGLNNRGTHNAESWVRNQFRDWTLM 267  
DB 180 QRWGFDATINSRYNDLTRLIQNTTHAVRVNTGLERVWGPDSRDWIRYNQFRELTLT 239  
QY 268 VLDLVALPSPYDTOMYPKITTAQLTRVYTDALGTGVHPSPFTSTWYNNAPFSATEA 327  
DB 240 VLDIVSLFPNVDSPYPIRTVSQLREIYNPV-----LENFDGSFRALAQ 285  
QY 328 AV---VRNPHLLDFLEQVITYLSLLSR-----WSNTQYNNM---WGHKLEPRTIGTGNIS 377  
DB 286 GIEGSIKPSPLMDILNSIITYTDAHGEYWSGQIMASPVGFGPEFTPLYGTMGNA 345  
QY 378 TQGSNTSINPVTLPSTSDVRYTESLAGLNLPLOTVPNGVPRVDFHWKFTVTHIASDNF 437  
DB 346 PQORIVALQGVRYRTLSLTLYRPNIGIN---NQOLSVLDTGTEFAYG-----TSSNL 396  
QY 438 YPGYAGITQLOQDSENELPPEATGPNVYESYHRLSHIGLI-----SASHVKALVYS 490  
DB 397 PSADVTKSGT--VDSLDEIPQNNVPPRQGFGRHLSHVSFMFRSGFNSSVSIIRAPMFS 454  
QY 491 WTHRSADRNTIENPSITQIPLVKAPNLSSGAAVGPGFTGGILRRTNTGTGDIRVN 550  
DB 455 WTHRSAEFNNIIPSSQITQIPITKSNLGSIGTSVKVGPGFTGGDILRRTSPQISTLRVN 514  
QY 551 INPPFAQRYRVRVYASTTDLQHTSINGKAINQGNFSAATMNGEDLDYKTRTVRGFTTP 610  
DB 515 ITAPLSQRVVRVIRVASTNTLQHTSIDGRPINQGNFSAATMSSGSLNLSQGSFRIVGFTTP 574  
QY 611 RSFLVDQSTFTTIGANNFSSGNEVYIDRIEFVPVEVYEAEDYDEKAEKVYALTSTNPR 670  
DB 575 FNFSGSVFTLSAHVFNSGNEVYIDRIEFVPAEVTFEAEYDLEAQAQVNELFTSSNQI 634  
QY 671 GLKTDVXVHIDQVSNLVSLSDEFYLDDEKRELFEIVKYAKQLHIERNM 719  
DB 635 GLKTDVTDVHIDQVSNLVSLSDEFCLDEKKESEKVKHAKRLSDERNL 683

RESULT 10  
S32649

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parasporal crystal protein cry1Ab3 - Bacillus thuringiensis
C:Species: Bacillus thuringiensis
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S32649
R:Lambert, B.
submitted to the EMBL Data Library, April 1993
A:Reference number: S32645
A:Accession: S32649
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1174 <LAM>
A:Cross-references: UNIPROT:Q45749; EMBL:222512; NID:G295865; PIDN:CAA80235.1; PID:G2958
C:Superfamily: parasporal crystal protein
C:Keywords: delta-endotoxin

Query Match 39.1%; Score 1471; DB 2; Length 1174;
Best Local Similarity 44.8%; Pred. No. 5.8e-95;
Matches 325; Conservative 103; Mismatches 202; Indels 96; Gaps 17;

QY 36 NINHE---DCLQSEYENVEPVSASTIQIGIA-GKILGTLGVPPAGQVASYFIL 90
DB 4 NQNCVYNCLSNPVEVILSEESTGTGLPDLISLSTRFLLSFVGVGVAGFLDLIW 63
QY 91 GELWPKGNQWEIFMEHVEEIIINQKISTYARNKALTDLKGIGDALAVYHDSLESWGNRN 150
DB 64 GPITP---SEWSLFLQIEQRIETLERNRAITTLRGLADSYEVYVLEALREWEENPN 120
QY 151 NTRASVYKSVQVIALEMFVKLPSFAVSGEVPILPIYAQAANLHLLLRDASIFCKEW 210
DB 121 NAQLREDVRIKFRATDDALITAINNFTLSFEIPLSVYQAANLHLLLRDAVSFCQGW 160
QY 211 GLSSEISTFYNRQVERAGDYSHCWKVYSTGLANLRTNAESVWRYNQFRDMTLMVLD 270
DB 181 GLDIATVNNHYNRLNLIHRTVEHCLDTYNGLENLRTNFRWSRFNQFRREULTVLVD 240
QY 271 LVALPSTDTQYPIKTAQTRVYTDATGTVHPHSFSTTWNNAAPS-FAAIAAV 329
DB 241 IVALEPNYDAARYPIQTSQRTREIYTSV--IEDSP-----VSANIENGFRABFG- 290
QY 330 VKNPHLLDFEQVITYSLRSWNTQYNNMNGHKLFRITGTTGLNISTQGSTNTSNPV 389
DB 291 VRPHLMDFMN-----SLFVTAETVRSQTVNGHLV-----SSRTAGNPI 331
QY 390 TLPP-----TSRDVYRTESLAGLNLFTQPVNGVPRVDFHWKFTVTHIAS 434
DB 332 NFPIYGIENPGGAIWADEDPPFYRT-----LSDPV-----FVRGGFGN 371
QY 435 DNFPYGPVAGITGLQ-----DSENLPEATGQNVESYSHRLSHI----- 476
DB 372 PH-VYLGURGVAFQQTGNTHTRTFNSTGIDSLDEIPQDNGAPNDYSHVNLHVTFVR 430
QY 477 --GLISASHV-KALVYSWTHSADRTNIENSTIQPLVKAPNLSSGAAVRPGFTGG 533
DB 431 WPGETIAGSDSWRAPMFSWTHSADRTNIENSTIQPLVKAPNLSSGAAVRPGFTGG 490
QY 534 DILRRTNGTGDIVNINPPAQRVYRIRYASTDLOQHTSNGKAINQNFSAFMNR 593
DB 491 DLLRRTNGTGDIVNINPPAQRVYRIRYASTDLOQHTSNGKAINQNFSAFMNR 550
QY 594 GEDLDYKTRTVGFTTFFSDVQSTFTIGAMNFSNGNEVYIDRIEFPVVEVYAEYDF 653
DB 551 GGNLESNGFRTAGFTSPFSNAQSTFTLGTAQFSN-QEVYIDRIEFPVPAEVTFAESDL 609
QY 654 EKAQEKVATLSTNPRGLKTDVYHLDQVSNLVSLSDBFYLDKXELFEIVKYAKOL 713
DB 610 ERAQKAVNALFTSTSQLGKTNVTGYHLDQVSNLVACLSDBFCDEKRELSKRVKARRL 669
QY 714 HIERNM 719
DB 670 SDRKRL 675

RESULT 11

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JD00002
parasporal crystal protein cry1Ab3 - Bacillus thuringiensis
N:Alternate names: delta-endotoxin-2; entomocidal protoxin; entomopathogenic crystal prot
C:Species: Bacillus thuringiensis
C:Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004
C:Accession: A90025; A91560; A90955; S14555; A26461; A24172; A29043; JD00002
R:Kondo, S.; Tamura, N.; Kunitate, A.; Hattori, M.; Akashi, A.; Ohmori, I.
Agric. Biol. Chem. 51: 455-463, 1987
A:Title: Cloning and nucleotide sequencing of two insecticidal delta-endotoxin genes from
A:Reference number: A90025
A:Accession: A90025
A:Molecule type: mRNA
A:Residues: 1-1155 <KON>
A:Cross-references: UNIPROT:P06578
A:Experimental source: subsp. kurstaki
R:Geisler, M.; Schweitzer, S.; Grimm, C.
Gene 48, 109-118, 1986
A:Title: The hypervariable region in the genes coding for entomopathogenic crystal protei
A:Reference number: A91560; MUID:87163505; PMID:3557124
A:Accession: A91560
A:Molecule type: DNA
A:Residues: 1-1155 <GET>
A:Cross-references: GB:M15271; NID:G143123; PIDN:AAA22561.1; PID:G143124
A:Experimental source: subsp. kurstaki
R:Mabiko, H.; Raymond, K.C.; Bulla Jr., L.A.
DNA 5, 305-314, 1986
A:Title: Bacillus thuringiensis entomocidal protoxin gene sequence and gene product anal
A:Reference number: A90955; MUID:86300092; PMID:3743328
A:Accession: A90955
A:Molecule type: DNA
A:Residues: 1-1155 <WAB>
A:Cross-references: GB:M13898; NID:G142719; PIDN:AAA22330.1; PID:G142720
A:Experimental source: subsp. berliner
R:Chak, K.F.; Jen, J.C.
submitted to the EMBL Data Library, October 1990
A:Description: Complete nucleotide sequence and expression in Escherichia coli of a cry
A:Reference number: S14555
A:Accession: S14555
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1155 <CHA>
A:Cross-references: EMBL:X54939; NID:G40272; PIDN:CAA38701.1; PID:G40273
R:Hofe, H.; de Grave, H.; Seurinck, J.; Janssens, S.; Mahillon, J.; Ampe, C.; Vandekerck
Eur. J. Biochem. 161, 273-280, 1986
A:Title: Structural and functional analysis of a cloned delta endotoxin of Bacillus thuri
A:Reference number: A26461; MUID:87054026; PMID:3023091
A:Accession: A26461
A:Molecule type: DNA
A:Residues: 1-730, 'L', 732-784, 'R', 786-1155 <HOF>
A:Cross-references: GB:X04698; NID:G40254; PIDN:CAA28405.1; PID:G40255
A:Experimental source: strain berliner 1715
C:Comment: This toxin is lethal to the larvae of lepidopterans and dipterans.
C:Genetics:
A:Gene: cry-1-2; bct2
C:Superfamily: parasporal crystal protein
C:Keywords: delta-endotoxin
F:82-586/Product: toxic peptide #status predicted <TXP>
F:82-300/Region: toxic #status predicted
F:300-586/Region: insecticidal #status predicted

Query Match 39.0%; Score 1467; DB 2; Length 1155;
Best Local Similarity 44.5%; Pred. No. 1.1e-94;
Matches 316; Conservative 112; Mismatches 226; Indels 56; Gaps 13;

QY 36 NINHECLKMSYENVE-PFVSASTIQG-----IGIAGKILGTLGVPPAGQVASYLS 87
DB 4 NPNINECPYNCLSNPVEVLGGERIETGYTIDISLSTQFLSEF-VPGAGFVLGLVD 62
QY 88 FILGELWPKGNQWEIFMEHVEEIIINQKISTYARNKALTDLKGIGDALAVYHDSLESWVG 147
DB 63 IIWGIF---GPSQWDAFLVQIEQLNQRIEFAFNQAISRLGLESLNLYQIVAESGFREWEA 119
QY 148 NRNNTARSVYKSVQVIALEMFVKLPSFAVSGEVPILPIYAQAANLHLLLRDASIFG 207

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Db 120 DPTNPALREEMRIQFNDMNSALTTAIFLFAVQNYQVPLLSVYVQAAANLHLVLSDVSFVG 179  
Qy 208 KEWGLSSSEISTFYNRQVERAGDYSCHCVKQWYSTGLNNLRTGNAESWRYNQFRDWTLM 267  
Db 180 QRWGFDAAATINSRYNDLTRLIGNYTHAVRYNTGLERWGPDSRDWIRYNQFRRELTLT 239  
Qy 268 VLDLVALFPDYDQWYPIKTTAQLTRVYVDAIGTVHPHPSFTSTWYNNAPSF-----S 323  
Db 240 VLDIVSLFPNDSPYPIRTVSQLTREIYTPV-----LENFDGSRGSAQ 285  
Qy 324 AIEAAVVRNPHLLDFLEQVITYSLLSR-----WSNTQYMMN---WGGHKLFRITGTLNI 376  
Db 286 GIEGS-IRSPHLMIDLINSITITDAHRGEYVWSGHQIMASPVGSGPFTTPLYGTMGNA 344  
Qy 377 STQGSTNTSINPVTLPFTSRQVRYTESLAGNLFLTPQVNGVPRVDFHMKFVTHPIASDN 436  
Db 345 APQQRIVAQGGVYRTLSLTYRRPFNIGIN---NQQLSVLDGTEFAYG-----TSSN 395  
Qy 437 FYYPGYAGITQOLQDSNELPPEATGQPNYESYSHRLSHIGLI-----SASHVKALVY 489  
Db 396 LPSAVYRKSGT--VDSLDEIPQNNVPPRQGSFHRLSHVMSFRSGFSNVSIIRAPMF 453  
Qy 490 SWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVRGPGTGGDILRLRTNTGTGDIRV 549  
Db 454 SWTHRSAEFNIIIPSSQITQIPLTKSTNLGSGTSVVKPGTGGDILRLRTSPQISTRV 513  
Qy 550 NINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDDLDYKTRTVGFTT 609  
Db 514 NITAPLSQRYRIRYASTTNLQFHTSIDGRPINQGNFSATMNSGSLQSGSFRIVGFTT 573  
Qy 610 PFSFLDVQSTFTIGAMFNSSGNEVYIDRIEFVPEVTEAEYDFEKAQKVTLFTSTNP 669  
Db 574 PFNFGSGSVFTLSAHVFNSSGNEVYIDRIEFVPAEVTFAEYDLERAQKAVNELFTSSNQ 633  
Qy 670 RLKTDVKDHYDIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719  
Db 634 IGLKTDVTDYHIDQVSNLVECLSDBFCLDEKSELSEKVKHAKRLSDERNL 683

## RESULT 12

A29125  
parasporal crystal protein Bt2 - Bacillus thuringiensis subsp. kurstaki (strain HD-1)  
C/Species: Bacillus thuringiensis subsp. kurstaki  
C/Date: 15-Dec-1998 #sequence\_revision 15-Dec-1998 #text\_change 09-Jul-2004  
C/Accession: A29125  
R/Fischhoff, D.A.; Bowdish, K.S.; Perlak, F.J.; Marrone, P.G.; McCormick, S.M.; Niederme  
Bio/Technology 5, 807-813, 1987  
A/Title: Insect tolerant transgenic tomato plants.  
A/Reference number: A29125  
A/Accession: A29125  
A/Status: not compared with conceptual translation  
A/Molecule type: DNA  
A/Residues: 1-1156 <FIS>  
A/Cross-references: UNIPROT:Q9P296; UNIPROT:Q93T21  
C/Superfamily: parasporal crystal protein  
C/Keywords: delta-endotoxin

Query Match 39.0%; Score 1467; DB 2; Length 1156;  
Best Local Similarity 44.5%; Pred. No. 1.1e-94;  
Matches 316; Conservative 112; Mismatches 226; Indels 56; Gaps 13;

Qy 36 NINHEDCLKMSEYENVE-PFVSASTIQTG-----IGIAGKILGTGLGVPPAGQVASLYS 87  
Db 4 NPNTNECIPYCNLSNPVEVLGGERIETGTPIDISLSLTQFLSEF-VPGAGFVLGLVD 62  
Qy 88 FILGELWPKGNQWEIEMEHVEEIIINQISTYARNKALTDLKGLGDALAVYHDSLSWVG 147  
Db 63 IINGIF---GPSQWDAFLVQIEQLINQRIEFARNQAISRLGSLNLYQIYAESFREWEA 119  
Qy 148 NNNTRARSVVKSVYIAELMFVQKLPSPAVSGEVPPLPIYVQAAANLHLULLLRDASIFG 207  
Db 120 DPTNPALREEMRIQFNDMNSALTTAIFLFAVQNYQVPLLSVYVQAAANLHLVLSDVSFVG 179

Qy 208 KEWGLSSSEISTFYNRQVERAGDYSCHCVKQWYSTGLNNLRTGNAESWRYNQFRDWTLM 267  
Db 180 QRWGFDAAATINSRYNDLTRLIGNYTHAVRYNTGLERWGPDSRDWIRYNQFRRELTLT 239  
Qy 268 VLDLVALFPDYDQWYPIKTTAQLTRVYVDAIGTVHPHPSFTSTWYNNAPSF-----LENFDGSRGSAQ 285  
Db 240 VLDIVSLFPNDSPYPIRTVSQLTREIYTPV-----LENFDGSRGSAQ 285  
Qy 324 AIEAAVVRNPHLLDFLEQVITYSLLSR-----WSNTQYMMN---WGGHKLFRITGTLNI 376  
Db 286 GIEGS-IRSPHLMIDLINSITITDAHRGEYVWSGHQIMASPVGSGPFTTPLYGTMGNA 344  
Qy 377 STQGSTNTSINPVTLPFTSRQVRYTESLAGNLFLTPQVNGVPRVDFHMKFVTHPIASDN 436  
Db 345 APQQRIVAQGGVYRTLSLTYRRPFNIGIN---NQQLSVLDGTEFAYG-----TSSN 395  
Qy 437 FYYPGYAGITQOLQDSNELPPEATGQPNYESYSHRLSHIGLI-----SASHVKALVY 489  
Db 396 LPSAVYRKSGT--VDSLDEIPQNNVPPRQGSFHRLSHVMSFRSGFSNVSIIRAPMF 453  
Qy 490 SWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVRGPGTGGDILRLRTNTGTGDIRV 549  
Db 454 SWTHRSAEFNIIIPSSQITQIPLTKSTNLGSGTSVVKPGTGGDILRLRTSPQISTRV 513  
Qy 550 NINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDDLDYKTRTVGFTT 609  
Db 514 NITAPLSQRYRIRYASTTNLQFHTSIDGRPINQGNFSATMNSGSLQSGSFRIVGFTT 573  
Qy 610 PFSFLDVQSTFTIGAMFNSSGNEVYIDRIEFVPEVTEAEYDFEKAQKVTLFTSTNP 669  
Db 574 PFNFGSGSVFTLSAHVFNSSGNEVYIDRIEFVPAEVTFAEYDLERAQKAVNELFTSSNQ 633  
Qy 670 RLKTDVKDHYDIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719  
Db 634 IGLKTDVTDYHIDQVSNLVECLSDBFCLDEKSELSEKVKHAKRLSDERNL 683

## RESULT 13

## A22798

parasporal crystal protein - Bacillus thuringiensis  
C/Species: Bacillus thuringiensis  
C/Date: 23-Aug-1987 #sequence\_revision 23-Aug-1987 #text\_change 09-Jul-2004  
C/Accession: A22798  
R/Shibano, Y.; Yamagata, A.; Nakamura, N.; Iizuka, T.; Sugisaki, H.; Takanami, M.  
Gene 34, 243-251, 1985  
A/Title: Nucleotide sequence coding for the insecticidal fragment of the Bacillus thuring  
A/Reference number: A22798; MUID:85232070; PMID:2989108  
A/Accession: A22798  
A/Molecule type: DNA  
A/Residues: 1-934 <SHI>  
A/Cross-references: UNIPROT:Q9SV8; GB:M10917; MID:g143100; PIDN:AAA22552.1; PID:g551713  
C/Comment: The authors translated the codon ACA for residue 264 as Ser.  
C/Superfamily: parasporal crystal protein  
C/Keywords: delta-endotoxin

Query Match 38.7%; Score 1454.5; DB 2; Length 934;  
Best Local Similarity 43.5%; Pred. No. 5.8e-94;  
Matches 310; Conservative 119; Mismatches 222; Indels 61; Gaps 12;

Qy 36 NINHEDCLKMSEYENVE-PFVSASTIQTG-----IGIAGKILGTGLGVPPAGQVASLYS 87  
Db 4 NPNTNECIPYCNLSNPVEVLGGERIETGTPIDISLSLTQFLSEF-VPGAGFVLGLVD 62  
Qy 88 FILGELWPKGNQWEIEMEHVEEIIINQISTYARNKALTDLKGLGDALAVYHDSLSWVG 147  
Db 63 IINGIF---GPSQWDAFLVQIEQLINQRIEFARNQAISRLGSLNLYQIYAESFREWEA 119  
Qy 148 NNNTRARSVVKSVYIAELMFVQKLPSPAVSGEVPPLPIYVQAAANLHLULLLRDASIFG 207  
Db 120 DPTNPALREEMRIQFNDMNSALTTAIFLFAVQNYQVPLLSVYVQAAANLHLVLSDVSFVG 179  
Qy 208 KEWGLSSSEISTFYNRQVERAGDYSCHCVKQWYSTGLNNLRTGNAESWRYNQFRDWTLM 267

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Db 180 QRWGDAATINSRYNDLRLIGNYDYAVRWYNTGLERVWGPDSRDVRYNQFRELTILT 239
QY 268 VLDLVALPFSYDTQMPYPIKTAQLTREYVYDAIGTVHPPHPSFTSTWYNNAPSAIEA 327
Db 240 VLDLVALFNSYDSRRYPRTVSQLTREIYTNPV-----LENFDGSPRGMAQ 285
QY 328 AV---VRPHLLDFLEQVITYLSLRSWNTQYMMWGGHKLBFRTIGT---LNISTQGS 381
Db 286 RIEQNIROPHLMDILNRIITYYDVHRG-----FNWSGHQITASVPGSGPEFAFPLFEN 340
QY 382 TMTSINPVTLPFTSRDVRVTESSL-----AGNLFLTPQVNGVPRVDFHFWKVTTHPI 432
Db 341 AGNAAPPVLSVLTGLGIFRTLSSPLRYRIILGSGPN---NQELFVLDGTETFSASLTNLT 397
QY 433 ASDNFYYPGAGIGTQLODSENELPPEATGQPNVYESYHRLSHLGLISAS-----HVKAL 487
Db 398 PSTIYRQRTV-----DSLVDIPPQDQNSVPPRAGFSHRLSHVMTLSQAAGAVYTLRAP 450
QY 488 VYSWTHRSADRNTTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTNTGTGDI 547
Db 451 TFSWQHRSABFNFIIPSSQITQIPLTKSTNLGSGTSVVKGPGFTGGDILRRTSPQISTL 510
QY 548 RVNINPPFAQRYRVRIRVASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYKTRTVGF 607
Db 511 RVNITAPLSQRYRVRIRVASTTDLQFHTSIDGRPINQGNFSAATMNRGSGSFRTVGF 570
QY 608 TTPFSFLDVQSTFTIGANNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQKVTALFTST 667
Db 571 TTPFNFGSSVFTLSAHVFNSSGNEVYIDRIEFVPAEVTFEAEYDLERAQKAVNELFTSS 630
QY 668 NPRGLKTDVYHIDQVSNLVESLSDEFYLDKRELFEIVYAKQLHIERNM 719
Db 631 NQIGLKTVDYHIDQVSNLVESLSDEFCLDEKQELSEKVKHAKLSDERNL 682

RESULT 14
JT0241
parasporal crystal protein - Bacillus thuringiensis (strain aizawai IPL7)
N/Alternate names: 135K insecticidal protein
C/Species: Bacillus thuringiensis
C/Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C/Accession: JT0241
R/Shimizu, M.; Oshie, K.; Nakamura, K.; Takada, Y.; Oeda, K.; Ohkawa, H.
Agric. Biol. Chem. 52, 1565-1573, 1988
A/Title: Cloning and expression in Escherichia coli of the 135-kDa insecticidal protein
A/Reference number: JT0241
A/Accession: JT0241
A/Molecule type: DNA
A/Residues: 1-1176 <SHI>
A/Cross-references: UNIPROT:P02965
A/Note: B. thuringiensis aizawai IPL7 produces similar 130K and 135K insecticidal protein
C/Comment: The 135K protein has insecticidal activity against Plutella xylostella larvae
C/Superfamily: parasporal crystal protein
C/Keywords: delta-endotoxin

Query Match 38.7%; Score 1453.5; DB 2; Length 1176;
Best Local Similarity 43.5%; Pred. No. 9.9e-94; Mismatches 223; Indels 61; Gaps 12;
Matches 310; Conservative 118;

QY 36 NINHEDECLKMSYEYENVE-PFVSASTIQTG-----IGIAGKILGTGLGVPPAGQVASLYS 87
Db 4 NPNINECIPYCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEF-VPGAGFVLGLVD 62
QY 88 FILGELWFKGNQWEIFMEHVEEINQKISITYARNKALTDLGLDALAVYHDSLESWVG 147
Db 63 IIWGIF---GPSQDAFLVQEQLNQRIBEFARNQIRLEGLSNLYQIYAESFREWEA 119
QY 148 NNNNTRARSVVKSQVIALELMFVQKLPQSFVSGSBEVPLPIYQAANLHLLLRDASIFG 207
Db 120 DPTNPALREEMRIQPDNNSALTATPLFAVQNVQVPLSVYVQAANLHLSVLEDVSFVG 179
QY 208 KEWGLSSSEISTFYNRQVERAGDYSCHCVKYSTGLNLRNLTGNAESWRYNQFRDFTLM 267

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Db 180 QRWGDAATINSRYNDLRLIGNYDYAVRWYNTGLERVWGPDSRDVRYNQFRELTILT 239
QY 268 VLDLVALPFSYDTQMPYPIKTAQLTREYVYDAIGTVHPPHPSFTSTWYNNAPSAIEA 327
Db 240 VLDLVALFNSYDSRRYPRTVSQLTREIYTNPV-----LENFDGSPRGMAQ 285
QY 328 AV---VRPHLLDFLEQVITYLSLRSWNTQYMMWGGHKLBFRTIGT---LNISTQGS 381
Db 286 RIEQNIROPHLMDILNRIITYYDVHRG-----FNWSGHQITASVPGSGPEFAFPLFEN 340
QY 382 TMTSINPVTLPFTSRDVRVTESSL-----AGNLFLTPQVNGVPRVDFHFWKVTTHPI 432
Db 341 AGNAAPPVLSVLTGLGIFRTLSSPLRYRIILGSGPN---NQELFVLDGTETFSASLTNLT 397
QY 433 ASDNFYYPGAGIGTQLODSENELPPEATGQPNVYESYHRLSHLGLISAS-----HVKAL 487
Db 398 PSTIYRQRTV-----DSLVDIPPQDQNSVPPRAGFSHRLSHVMTLSQAAGAVYTLRAP 450
QY 488 VYSWTHRSADRNTTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTNTGTGDI 547
Db 451 TFSWQHRSABFNFIIPSSQITQIPLTKSTNLGSGTSVVKGPGFTGGDILRRTSPQISTL 510
QY 548 RVNINPPFAQRYRVRIRVASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYKTRTVGF 607
Db 511 RVNITAPLSQRYRVRIRVASTTDLQFHTSIDGRPINQGNFSAATMNRGSGSFRTVGF 570
QY 608 TTPFSFLDVQSTFTIGANNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQKVTALFTST 667
Db 571 TTPFNFGSSVFTLSAHVFNSSGNEVYIDRIEFVPAEVTFEAEYDLERAQKAVNELFTSS 630
QY 668 NPRGLKTDVYHIDQVSNLVESLSDEFYLDKRELFEIVYAKQLHIERNM 719
Db 631 NQIGLKTVDYHIDQVSNLVESLSDEFCLDEKQELSEKVKHAKLSDERNL 682

RESULT 15
S02134
parasporal crystal protein cryIC1 - Bacillus thuringiensis (strain aizawai IC1)
N/Alternate names: delta-endotoxin IC1; entomocidal crystal protein
C/Species: Bacillus thuringiensis
A/Variety: strain aizawai IC1
C/Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C/Accession: S02134; S04994
R/Haider, M.Z.; Ellar, D.J.
Nucleic Acids Res. 16, 10927, 1988
A/Title: Nucleotide sequence of a Bacillus thuringiensis aizawai IC1 entomocidal crystal
A/Reference number: S02134; MUID:89083518; PMID:3205732
A/Accession: S02134
A/Status: translation not shown
A/Molecule type: DNA
A/Residues: 1-1155 <HAI>
A/Cross-references: UNIPROT:P06578; EMBL:X13233; NID:G40277; PIDN:CAA31620.1; PID:G40278
A/Experimental source: strain aizawai IC1
R/Haider, M.Z.; Ellar, D.J.
J. Mol. Biol. 208, 183-194, 1989
A/Title: Functional mapping of an entomocidal delta-endotoxin. Single amino acid changes
A/Reference number: S04994; MUID:89362455; PMID:2769751
A/Accession: S04994
A/Molecule type: DNA
A/Residues: 429-449; 'A', 451-724 <HAW>
A/Cross-references: EMBL:X16315
A/Experimental source: strain aizawai IC1
C/Comment: This toxin is lethal to the larvae of lepidopterans and dipterans.
C/Superfamily: parasporal crystal protein
C/Keywords: delta-endotoxin

Query Match 38.6%; Score 1450; DB 2; Length 1155;
Best Local Similarity 44.1%; Pred. No. 1.7e-93;
Matches 313; Conservative 112; Mismatches 223; Indels 56; Gaps 13;

QY 36 NINHEDECLKMSYEYENVE-PFVSASTIQTG-----IGIAGKILGTGLGVPPAGQVASLYS 87

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Db 4 NPNINECIPYNCLNSPEVEVLQGERIETGYTFIDISLSLTQFLSEF-VPGAGFVLGLVD 62  
Qy 88 FILGELMPKKNQWEIIFMEHVEEIIINQKISTYARKALTDLKGGLDALAVYHDSLESWVG 147  
Db 63 IIWGIF--GPSQWDAFLVQIEQLINQRIEEFARNCAISRLEGSLNLYQIYAESPWEA 119  
Qy 148 NRNNTARSVKXSOYIALSLMFVQKLPSPAVSGEEVPLLPYAOAANLHLLLRDASIFG 207  
Db 120 DPTNPALREEMRIQFNDMNSALTITAIPLFAVQNYQVELLSVYVQAAHLHSLVLRDVSFVG 179  
Qy 208 KEWGLSSSIITFYNRQVRAGDYSDHCVKYSTGLNLRGTNAESWVRYNQOFREDMTLM 267  
Db 180 QRGFPAAATINSEYNDLTFLIGNYTDHAYRYNTGLERVWGPDSRDWIRYNQOFRELTIT 239  
Qy 268 VLDLVALFSPYQOMYPIKTKTQLTREVYTDAGTVHPHPSFTSTTWYNNAPSP----S 323  
Db 240 VLDIVSLFFNYDSRTYPIRTVSQLTREIYTNPV-----LENFDGSPRGSQAQ 285  
Qy 324 AIEAAVVRPHLLDLEQVITVYLSLR---WSNTQYMNW---WGHKLEFRTIGGTINI 376  
Db 286 GIEGS--IRSPHLMIDILNSITIIYDAHRGEYWSGHQIMASPVGFSQPEFTFPLYGTMGNA 344  
Qy 377 STQGSTNTSINPVTLPFTGRDVRVYTESLAGLNLFLTQPVNGVRVDFHMKFVTHPIASDN 436  
Db 345 APQQRIVAQLOGGVYRTLSSTLYRRPPENIGIN---NQQLSVLDGTETAYG-----TSSN 395  
Qy 437 FYYPGAGIGTQLODSENELPPEATQCPNVESYSHLSHIGLI-----SASHVKALVY 489  
Db 396 LPSAVYRKSGT--VDSLDEIPQNNVPPRGFHSRLSHVMSFRSGFSNSVSIIRPPMF 453  
Qy 490 SWTHRGADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNTGTGDIRV 549  
Db 454 SWTHRAEFNNIIPSSQITQIPLTKSTNLGSGTVVKVGPGFTGGDILRRITSPQISTLAV 513  
Qy 550 NINPPFAQRVVRIRYASTTDLOFHTSINGKAINQGNFSAATMNRGEDLDYKTFRTVGTFT 609  
Db 514 NITAPLSQRYVRIRYASTTNLQHTSIDGRIINQGNFSAATMSSGNLQSGSFRIVGTFT 573  
Qy 610 PPSFLDVQSTFTIGAMNFFSGNEVYIDRIEFVPEVTEAEYDFEKAQEKVATLFTSTNP 669  
Db 574 PFNFGSSVFTLSAHVFNSEVNEVYIDRIEFVPAEVTFEAEYDLERAQKAVNELFTSSNQ 633  
Qy 670 RGLKTDVKYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKOLHIERNM 719  
Db 634 IGLKTDVTDVYHIDQVSNLVESLSDEFCLDEKELSEKVKHAKLSDERNL 683

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Job time : 22.191 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

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Scoring table: BLOSUM62  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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  - 2: /cgn2\_6/prodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3760	100.0	719	17	US-10-782-020-10
2	3760	100.0	719	17	Sequence 10, Appl
3	3760	100.0	719	17	Sequence 8, Appl
4	3760	100.0	719	17	US-10-782-141-8
5	3476.5	92.5	710	14	US-10-782-096-10
6	2278.5	60.6	1228	16	US-10-782-570-7
7	2265.5	60.3	1207	10	US-10-428-961-42
8	2186.5	58.2	1227	14	US-10-809-953-10
9	2171.5	57.8	1186	9	US-09-988-462-7
10	2116	56.3	1228	14	US-10-428-961-63
11	2116	56.3	1228	15	US-10-428-961-38
12	1932.5	51.4	643	9	US-10-614-524-2
13	1722.5	45.8	1167	14	US-09-826-660-25
					Sequence 1, Appl

14	1681.5	44.7	653	14	US-10-428-961-6	Sequence 6, Appl
15	1670.5	44.4	1157	17	US-10-782-141-16	Sequence 16, Appl
16	1670.5	44.4	1157	17	US-10-782-096-17	Sequence 17, Appl
17	1670.5	44.4	1157	17	US-10-782-570-13	Sequence 13, Appl
18	1511	40.2	1206	13	US-10-032-717-2	Sequence 2, Appl
19	1511	40.2	1206	14	US-10-414-637-2	Sequence 2, Appl
20	1511	40.2	1206	15	US-10-606-320-2	Sequence 2, Appl
21	1511	40.2	1206	17	US-10-746-914-2	Sequence 4, Appl
22	1495	39.8	1210	13	US-10-032-717-4	Sequence 4, Appl
23	1495	39.8	1210	14	US-10-414-637-4	Sequence 4, Appl
24	1495	39.8	1210	15	US-10-606-320-4	Sequence 4, Appl
25	1495	39.8	1210	17	US-10-746-914-4	Sequence 4, Appl
26	1485.5	39.5	1156	14	US-10-099-285-72	Sequence 72, Appl
27	1485.5	39.5	1156	14	US-10-428-961-28	Sequence 28, Appl
28	1467	39.0	1155	9	US-09-756-643-2	Sequence 2, Appl
29	1467	39.0	1155	10	US-09-988-462-9	Sequence 9, Appl
30	1467	39.0	1155	14	US-10-136-998A-2	Sequence 2, Appl
31	1467	39.0	1177	14	US-10-035-060-6	Sequence 6, Appl
32	1467	39.0	1181	10	US-09-988-462-11	Sequence 11, Appl
33	1467	39.0	1181	10	US-09-988-462-13	Sequence 13, Appl
34	1467	39.0	1181	10	US-09-988-462-15	Sequence 15, Appl
35	1467	39.0	1181	10	US-09-988-462-17	Sequence 17, Appl
36	1467	39.0	1181	10	US-09-988-462-28	Sequence 28, Appl
37	1467	39.0	1181	14	US-10-136-998A-4	Sequence 4, Appl
38	1467	39.0	1181	14	US-10-136-998A-8	Sequence 8, Appl
39	1467	39.0	1181	14	US-10-136-998A-10	Sequence 10, Appl
40	1467	39.0	1181	14	US-10-136-998A-12	Sequence 12, Appl
41	1462	38.9	1177	14	US-10-035-060-2	Sequence 2, Appl
42	1460	38.8	1177	14	US-10-035-060-8	Sequence 8, Appl
43	1459	38.8	1177	14	US-10-102-469-24	Sequence 24, Appl
44	1443.5	38.4	1176	17	US-10-782-141-6	Sequence 6, Appl
45	1443.5	38.4	1176	17	US-10-782-096-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1

US-10-782-020-10  
; Sequence 10, Application US/10782020  
; Publication No. US20040197916A1  
; GENERAL INFORMATION:  
; APPLICANT: Carozzi, Nadine  
; APPLICANT: Hargiss, Tracy  
; APPLICANT: Kozziel, Michael G.  
; APPLICANT: Duck, Nicholas B.  
; APPLICANT: Carr, Brian  
; TITLE OF INVENTION: AXMI-004, A Delta-Endotoxin Gene and  
; FILE OF INVENTION: Methods for Its Use  
; FILE REFERENCE: 045600/274139  
; CURRENT APPLICATION NUMBER: US/10782,020  
; CURRENT FILING DATE: 2004-02-19  
; PRIOR APPLICATION NUMBER: 60/448,810  
; PRIOR FILING DATE: 2003-02-20  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 719  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
US-10-782-020-10

Query Match 100.0%; Score 3760; DB 17; Length 719;  
Best Local Similarity 100.0%; Pred. No. 2,7e-309;  
Matches 719; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MKLNQDQKHQSFSSNAKVDKISTDLSKNQETDIQLQNHEDCLKNSEVENPEPVSASTI	60
Db	1	MKLNQDQKHQSFSSNAKVDKISTDLSKNQETDIQLQNHEDCLKNSEVENPEPVSASTI	60
Qy	61	QTGIGIAGKILGTLGVPFAGQVASYLSYFILGELPKGNQWEIIFMEHVEEIIINQKISTYA	120
Db	61	QTGIGIAGKILGTLGVPFAGQVASYLSYFILGELPKGNQWEIIFMEHVEEIIINQKISTYA	120

QY 121 RNKALTDLKLGLDALAVYHDSLEWVGNNRNRARSVVKSOYIALELMFVQKLPSPAVSG 180  
 DB 121 RNKALTDLKLGLDALAVYHDSLEWVGNNRNRARSVVKSOYIALELMFVQKLPSPAVSG 180  
 QY 181 BEVPLLPPIYAQAANLHLLLDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHCVKWS 240  
 DB 181 BEVPLLPPIYAQAANLHLLLDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHCVKWS 240  
 QY 241 TGLNNLRGTNAESWVRYNQFRDMLVLDLVALFPSTDMYPIKTTAQLTREVTYDAI 300  
 DB 241 TGLNNLRGTNAESWVRYNQFRDMLVLDLVALFPSTDMYPIKTTAQLTREVTYDAI 300  
 QY 301 GTVHPHPSFTSTTWNNNAPSFAIEAAVVRNPHLLDLEQVTIYSLLSWSNTQYNNMW 360  
 DB 301 GTVHPHPSFTSTTWNNNAPSFAIEAAVVRNPHLLDLEQVTIYSLLSWSNTQYNNMW 360  
 QY 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRYSYSHRSLSHIGLIS 480  
 DB 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRYSYSHRSLSHIGLIS 480  
 QY 421 VDFHWKFVTHPIASDNFYPGYAGIGTQLODSENELPPEATGQPNYESYSHRSLSHIGLIS 540  
 DB 421 VDFHWKFVTHPIASDNFYPGYAGIGTQLODSENELPPEATGQPNYESYSHRSLSHIGLIS 540  
 QY 481 ASHVKALVYSWTHRSADRTNIENSITQIPLVKAFLSSGAAVVRGPGTGGDILRRTN 600  
 DB 481 ASHVKALVYSWTHRSADRTNIENSITQIPLVKAFLSSGAAVVRGPGTGGDILRRTN 600  
 QY 541 TGTGDIRVNIINPPPAQRYRIRIYASTDLOPHTSINGKAINQGNFSATWNGEDLDYK 660  
 DB 541 TGTGDIRVNIINPPPAQRYRIRIYASTDLOPHTSINGKAINQGNFSATWNGEDLDYK 660  
 QY 601 TFRVGTTPPSFLDVQSTFTIGAWNFSNGNEVYIDRIEFVPEVTVYEAEDPEKAQEKV 719  
 DB 601 TFRVGTTPPSFLDVQSTFTIGAWNFSNGNEVYIDRIEFVPEVTVYEAEDPEKAQEKV 719  
 QY 661 TALFTSTNPRGLKTDVVDYHIDQVSNLVSLSDBFYLDKEKELFEIVKYAKQLHIERNM 719  
 DB 661 TALFTSTNPRGLKTDVVDYHIDQVSNLVSLSDBFYLDKEKELFEIVKYAKQLHIERNM 719  
 RESULT 2  
 US-10-782-141-8  
 ; Sequence 8, Application US/10782141  
 ; Publication No. US20040197917A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Carozzi, Nadine  
 ; APPLICANT: Hargiss, Tracy  
 ; APPLICANT: Koziel, Michael G.  
 ; APPLICANT: Duck, Nicholas B.  
 ; APPLICANT: Carr, Brian  
 ; TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and  
 ; TITLE OF INVENTION: Methods for Its Use  
 ; FILE REFERENCE: 045600/274143  
 ; CURRENT APPLICATION NUMBER: US/10782,141  
 ; PRIOR FILING DATE: 2004-02-20  
 ; PRIOR APPLICATION NUMBER: 60/448,632  
 ; PRIOR FILING DATE: 2003-02-20  
 ; NUMBER OF SEQ ID NOS: 23  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 8  
 ; LENGTH: 719  
 ; TYPE: PRT  
 ; ORGANISM: Bacillus thuringiensis  
 US-10-782-141-8  
 Query Match 100.0%; Score 3760; DB 17; Length 719;  
 Best Local Similarity 100.0%; Pred. No. 2,7e-309; Indels 0; Gaps 0;  
 Matches 719; Conservative 0; Mismatches 0;  
 QY 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNIHEDCLKMSEYENVEPFFVASTI 60  
 DB 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNIHEDCLKMSEYENVEPFFVASTI 60

DB 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNIHEDCLKMSEYENVEPFFVASTI 60  
 QY 61 QTGIGIAGKILGTGVPFAGVASIYSITIGELWPKGNQWEIEMHVEEIIINOKISTYA 120  
 DB 61 QTGIGIAGKILGTGVPFAGVASIYSITIGELWPKGNQWEIEMHVEEIIINOKISTYA 120  
 QY 121 RNKALTDLKLGLDALAVYHDSLEWVGNNRNRARSVVKSOYIALELMFVQKLPSPAVSG 180  
 DB 121 RNKALTDLKLGLDALAVYHDSLEWVGNNRNRARSVVKSOYIALELMFVQKLPSPAVSG 180  
 QY 181 BEVPLLPPIYAQAANLHLLLDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHCVKWS 240  
 DB 181 BEVPLLPPIYAQAANLHLLLDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHCVKWS 240  
 QY 241 TGLNNLRGTNAESWVRYNQFRDMLVLDLVALFPSTDMYPIKTTAQLTREVTYDAI 300  
 DB 241 TGLNNLRGTNAESWVRYNQFRDMLVLDLVALFPSTDMYPIKTTAQLTREVTYDAI 300  
 QY 301 GTVHPHPSFTSTTWNNNAPSFAIEAAVVRNPHLLDLEQVTIYSLLSWSNTQYNNMW 360  
 DB 301 GTVHPHPSFTSTTWNNNAPSFAIEAAVVRNPHLLDLEQVTIYSLLSWSNTQYNNMW 360  
 QY 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRYSYSHRSLSHIGLIS 480  
 DB 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRYSYSHRSLSHIGLIS 480  
 QY 421 VDFHWKFVTHPIASDNFYPGYAGIGTQLODSENELPPEATGQPNYESYSHRSLSHIGLIS 540  
 DB 421 VDFHWKFVTHPIASDNFYPGYAGIGTQLODSENELPPEATGQPNYESYSHRSLSHIGLIS 540  
 QY 481 ASHVKALVYSWTHRSADRTNIENSITQIPLVKAFLSSGAAVVRGPGTGGDILRRTN 600  
 DB 481 ASHVKALVYSWTHRSADRTNIENSITQIPLVKAFLSSGAAVVRGPGTGGDILRRTN 600  
 QY 541 TGTGDIRVNIINPPPAQRYRIRIYASTDLOPHTSINGKAINQGNFSATWNGEDLDYK 660  
 DB 541 TGTGDIRVNIINPPPAQRYRIRIYASTDLOPHTSINGKAINQGNFSATWNGEDLDYK 660  
 QY 601 TFRVGTTPPSFLDVQSTFTIGAWNFSNGNEVYIDRIEFVPEVTVYEAEDPEKAQEKV 719  
 DB 601 TFRVGTTPPSFLDVQSTFTIGAWNFSNGNEVYIDRIEFVPEVTVYEAEDPEKAQEKV 719  
 QY 661 TALFTSTNPRGLKTDVVDYHIDQVSNLVSLSDBFYLDKEKELFEIVKYAKQLHIERNM 719  
 DB 661 TALFTSTNPRGLKTDVVDYHIDQVSNLVSLSDBFYLDKEKELFEIVKYAKQLHIERNM 719  
 RESULT 3  
 US-10-782-096-10  
 ; Sequence 10, Application US/10782096  
 ; Publication No. US20040210964A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Carozzi, Nadine  
 ; APPLICANT: Hargiss, Tracy  
 ; APPLICANT: Koziel, Michael G.  
 ; APPLICANT: Duck, Nicholas B.  
 ; APPLICANT: Carr, Brian  
 ; TITLE OF INVENTION: AXMI-009, A Delta-Endotoxin Gene and  
 ; TITLE OF INVENTION: Methods for Its Use  
 ; FILE REFERENCE: 045600/274148  
 ; CURRENT APPLICATION NUMBER: US/10782,096  
 ; CURRENT FILING DATE: 2004-02-19  
 ; PRIOR APPLICATION NUMBER: 60/448,633  
 ; PRIOR FILING DATE: 2003-02-20  
 ; NUMBER OF SEQ ID NOS: 23  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 10  
 ; LENGTH: 719  
 ; TYPE: PRT  
 ; ORGANISM: Bacillus thuringiensis  
 US-10-782-096-10  
 Query Match 100.0%; Score 3760; DB 17; Length 719;



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Best Local Similarity 100.0%; Pred. No. 2.7e-309;
Matches 719; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKLNQDQKQSFSSNAKVDKISTDSLNKNETDIELQNHEDCLKMSSEYENVEPFSASTI 60
Db 1 MKLNQDQKQSFSSNAKVDKISTDSLNKNETDIELQNHEDCLKMSSEYENVEPFSASTI 60
Qy 61 QTGIGTAGKILGTLGVPPAGQVAVSLYFILGELWPKGKNQWEIIFMEHVEEIIINOKISTYA 120
Db 61 QTGIGTAGKILGTLGVPPAGQVAVSLYFILGELWPKGKNQWEIIFMEHVEEIIINOKISTYA 120
Qy 121 RNKALTDLKLGDALAVYHDSLSWGNRNNTARSVVKSYQYIALELMFVKLPSPFAVSG 180
Db 121 RNKALTDLKLGDALAVYHDSLSWGNRNNTARSVVKSYQYIALELMFVKLPSPFAVSG 180
Qy 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSCHVKWYS 240
Db 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSCHVKWYS 240
Qy 241 TGLNNLRGTNAESWVRYNQFRDWTLMVLDLVALFPSYDTQMPYIKTTAQLTREYITDAI 300
Db 241 TGLNNLRGTNAESWVRYNQFRDWTLMVLDLVALFPSYDTQMPYIKTTAQLTREYITDAI 300
Qy 301 GTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTTIYSLLSRWNTQYMNW 360
Db 301 GTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTTIYSLLSRWNTQYMNW 360
Qy 361 GGHKLEPRTTGGTLNISTQGSTNTSINPVLPTSDRDVYTESLAGINLFLTOPVNGVPR 420
Db 361 GGHKLEPRTTGGTLNISTQGSTNTSINPVLPTSDRDVYTESLAGINLFLTOPVNGVPR 420
Qy 421 VDFHWKFTVTHPIASDNFYPGYAGIGTQLODSENLPEPEATQPNYESYSHRLSHIGLIS 480
Db 421 VDFHWKFTVTHPIASDNFYPGYAGIGTQLODSENLPEPEATQPNYESYSHRLSHIGLIS 480
Qy 481 ASHVKALVYSWTHRSADRTNITPNSITQIPLVKAENLSSGAAVVRGPGFTGGDILRRTN 540
Db 481 ASHVKALVYSWTHRSADRTNITPNSITQIPLVKAENLSSGAAVVRGPGFTGGDILRRTN 540
Qy 541 TGTFGDIRVNINPPFAQRYVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
Db 541 TGTFGDIRVNINPPFAQRYVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
Qy 601 TFRTVGFTTTPSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEKV 660
Db 601 TFRTVGFTTTPSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEKV 660
Qy 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719
Db 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 4
US-10-782-570-7
; Sequence 7, Application US/10782570
; Publication No. US20040210965A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-007, A Delta-Endotoxin Gene and
; TITLE OF INVENTION: Methods for Its Use
; FILE REFERENCE: 045600/274144
; CURRENT APPLICATION NUMBER: US/10/782,570
; PRIOR FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: 60/448,812
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 719
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TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-782-570-7

Query Match 100.0%; Score 3760; DB 17; Length 719;
Best Local Similarity 100.0%; Pred. No. 2.7e-309;
Matches 719; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKLNQDQKQSFSSNAKVDKISTDSLNKNETDIELQNHEDCLKMSSEYENVEPFSASTI 60
Db 1 MKLNQDQKQSFSSNAKVDKISTDSLNKNETDIELQNHEDCLKMSSEYENVEPFSASTI 60
Qy 61 QTGIGTAGKILGTLGVPPAGQVAVSLYFILGELWPKGKNQWEIIFMEHVEEIIINOKISTYA 120
Db 61 QTGIGTAGKILGTLGVPPAGQVAVSLYFILGELWPKGKNQWEIIFMEHVEEIIINOKISTYA 120
Qy 121 RNKALTDLKLGDALAVYHDSLSWGNRNNTARSVVKSYQYIALELMFVKLPSPFAVSG 180
Db 121 RNKALTDLKLGDALAVYHDSLSWGNRNNTARSVVKSYQYIALELMFVKLPSPFAVSG 180
Qy 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSCHVKWYS 240
Db 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSCHVKWYS 240
Qy 241 TGLNNLRGTNAESWVRYNQFRDWTLMVLDLVALFPSYDTQMPYIKTTAQLTREYITDAI 300
Db 241 TGLNNLRGTNAESWVRYNQFRDWTLMVLDLVALFPSYDTQMPYIKTTAQLTREYITDAI 300
Qy 301 GTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTTIYSLLSRWNTQYMNW 360
Db 301 GTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTTIYSLLSRWNTQYMNW 360
Qy 361 GGHKLEPRTTGGTLNISTQGSTNTSINPVLPTSDRDVYTESLAGINLFLTOPVNGVPR 420
Db 361 GGHKLEPRTTGGTLNISTQGSTNTSINPVLPTSDRDVYTESLAGINLFLTOPVNGVPR 420
Qy 421 VDFHWKFTVTHPIASDNFYPGYAGIGTQLODSENLPEPEATQPNYESYSHRLSHIGLIS 480
Db 421 VDFHWKFTVTHPIASDNFYPGYAGIGTQLODSENLPEPEATQPNYESYSHRLSHIGLIS 480
Qy 481 ASHVKALVYSWTHRSADRTNITPNSITQIPLVKAENLSSGAAVVRGPGFTGGDILRRTN 540
Db 481 ASHVKALVYSWTHRSADRTNITPNSITQIPLVKAENLSSGAAVVRGPGFTGGDILRRTN 540
Qy 541 TGTFGDIRVNINPPFAQRYVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
Db 541 TGTFGDIRVNINPPFAQRYVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
Qy 601 TFRTVGFTTTPSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEKV 660
Db 601 TFRTVGFTTTPSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEKV 660
Qy 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719
Db 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 5
US-10-428-961-42
; Sequence 42, Application US/10428961
; Publication No. US20030237111A1
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Chu, Chih-Rei
; APPLICANT: Donovan, William P.
; APPLICANT: Gilmer, Amy J.
; APPLICANT: Rupar, Mark J.
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin
; FILE REFERENCE: MECO201--1
; CURRENT APPLICATION NUMBER: US/10/428,961
; CURRENT FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: 09/661,322
```

[illegible]

; GENERAL INFORMATION:

Db 656 FTWNPRLKTDYDHYDQVSNLVACLSDEFCLDEKRELEKVKYAKRLSDERNL 711

US-09-988-462-7

RESULT 7

Sequence 7, Application US/09988462

Publication No. US20030046726A1

GENERAL INFORMATION:

APPLICANT: Koziel, Michael G.

Desai, Nalini M.

Lewis, Kelly S.

Kramer, Vance C.

Warren, Gregory W.

Evola, Stephen V.

Crossland, Lydie D.

Wright, Martha S.

Merlin, Ellis J.

Lauais, Karen L.

TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED INSECTICIDAL ACTIVITY IN MAIZE

NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Syngenta Biotechnology, Inc.

STREET: 3054 Cornwallis Road

CITY: Research Triangle Park

STATE: NC

COUNTRY: USA

ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09988 462

FILING DATE: 20-NO. US20030046726A1-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/547,422

FILING DATE: 11-APR-2000

APPLICATION NUMBER: US 08/459,504

FILING DATE: 02-JUN-1995

APPLICATION NUMBER: US 07/951,715

FILING DATE: 25-SEP-1992

APPLICATION NUMBER: US 07/772,027

FILING DATE: 04-OCT-1991

ATTORNEY/AGENT INFORMATION:

NAME: Meigs, J. Timothy

REGISTRATION NUMBER: 38,241

REFERENCE/DOCKET NUMBER: S-188051

TELEPHONE: (919)541-8587

TELEFAX: (919)541-8689

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 1207 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 7:

US-09-988-462-7

Query Match 60.3%; Score 2265.5; DB 10; Length 1207;

Best Local Similarity 64.3%; Pred. No. 2.6e-182;

Matches 442; Conservative 78; Mismatches 154; Indels 13; Gaps 5;

Qy 40 EDCLKMEYENVPFVSASTIQTGIGIAGKILGTGVFPAGQVASYSLFGLBWPCKGN 99

Db 10 EDSLICIAEGNIDPFVSASTVQIGINAGRIILGVLPFAGQLASFYSLFVGLWPRGRD 69

Qy 100 QWEIFMHEVEINQKISTVARNKALTDLKGDLALAVYHDSLESVGNRNNTARSVK 159

Db 70 QWEIFLHVQLINQKITENARNALTARLQGLGDSFRAYQQSLDLENRRDARTSVLY 129

Qy 160 SOYIALELMFVOKLPSPFAVSGEEVPLLPYIAQAANLHLLLRDASIFPKENGLSSSEIST 219

Db 130 TOYIALELDFLNPMPFAIRNQEVPLLMVYQAANLHLLLRDASLFGSEFGLTSQEIQR 189

Qy 220 FYNROVERAGDYSDHCVKWYSTGLNNLSTGNAESWVRYNQFRDRMTLAVLDVALFPSSYD 279

Db 190 YIEROVERTRDYSDYCVWEYNTGLNSLSTGNAESWVRYNQFRDRMTLAVLDVALFPSSYD 249

Qy 280 TOMYPIKTTAQLTREVTYDAIGTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFL 339

Db 250 TRTYPINTSAQLTREVTYDAIGAT--GVNMAWMWYNNNAPSFAIEAAVVRNPHLLDFL 307

Qy 340 EOVTVYSLLSRWSNTQVYNNMGCHLERTTGGTLNISTGTSNTSINPVTLPFTSRDVTY 399

Db 308 EQLTIFSSASRWSNTRHWYWRGHTIQSRPIQGGTLNISTGTSNTSINPVTLPFTSRDVTY 367

Qy 400 RTESLAGLNLFP--LTQPVNGVPRVDFHWKFVTHP-----IASDNFYFYGAGIGTQLQDS 452

Db 368 RTESYAGVLLWGIYDEPIHGVTVRNF--TNPQNISDRGTANYSQP-YESPGQLKDS 423

Qy 453 ENELPREATGQPNYESYSHRLSHIGLISASHVKALVYSWTHRSADRTNITSPNSITQIPL 512

Db 424 ETELPETTERPNYESYSHRLSHIGIILQSRVNVVSVWTHRSADRTNITGPNRITQIPM 483

Qy 513 VKAFNLSSGAAVVRGPGTGGDILRRNTGTGDIRVNNPFPFAQRYVRVRYASTTDLQ 572

Db 484 VKASELPQGTTVRGPGTGGDILRRNTGTGDIRVNVGPGPIRVTVNGPLTORYRIGRYASTVDFD 543

Qy 573 FHTSINGKAINQGNFSATMNGEDLDYKTFRTVGTGTFPSFLDVQSTTTIGANWSSNE 632

Db 544 FVSRGGTTVNNFRFLRTMNSGDELKYGNFVRAFTTFTTQIQDIIRTSIQGLSGNGE 603

Qy 633 VVIDRIEFPVVEVTVEAEYDEKAEKVYALTFTSNRGLKTDVKDYHIDQVSNLIVESLS 692

Db 604 VVIDKILIPVTATPEAEYDLERAGEAVNALFTNPRKTDVTDYHIDQVSNLIVACLS 663

Qy 693 DEFYLDKRELFPIVYKAKQLHIERNM 719

Db 664 DEFCLDEKRELEKVKYAKRLSDERNL 690

RESULT 8

US-10-428-961-63

Sequence 63, Application US/10428961

Publication No. US20030237111A1

GENERAL INFORMATION:

APPLICANT: Baum, James A.

APPLICANT: Chu, Chih-Rei

APPLICANT: Donovan, William P.

APPLICANT: Gilmer, Amy J.

APPLICANT: Ruper, Mark J.

TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin

FILE REFERENCE: MECO201-1

CURRENT APPLICATION NUMBER: US/10/428,961

PRIOR FILING DATE: 2003-05-02

PRIOR APPLICATION NUMBER: 09/661,322

PRIOR FILING DATE: 2000-09-13

PRIOR APPLICATION NUMBER: 60/153,995

PRIOR FILING DATE: 1999-09-15

NUMBER OF SEQ ID NOS: 63

SOFTWARE: PatentIn version 3.2

SEQ ID NO 63

LENGTH: 1227

TYPE: PRT

ORGANISM: Bacillus thuringiensis

US-10-428-961-63

Query Match 58.2%; Score 2186.5; DB 14; Length 1227;

Best Local Similarity 59.2%; Pred. No. 1.3e-175;

Matches 423; Conservative 105; Mismatches 173; Indels 13; Gaps 3;

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QY 13 SSNAKVDKISTDSLXN-----ETDIELQNIHEDCLKMSYENVEPFSASTIQTGIG 65
Db 7 NENEINALSIPAVNSHSAQNLSTDARI-----EDSLCIAEGNNIDPFSASVTQTGIN 61
QY 66 IAGKILGTGVFPAGQVASFILGELWPKGKQWEIFMEHVEEIIINQKISTYARNKAL 125
Db 62 IAGRILGVLPFAGQIASFYSFLVGLWPRGRDPWEIFLVEHVEHLIRQQVTENTRTAL 121
QY 126 TDLKGLDALAVYHDSLESWGNRNNTPARSVVKSQYIALELMFVQKLPSPFVSGEVP 185
Db 122 ARLOGLGNSFRAYQOSLEDWLENRDDARTSRVLYTQYIALELDFLNAWPLFAIRNQEVPL 181
QY 186 LPIYAQAANLHLLLRDASIFGKEWGLSSSISFYKNOVERAGDYSDHCVKWTSTGLNN 245
Db 182 LMVYAQAANLHLLLRDASLFGSEFGLTSQBIQRYERQVEKTRYSYDVCARWNTGLNN 241
QY 246 LRGTNAESWVRYNQPRRDMTLMVLDLVALFPSTYDTQMPYIKTTAQLTREYVYDAIGTVHP 305
Db 242 LRGTNAESWLRYNQPRRDLTLGVLDLVALFPSTYDTRVYPMNTSAQLTREIYDPIGRNA 301
QY 306 HPSFTSTWYNNAPSFSAIAEAAVVRNPHLLDPLEQVITYLSLRSWNTQYMNWGGHKL 365
Db 302 PSGFASTWNNFNNAPSFSAIAEAAVVRNPHLLDPLEQVITYLSLRSWNTQYMNWGGHKL 361
QY 366 EFRITGGTLNISTQGSTNTSINPVLTPFTSRDVRVYTESLAGLNLFLTQPVNGVPRVDPHW 425
Db 362 ESRTIRGSLSTWHTGNTNTSINPVLQFTSRDVRVYTESFAGINILLTTPVNGVPRVAFNW 421
QY 426 KFTVTHPIASDNFYPGYAGIGTQLODSENELPPEATQPNYESYSHLSHIGLISASHVK 485
Db 422 RNPLSLRGSLTYTIGYTGVGTLQFDSSELPETTERPNYESYSHLSHIGLISASHVK 481
QY 486 ALVYSWTHRSADRNTIIPNPSITQIPLVKAPNLSGAAVVRGPGTGGDIILRTNTGTFG 545
Db 602 EFPVGISASGQ-TAGISISNAGSQTHFDFKIEPITATFEAYEDLERAQEAVALFT 660
QY 666 STNPRGLKTDVKDHYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKOLHIERNM 719
Db 661 NTNPRRLKGTVDYHIDVSNLVSLSDEFYLDKRELFEIVKYAKOLHIERNM 714

```

## RESULT 9

US-09-826-660-23

; Sequence 23, Application US/09826660

; Patent No. US20010026940A1

; GENERAL INFORMATION:

; APPLICANT: Cardineau, Guy A.

; APPLICANT: Stelman, Steven J.

; APPLICANT: Narva, Kenneth E.

; TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins

; FILE REFERENCE: MA-714XC2D1

; CURRENT APPLICATION NUMBER: US/09/826,660

; CURRENT FILING DATE: 2001-04-05

; PRIOR APPLICATION NUMBER: 09/178,252

; PRIOR FILING DATE: 1998-10-23

; PRIOR APPLICATION NUMBER: 60/065,215

; PRIOR FILING DATE: 1997-11-12

; PRIOR APPLICATION NUMBER: 60/076,445

; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 23

; LENGTH: 1186

; TYPE: PRT

; ORGANISM: Artificial Sequence

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; FEATURE:
; OTHER INFORMATION: Toxin encoded by synthetic B.t. gene
US-09-826-660-23

```

Query Match 57.8%; Score 2171.5; DB 9; Length 1186;

Best Local Similarity 59.0%; Pred. No. 2.4e-174;

Matches 421; Conservative 108; Mismatches 172; Indels 13; Gaps 3;

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QY 13 SSNAKVDKISTDSLXN-----ETDIELQNIHEDCLKMSYENVEPFSASTIQTGIG 65
Db 7 NENEINALSIPAVNSHSAQNLSTDARI-----EDSLCIAEGNNIDPFSASVTQTGIN 61

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```

QY 66 IAGKILGTGVFPAGQVASFILGELWPKGKQWEIFMEHVEEIIINQKISTYARNKAL 125
Db 62 IAGRILGVLPFAGQIASFYSFLVGLWPRGRDPWEIFLVEHVEHLIRQQVTENTRTAL 121

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```

QY 126 TDLKGLDALAVYHDSLESWGNRNNTPARSVVKSQYIALELMFVQKLPSPFVSGEVP 185
Db 122 ARLOGLGNSFRAYQOSLEDWLENRDDARTSRVLYTQYIALELDFLNAWPLFAIRNQEVPL 181

```

```

QY 186 LPIYAQAANLHLLLRDASIFGKEWGLSSSISFYKNOVERAGDYSDHCVKWTSTGLNN 245
Db 182 LMVYAQAANLHLLLRDASLFGSEFGLTSQBIQRYERQVEKTRYSYDVCARWNTGLNN 241

```

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QY 246 LRGTNAESWVRYNQPRRDMTLMVLDLVALFPSTYDTQMPYIKTTAQLTREYVYDAIGTVHP 305
Db 242 LRGTNAESWLRYNQPRRDLTLGVLDLVALFPSTYDTRVYPMNTSAQLTREIYDPIGRNA 301

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QY 306 HPSFTSTWYNNAPSFSAIAEAAVVRNPHLLDPLEQVITYLSLRSWNTQYMNWGGHKL 365
Db 302 PSGFASTWNNFNNAPSFSAIAEAAVVRNPHLLDPLEQVITYLSLRSWNTQYMNWGGHKL 361

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QY 366 EFRITGGTLNISTQGSTNTSINPVLTPFTSRDVRVYTESLAGLNLFLTQPVNGVPRVDPHW 425
Db 362 ESRTIRGSLSTWHTGNTNTSINPVLQFTSRDVRVYTESFAGINILLTTPVNGVPRVAFNW 421

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QY 426 KFTVTHPIASDNFYPGYAGIGTQLODSENELPPEATQPNYESYSHLSHIGLISASHVK 485
Db 422 RNPLSLRGSLTYTIGYTGVGTLQFDSSELPETTERPNYESYSHLSHIGLISASHVK 481

```

```

QY 486 ALVYSWTHRSADRNTIIPNPSITQIPLVKAPNLSGAAVVRGPGTGGDIILRTNTGTFG 545
Db 602 EFPVGISASGQ-TAGISISNAGSQTHFDFKIEPITATFEAYEDLERAQEAVALFT 660

```

```

QY 666 STNPRGLKTDVKDHYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKOLHIERNM 719
Db 661 SSNOIGLKTVDYHIDVSNLVSLSDEFYLDKRELFEIVKYAKOLHIERNM 714

```

## RESULT 10

US-10-428-961-38

; Sequence 38, Application US/10428961

; Publication NO. US20030237111A1

; GENERAL INFORMATION:

; APPLICANT: Baum, James A.

; APPLICANT: Chu, Chih-Rei

; APPLICANT: Donovan, William P.

; APPLICANT: Gilmer, Amy J.

; APPLICANT: Rupar, Mark J.

; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin

; TITLE OF INVENTION: Polynucleotides, Compositions, and Methods of Use (Amended)

; FILE REFERENCE: MECO201--1

; CURRENT APPLICATION NUMBER: US/10/428,961

; CURRENT FILING DATE: 2003-05-02

; PRIOR APPLICATION NUMBER: 09/661,322

```

; PRIOR FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: 60/153,995
; PRIOR FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 38
; LENGTH: 1228
; TYPE: PR1
; ORGANISM: Bacillus thuringiensis
US-10-428-961-38

Query Match          56.3%; Score 2116; DB 14; Length 1228;
Best Local Similarity 59.5%; Pred. No.1.3e-169;
Matches 424; Conservative 98; Mismatches 181; Indels 10; Gaps 17;

QY 13 SSNAKVDKISDLSKN-ETDIELQ-NINHPDCLKNSEYENVEPVFSASTIQTGTGIGAKI 70
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
7 NENEINALSIPAVSNHSTOMDLSPFDARIEDSLCIAEGNNINPIUSASTVQTGINIAGRI 66
QY 71 LGTLGVFPAGVASLYSIFLIGELMPKGNOWEIFMEHVEEIIINOKISTYARNKALTDLKG 130
Db 67 LGVLGVFPAGQIASFYSLFVGLMPWRGRDQWEIFLEHVEQILINQOITENANTALALQGG 126
QY 131 LGDALAYVHDSLESWGVRNNRNNTRARSVVKVQYIALLEMFVKLPSPFASVEEPLLIPIYA 190
Db 127 LGDSFRAYQQSLEDWLENRDRDARTSRVLYTQYIALELDFNAMLPFAIRNQVEVELLMVYA 186
QY 191 QAAHLHLLLRDASIFCKEWGLSSSEISTFNNROVERAGDYSDDCVKQWYTGILNLRGTN 250
Db 187 QAAHLHLLLRDASLFGSEFGLTSQBIQRYRVERQEQTRDYSYCVIEWYNTGLNSLRGTN 246
QY 251 AESWVRYNQFRDRMTLMLDLVALFPSSDYQMPIKTTAQLTRREYVYDAIGTVHPHPSFT 310
Db 247 AASWVRYNQFRDLTLGVLDLVALFPDYDIRTYPINTSAQLTRREYVYDAIGAT--GVNMA 304
QY 311 STTWYNNAPSPSAIEAAVVRNPHLLDFLQVITYISLLRWSNTQYNNMGGHKLPRTI 370
Db 305 SMWYNNAPSPSAIEAVIRSPHLLDFLEQLTIFSTSRSWSATRHMTYWRGHTIQSRPI 364
QY 371 GGTINTSTCGSTWTSINPVLPTTSRDVRYTESLAGNLNF--LTQPVNGVPRVDFHWKEV 428
Db 365 GGGINTSTHGSTWTSINPVLSPFSRDVRYTESVAGVLLWGLYLEPIHGVTYVRFNRP 424
QY 429 --THPIASDNFYVPGYAGITQLQDSNELPPEATQGPNYESYSHRLSHIGLISASHVKA 486
Db 425 QNTFERGTANYSP--YESPGQLKDSLETLPPTTERPNYESYSHRLSHIGLISQSRVHV 483
QY 487 LVYSWTHRSADRTNTEPNSTIQLPKVAKNLSSGAAVRPGFTGGDIILRRNTGTGFGD 546
Db 484 PVSWSWTHRSADRTNTEISSDSITQPLVKSFNLSNGTSVVSQPGFTGGDIILRRNVGSLVS 543
QY 547 IRYNINPPFAQRYRIRYASTTDLPHTSINKAKINQGNFSAIMNRGEDLDVKTFTVVG 606
Db 544 MGLNFNNTSLQRYRVRVRYAASQTWVLRLVVGSTTFDQGPSTMSANESLTSQSFFAE 603
QY 607 FTFPFGLDVQSTFTTGAMNFPSSGNEVYIDRIEFPVPEVITYEAEYDFEKAQEKVTLFTS 666
Db 604 FPGVIGSAGSQ--TAGISISNNAGRTQTFHFKDIEFIPITATFEAYDLERACEAVNALFTN 662
QY 667 TNPRLKLTVDKVDHIDOVSNLVSLSDEFYLDKRELFEIVKYAKOLHIERNM 719
Db 663 TNPRLKLTVDTHIDOVSNLVACLSDEFCLDKRELLEKVKYAKRLSDERNL 715

RESULT 11
US-10-614-524-2
; Sequence 2, Application US/10614524
; Publication No. US2004001602A1
; GENERAL INFORMATION:
; APPLICANT: Arnaut, Greta
; APPLICANT: Boets, Annemie
; APPLICANT: Damme, Nicole
; APPLICANT: Mathieu, Eva

```

? APPLICANT: Vanneste, Stijn  
 ? APPLICANT: Van Rie, Jeroen  
 ? TITLE OF INVENTION: Insecticidal proteins from Bacillus thuringiensis.  
 ? FILE REFERENCE: NEWTISUS2  
 ? CURRENT APPLICATION NUMBER: US/10/614,524  
 ? CURRENT FILING DATE: 2003-07-08  
 ? PRIOR APPLICATION NUMBER: US/09/739,243  
 ? PRIOR FILING DATE: 2000-12-19  
 ? PRIOR APPLICATION NUMBER: 60/173387  
 ? PRIOR FILING DATE: 1999-12-28  
 ? NUMBER OF SEQ ID NOS: 13  
 ? SOFTWARE: PatentIn Ver. 2.0  
 ? SEQ ID NO 2  
 ? LENGTH: 1228  
 ? TYPE: PRT  
 ? ORGANISM: Bacillus thuringiensis  
 ? US-10-614-524-2

Query Match	56.3%	Score 2116	DB 15	Length 1228
Best Local Similarity	59.5%	Pred. No. 1.3e-169		
Matches 424	Conservative 98	Mismatches 181	Indels 10	Gaps 7
QY	13	SSNAKVDKISTDSLKN-ETDIELQ-NINHEDCLMKSEYENVEPFVSASTIQTIGIGIAGKI	70	
Db	7	NENEIINALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVASIVQTGINIAGRI	66	
QY	71	LGTGLVPPAGQVASLYSHFLOELMPKGNOWELFMHVEBIIINQKISTYARNKALTDLKG	130	
Db	67	LGLVGVPPAGTASFYSFLVAGELMPRGDOWEIFLEHVEQLINQQITENARNALTARLOG	126	
QY	131	LGICALVAHDSLEGSWGNRRNTRASVVKSQYIALELMFVKPLSPFAVSGEVPILPIYA	190	
Db	127	LGDSFRAVCQSLEDWLENRDDARTSVLYTQYIALELDPLNAMPLEFAIRNQEVPLIMYA	186	
QY	191	QAANLHLHLLLDASIPKKEWGLSSSEISTPYNQVERAGDYSDHCVKVYSTGLNNLRGN	250	
Db	187	QAANLHLHLLLDASLGFSEFGLTSQETQRYERQVEQTRDYSYDCVEMVNTGLNSLRGN	246	
QY	251	ABSWRYNQFRDMTMLVLDLVALFPSSYDTOMYPIKTTAQLTRREVYTDAGTGVHPHPT	310	
Db	247	AASWRYNQFRDITLGVLDLVALFPSSYDRTPTINTSQAQLTRREVYTDAGAT--GVNWA	304	
QY	311	STTWNNNAPSFSAIEAAVVRNPHLLDFLEQVTIYISLLSRWNTQYNNWGGHKLEFTRI	370	
Db	305	SNWYNNNAPSFSAIETAVIRSPLLDFLEQLTIFSTSRWSATRMITYRGTHTIQSRPI	364	
QY	371	GGTLMISTGGSTNTSINPVTLPTFSRDRVYRTESLAGLNLP--LTQPVNGVPRVDFHMKFV	428	
Db	365	GGGLNTSTHGSTNTSINPVLSPFSRDRVYRTESYAGVLLWGLYLRPIHGVPVTRFNRP	424	
QY	429	--THPIASDNFPYCGYAGIGTQLODSENLPPATQCPNYESYSHRLSHIGIISASHVKA	486	
Db	425	QNTFERGTANYSQP-YESPGQLQKDSEITELPPETTERPNYESYSHRLSHIGIISQSRVHV	483	
QY	487	LVYSWTHRSADRTNTIIPNSITQIPLVKAPNLSSGAAVVRGPGFTGGDILRLRTNTGTGCD	546	
Db	484	PVYSWTHRSADRTNTIISDSITQIPLVKSPLNSGTSVVSGPFGTGGDILIRTNVNGSVLS	543	
QY	547	IRVINPPEFAQYRVIRYRISTDLOFHTSINGKAINQCNFSATNMRGDDLDYKTRFTVG	606	
Db	544	MGLNFNNITSLQRYRVRYRVAASQTMVLRVTVGSTTFFDQFPSTWSANESLTQSFRFAE	603	
QY	607	FTTTPFSLDVQSTFTICAWNFSSGNEVYIDRIEFVEVEVTEABEDFEKAQEKVVALTFS	666	
Db	604	FPVGISAGSQ--TAGISISNNAAGRTFHFDKTEFPIATFAEVDLERAQAVNALLFTN	662	
QY	667	TNPRGLKTDVKDHYHIDOVSNLVSLSDEFLVDKELFEIVKYAKQLHIERNM	719	
Db	663	TNPRRLKTDVTDYHIDOVSNLVAACLDEFCLEKRELLKVKYAKRLSDERNL	715	

RESULT 12  
US-09-826-660-25





us-10-019-823b-55.rapb

Fri Oct 29 15:06:24 2004

QY	397	DVYTESLAGLNLFLTOPVNGVPRVDFHMKFVTHPIASDNFY-----YPGYAGIGTQLOD	451
Db	409	DIFFEINSTVANLANYOKAYGVGFSWFH--MVKEGTSSTAYLYSKTHLTALQGC-TQVYE	465
QY	452	SENELPPEATGQPNYESYSHRLSHI-----GLISASHVKALVYSWTHRSADRNTIE	503
Db	466	SSDEIPLDRT-VPVAESYSHRLSHITSHSPSKNG--SAYYCSFPFVFWTHTSADLNTIY	522
QY	504	PNSITOTPLKAFNLSSGAAVRCGPGTGGDILLRRTNTGTDIRVNINPPFAQRYRVRI	563
Db	523	SDKITQIPAVKGDMLYLGGSVVQGGFTGGDILKRTNPSILGTFAVTVNGSLSQRYRVRI	582
QY	564	RYASTTDLOFHTSINGKAINQGNFSATMNRGEDLDYKTFRTVGTFTTPTPFLDVQSTFTIG	623
Db	583	RYASTTDPEF-TLYLGDTIEKNRFTKMTDNGASLTETFKFASFTTDFQFRETQDKILLS	641
QY	624	AWNFSSGNEVYIDRIEFVPVEVYEAEDPEKAQKVTAFTSTNPRGLXTDVKDYHIDQ	683
Db	642	MGDFSSGOEVYIDRIEFIPVDEYEAODLEAKKAVNALFTNPKD-GLRPGVTDIEVNQ	700
QY	684	VSNLVESSLDEFYLDKEKRELFYIVKYAKQLHIERNM	719
Db	701	AANLVECLSDDLYPNEKELLFPAVREAKRLSGARNL	736

Search completed: October 28, 2004, 18:40:56  
Job time : 68.6795 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 28, 2004, 17:52:12 ; Search time 98.2996 Seconds  
(without alignments)  
4202.652 Million cell updates/sec

Title: US-10-019-823B-54

Perfect score: 3749

Sequence: 1 MKLKNQDKHQSFSNAKVDK.....KRELFIVKYAKQLHIERNM 718

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_02.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	3722.5	99.3	719	1 CLIA_BACTK	Q45752 bacillus th
2	3722.5	99.3	719	2 O6X181	O6X181 bacillus th
3	3722.5	99.3	719	2 AAP86782	AAP86782 bacillus th
4	3717.5	99.2	719	2 Q93NM5	Q93NM5 bacillus th
5	3716.5	99.1	719	2 O85796	O85796 bacillus th
6	3714.5	99.1	719	2 CAC85964	CAC85964 bacillus th
7	3587.5	95.7	719	2 O8KY61	O8KY61 bacillus th
8	3513.5	93.7	719	2 Q9F0P8	Q9F0P8 bacillus th
9	3482.5	92.9	719	1 CLIB_BACTE	CLIB_BACTE
10	3359.5	89.6	719	1 CLID_BACTU	CLID_BACTU
11	3358.5	89.6	719	1 CLIC_BACTU	CLIC_BACTU
12	2415	64.4	1223	1 C1BB_BACTU	C1BB_BACTU
13	2415	64.4	1233	1 C1BC_BACTM	C1BC_BACTM
14	2249	60.0	1228	2 Q93T75	Q93T75
15	2248	60.0	1228	1 C1BA_BACTK	C1BA_BACTK
16	2240	59.7	1228	2 Q93NM5	Q93NM5
17	2165	57.7	849	2 Q6PYW8	Q6PYW8
18	2165	57.7	849	2 AAS93797	AAS93797
19	2165	57.7	1227	1 C1BE_BACTU	C1BE_BACTU
20	2089	55.7	1231	2 Q8KNY2	Q8KNY2
21	2084	55.6	1231	1 C1BD_BACT2	C1BD_BACT2
22	1974	52.7	1215	1 C1KA_BACTM	C1KA_BACTM
23	1895	50.5	381	2 Q45740	Q45740
24	1652	44.1	1157	1 C8AA_BACUK	C8AA_BACUK
25	1643.5	43.8	1144	2 O8KZL7	O8KZL7
26	1480.5	39.5	1157	1 C9CA_BACTO	C9CA_BACTO
27	1473	39.3	1169	1 C8BA_BACUK	C8BA_BACUK
28	1462	39.0	1166	1 C1GA_BACTU	C1GA_BACTU
29	1451.5	39.0	1169	1 C1FB_BACTU	C1FB_BACTU
30	1456.5	38.9	1167	1 C1JF_BACTU	C1JF_BACTU
31	1455.5	38.8	1174	2 Q45749	Q45749 bacillus th

32	1445.5	38.6	1118	2 Q9AM83	Q9AM83 bacillus th
33	1441.5	38.5	1155	1 CLAB_BACTK	P08578 bacillus th
34	1441.5	38.5	1155	2 Q7BE98	Q7BE98 bacillus th
35	1441.5	38.5	1155	2 Q9F296	Q9F296 bacillus th
36	1441.5	38.5	1155	2 AAN76494	AAN76494 bacillus th
37	1441.5	38.5	1155	2 AAO13302	AAO13302 bacillus th
38	1436.5	38.3	1156	2 O6GUA7	O6GUA7 bacillus th
39	1433	38.2	1180	2 Q8S5V8	Q8S5V8 bacillus th
40	1432	38.2	1176	2 QWZT9	Q7WZT9 bacillus th
41	1431.5	38.2	1177	2 Q6EIX3	Q6EIX3 bacillus th
42	1430	38.1	793	2 Q6PYW7	Q6PYW7 bacillus th
43	1430	38.1	793	2 AAS93798	AAS93798 bacillus th
44	1429.5	38.1	1155	2 Q93T21	Q93T21 bacillus th
45	1426	38.0	1176	2 Q45736	Q45736 bacillus th

## ALIGNMENTS

### RESULT 1

ID CLIA\_BACTK STANDARD; PRT: 719 AA.  
AC Q45752; P71092; Q45750; Q45751; Q45756;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DE Pesticidal crystal protein cryIIa (Insecticidal delta-endotoxin)  
DE CryII(a) (Crystalline entomocidal protoxin) (81 kDa crystal protein).  
GN Name-cryIIa; Synonyms=cryII(a), cryV, cryVI, CGCryV;  
OS Bacillus thuringiensis (subsp. kurstaki).  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=23339;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=DSIR732;  
RX MEDLINE=93298009; PubMed=8517758;  
RA Gleave A.P., Williams R., Hedges R.J.;  
RT "Screening by polymerase chain reaction of Bacillus thuringiensis  
RT serotypes for the presence of cryV-like insecticidal protein genes and  
RT characterization of a cryV gene cloned from B. thuringiensis subsp.  
RT kurstaki.";  
RL Appl. Environ. Microbiol. 59:1683-1687(1993).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=JHCC4835;  
RX MEDLINE=92269582; PubMed=1588820;  
RA Tailor R., Tippet J., Gibb G., Pells S., Pike D., Jordan L., Ely S.;  
RT "Identification and characterization of a novel Bacillus thuringiensis  
RT delta-endotoxin entomocidal to coleopteran and lepidopteran larvae.";  
RL Mol. Microbiol. 6:1211-1217(1992).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=HD-1;  
RX MEDLINE=95314293; PubMed=7793960;  
RA Shin B.-S., Park S.-H., Choi S.-K., Koo B.T., Lee S.T., Kim J.I.;  
RT "Distribution of cryV-type insecticidal protein genes in Bacillus  
RT thuringiensis and cloning of cryV-type genes from Bacillus  
RT thuringiensis subsp. kurstaki and Bacillus thuringiensis subsp.  
RT entomocidus.";  
RL Appl. Environ. Microbiol. 61:2402-2407(1995).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=AB88;  
RX MEDLINE=96178985; PubMed=8606196;  
RA Kostichka K., Warren G.W., Mullins M., Mullins A.D., Palakar N.V.,  
RA Craig J.A., Koziel M.G., Estruch J.J.;  
RT "Cloning of a cryV-type insecticidal protein gene from Bacillus  
RT thuringiensis: the cryV-encoded protein is expressed early in  
RT stationary phase.";  
RL J. Bacteriol. 178:2141-2144(1996).  
RN [5]  
RP SEQUENCE FROM N.A.  
RC STRAIN=61;

RA Selvapandian A., Bhatnagar R.K.;  
 RT "Isolation, cloning and expression of cryV gene."  
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Promotes colloidomic lysis by binding to the midgut  
 CC epithelial cells of certain coleopteran and lepidopteran species.  
 CC Active on *Plutella xylostella* and *Bombyx mori*.  
 CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during  
 CC sporulation and is accumulated both as an inclusion and as part  
 CC of the spore coat.  
 CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-  
 CC terminus.  
 CC -!- SIMILARITY: Belongs to the delta endotoxin family.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC with the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (see [http://www.isb-sib.ch/](http://www.isb-sib.ch/announce/)  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC -----  
 CC EMBL; M98544; AA222354.1; -  
 CC EMBL; X62821; AAC44633.1; -  
 CC EMBL; L36338; AAC36999.1; -  
 CC EMBL; L49391; AAB00958.1; -  
 CC EMBL; Y08920; CAA70124.1; -  
 CC F01; I39815; I39815.  
 CC F01; S25383; S25383.  
 CC HSP; P02965; IC1Y.  
 CC InterPro; IPR001178; Endotoxin.  
 CC InterPro; IPR005638; endotoxin\_C.  
 CC InterPro; IPR005639; endotoxin\_N.  
 CC InterPro; IPR008979; Gal\_bind\_like.  
 CC Pfam; PF03944; Endotoxin\_C; 1.  
 CC Pfam; PF00555; Endotoxin\_M; 1.  
 CC Pfam; PF03945; Endotoxin\_N; 1.  
 CC Sporulation; Toxin.  
 KW VARIANT 159 159 K -> R (in strain 61).  
 FT VARIANT 233 233 D -> Y (in strain JHCC4835 and strain HD-  
 FT VARIANT 443 443 A -> V (in strain AB88).  
 FT VARIANT 711 712 KO -> NE (in strain HD-1 and strain 61).  
 FT SEQUENCE 719 AA; 81216 MW; 3627ESA6C25DAFF5 CRC64;  
 SQ  
 Query Match 99.3%; Score 3722.5; DB 1; Length 719;  
 Best Local Similarity 99.4%; Pred. No. 1.2e-251;  
 Matches 715; Conservative 0; Mismatches 3; Indels 1; Gaps 1;  
 QY 1 MKLNQDKHQSFSSNAKVDKISTSLKNETDIELQNHEDCLKXSEYENVEPVSASTI 60  
 DB 1 MKLNQDKHQSFSSNAKVDKISTSLKNETDIELQNHEDCLKXSEYENVEPVSASTI 60  
 QY 61 QTGIGIAGKILGTGVPPAGQVASLYSFILGELWPKGNQWEI FWEHVEEII NQKISTYA 120  
 DB 61 QTGIGIAGKILGTGVPPAGQVASLYSFILGELWPKGNQWEI FWEHVEEII NQKISTYA 120  
 QY 121 RNKALTDLKGDLALAVYHDSLESWGNNRNTARSVVKSOYIALELMFVKLPSPFAVSG 180  
 DB 121 RNKALTDLKGDLALAVYHDSLESWGNNRNTARSVVKSOYIALELMFVKLPSPFAVSG 180  
 QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFFNROVERAGDYSYHCVKWS 240  
 DB 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFFNROVERAGDYSYHCVKWS 240  
 QY 241 TGLNLRGTNAESWRYNQFRDMLVLDLVALPSPYDTQMPYIKTTAQLTREVVYDAI 300  
 DB 241 TGLNLRGTNAESWRYNQFRDMLVLDLVALPSPYDTQMPYIKTTAQLTREVVYDAI 300  
 QY 301 GTVHPHPSTSTWNNAPSAEAAAVRNPHLLDFLEQVTYISLLSRWSNTQYNNMW 360  
 DB 301 GTVHPHPSTSTWNNAPSAEAAAVRNPHLLDFLEQVTYISLLSRWSNTQYNNMW 360  
 QY 361 GGHKLEFRITGTLNIS\*QGSNTSINPVTLPFTSRDYRTESLAGLNLFTQPVN-VPR 419

DB 361 GGHKLEFRITGTLNIS\*QGSNTSINPVTLPFTSRDYRTESLAGLNLFTQPVN-VPR 420  
 QY 420 VDFHFKVTHPIASDNFFYPGAGIGTQDSSENLPEPEATQPNYESYSHRLSHIGLIS 479  
 DB 421 VDFHFKVTHPIASDNFFYPGAGIGTQDSSENLPEPEATQPNYESYSHRLSHIGLIS 480  
 QY 480 ASHVXALVSWTHRSADRTNIEPNSITQIPLVKAFNLSSGAUVRGSGFTGGDLIRTN 539  
 DB 481 ASHVXALVSWTHRSADRTNIEPNSITQIPLVKAFNLSSGAUVRGSGFTGGDLIRTN 540  
 QY 540 TGTFGDIRVNIINPPPAQRYRVAIRYASTDLDQFHTSINGKAINQGNFSATWNRGDDLYK 599  
 DB 541 TGTFGDIRVNIINPPPAQRYRVAIRYASTDLDQFHTSINGKAINQGNFSATWNRGDDLYK 600  
 QY 600 TPTXVGFTTPPSLLDVQSTFTIGAWNFSNGNEVYIDRIEFVPEVYTYEAEYDFEKAQEKV 659  
 DB 601 TPTXVGFTTPPSFLDVQSTFTIGAWNFSNGNEVYIDRIEFVPEVYTYEAEYDFEKAQEKV 660  
 QY 660 TALFTSTNPRGLKTDVQYHIDQVSNLVESLSDEFYLDKRELFELVYAKQLHIERNM 718  
 DB 661 TALFTSTNPRGLKTDVQYHIDQVSNLVESLSDEFYLDKRELFELVYAKQLHIERNM 719  
 RESULT 2  
 Q6X181 PRELIMINARY; PRT; 719 AA.  
 AC Q6X181;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE CryII.  
 GN Name=CryII;  
 OS *Bacillus thuringiensis*.  
 OC Bacteria, Firmicutes, Bacillales; Bacillaceae; Bacillus.  
 CX NCBI\_TaxID=1428;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RL Espindola R., Lemos M.V.F., Lemos E.G.M., Sena J.A.D.;  
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY262167; AAP86782.1; -  
 DR InterPro; IPR001178; Endotoxin.  
 DR InterPro; IPR005638; endotoxin\_C.  
 DR InterPro; IPR005639; endotoxin\_N.  
 DR InterPro; IPR008979; Gal\_bind\_like.  
 DR Pfam; PF03944; Endotoxin\_C; 1.  
 DR Pfam; PF00555; Endotoxin\_M; 1.  
 DR Pfam; PF03945; Endotoxin\_N; 1.  
 SQ SEQUENCE 719 AA; 81216 MW; 3627ESA6C25DAFF5 CRC64;  
 Query Match 99.3%; Score 3722.5; DB 2; Length 719;  
 Best Local Similarity 99.4%; Pred. No. 1.2e-251;  
 Matches 715; Conservative 0; Mismatches 3; Indels 1; Gaps 1;  
 QY 1 MKLNQDKHQSFSSNAKVDKISTSLKNETDIELQNHEDCLKXSEYENVEPVSASTI 60  
 DB 1 MKLNQDKHQSFSSNAKVDKISTSLKNETDIELQNHEDCLKXSEYENVEPVSASTI 60  
 QY 61 QTGIGIAGKILGTGVPPAGQVASLYSFILGELWPKGNQWEI FWEHVEEII NQKISTYA 120  
 DB 61 QTGIGIAGKILGTGVPPAGQVASLYSFILGELWPKGNQWEI FWEHVEEII NQKISTYA 120  
 QY 121 RNKALTDLKGDLALAVYHDSLESWGNNRNTARSVVKSOYIALELMFVKLPSPFAVSG 180  
 DB 121 RNKALTDLKGDLALAVYHDSLESWGNNRNTARSVVKSOYIALELMFVKLPSPFAVSG 180  
 QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFFNROVERAGDYSYHCVKWS 240  
 DB 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFFNROVERAGDYSYHCVKWS 240  
 QY 241 TGLNLRGTNAESWRYNQFRDMLVLDLVALPSPYDTQMPYIKTTAQLTREVVYDAI 300  
 DB 241 TGLNLRGTNAESWRYNQFRDMLVLDLVALPSPYDTQMPYIKTTAQLTREVVYDAI 300

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QY 301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTTIYSLSRWSNTQYMNW 360
DB 301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTTIYSLSRWSNTQYMNW 360
QY 361 GGKLEPFTIGTINISQGSTNTSINPVTLPFTSRDVRVRESLAGNLFLTPQVNVPR 419
DB 361 GGKLEPFTIGTINISQGSTNTSINPVTLPFTSRDVRVRESLAGNLFLTPQVNVPR 420
QY 420 VDFHKKFVTHPIASDNFYYPGAGIGTQDSENELPPEATQPNYESYSHRSHIGLIS 479
DB 421 VDFHKKFVTHPIASDNFYYPGAGIGTQDSENELPPEATQPNYESYSHRSHIGLIS 480
QY 480 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 539
DB 481 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
QY 540 TGTGDIRVINPPFAQRYRVRIRYASTTDLQFHTSINGKAINOGNFSATMNRGEDLDYK 599
DB 541 TGTGDIRVINPPFAQRYRVRIRYASTTDLQFHTSINGKAINOGNFSATMNRGEDLDYK 600
QY 600 TFXVVGFTTTPSLLDVQSTFTIGANFSSGNEVYIDRIEFVPEVTVYEAEDFEKAQEKV 659
DB 601 TFRVVGFTTTPSLFDVQSTFTIGANFSSGNEVYIDRIEFVPEVTVYEAEDFEKAQEKV 660
QY 660 TALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDEFYLDKRELFVYKAKQLHIERNM 718
DB 661 TALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDEFYLDKRELFVYKAKQLHIERNM 719

RESULT 3
ID AAP86782 PRELIMINARY; PRT; 719 AA.
AC AAP86782;
DT 02-MAR-2004 (TREMELrel. 27, Created)
DT 02-MAR-2004 (TREMELrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMELrel. 27, Last annotation update)
DE CryII.
GN CryII.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
CX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=T01 328;
RA Espindola R., Lemos M.V.F., Lemos E.G.M., Sena J.A.D.;
RT "Complete sequence of cryII gene of isolate T01 328 from Bacillus
RT thuringiensis from Cubateo (SP, Brazil) soil.";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY262167; AAP86782.1; -.
SQ SEQUENCE 719 AA; 81216 MW; 3627E5A6C25DAFF5 CRC64;

Query Match 99.3%; Score 3722.5; DB 2; Length 719;
Best Local Similarity 99.4%; Pred. No. 1.2e-251;
Matches 715; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 MCLKNQDKHQSFSNAKVDKISTDSLKNETDIELQNHEDCLKMSEYENVEPVSASTI 60
DB 1 MCLKNQDKHQSFSNAKVDKISTDSLKNETDIELQNHEDCLKMSEYENVEPVSASTI 60
QY 61 QTGIGTAGKILGTGVPFAGQVSLYSFILGELWPKGNQWEIEMHVEIINOKISTYA 120
DB 61 QTGIGTAGKILGTGVPFAGQVSLYSFILGELWPKGNQWEIEMHVEIINOKISTYA 120
QY 121 RNKALTDLKLGLDALVYHDSLSVGNRNNTARSVWKSQVIALELMFVQKLSPFVSG 180
DB 121 RNKALTDLKLGLDALVYHDSLSVGNRNNTARSVWKSQVIALELMFVQKLSPFVSG 180
QY 181 EYVPLPIVQAANLHLLLRDASIFGKRWGLSSSEISIFYNQVRAGDYSYHCVKWS 240
DB 181 EYVPLPIVQAANLHLLLRDASIFGKRWGLSSSEISIFYNQVRAGDYSYHCVKWS 240

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QY 241 TGLNNLRGTNABSVRYNQFRDMDTLNVLDLVALPESYDTQMPIKTATQALREVYTDI 300
DB 241 TGLNNLRGTNABSVRYNQFRDMDTLNVLDLVALPESYDTQMPIKTATQALREVYTDI 300
QY 301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTTIYSLSRWSNTQYMNW 360
DB 301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTTIYSLSRWSNTQYMNW 360
QY 361 GGKLEPFTIGTINISQGSTNTSINPVTLPFTSRDVRVRESLAGNLFLTPQVNVPR 419
DB 361 GGKLEPFTIGTINISQGSTNTSINPVTLPFTSRDVRVRESLAGNLFLTPQVNVPR 420
QY 420 VDFHKKFVTHPIASDNFYYPGAGIGTQDSENELPPEATQPNYESYSHRSHIGLIS 479
DB 421 VDFHKKFVTHPIASDNFYYPGAGIGTQDSENELPPEATQPNYESYSHRSHIGLIS 480
QY 480 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 539
DB 481 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
QY 540 TGTGDIRVINPPFAQRYRVRIRYASTTDLQFHTSINGKAINOGNFSATMNRGEDLDYK 599
DB 541 TGTGDIRVINPPFAQRYRVRIRYASTTDLQFHTSINGKAINOGNFSATMNRGEDLDYK 600
QY 600 TFXVVGFTTTPSLLDVQSTFTIGANFSSGNEVYIDRIEFVPEVTVYEAEDFEKAQEKV 659
DB 601 TFRVVGFTTTPSLFDVQSTFTIGANFSSGNEVYIDRIEFVPEVTVYEAEDFEKAQEKV 660
QY 660 TALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDEFYLDKRELFVYKAKQLHIERNM 718
DB 661 TALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDEFYLDKRELFVYKAKQLHIERNM 719

RESULT 4
ID Q93NJ5 PRELIMINARY; PRT; 719 AA.
AC Q93NJ5;
DT 01-DEC-2001 (TREMELrel. 19, Created)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMELrel. 26, Last annotation update)
DE CryIIa.
GN Name=cryIIa;
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
CX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RA Song F., Zhang J., Gu A., Huang D., Li G.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF373207; AAK66742.1; -.
DR HSSP; P02965; 1CIY.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin N.
DR InterPro; IPR005639; endotoxin C.
DR InterPro; IPR008979; Gal bind like.
DR Pfam; PF03944; Endotoxin_C_1.
DR Pfam; PF00555; Endotoxin_W_1.
DR Pfam; PF03945; Endotoxin_W_1.
DR SEQUENCE 719 AA; 81225 MW; C629DF2C44827241 CRC64;

Query Match 99.2%; Score 3717.5; DB 2; Length 719;
Best Local Similarity 99.3%; Pred. No. 2.6e-251;
Matches 714; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1 MCLKNQDKHQSFSNAKVDKISTDSLKNETDIELQNHEDCLKMSEYENVEPVSASTI 60
DB 1 MCLKNQDKHQSFSNAKVDKISTDSLKNETDIELQNHEDCLKMSEYENVEPVSASTI 60
QY 61 QTGIGTAGKILGTGVPFAGQVSLYSFILGELWPKGNQWEIEMHVEIINOKISTYA 120

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Db	61	QTGIGIAGKILGTLGVPPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA	120
Qy	121	RNKALTDLKGGLDALAVYHDSLEWGNRNTRARSVVKSQYIALELMFVQKLPSPFAVSG	180
Db	121	RNKALTDLKGGLDALAVYHDSLEWGNRNTRARSVVKSQYIALELMFVQKLPSPFAVSG	180
Qy	181	BEVPLLPYIAQAANLHLLLRDASIFGKWEGLSSSEISTFVNRVERAGDYSYHCVKWS	240
Db	181	BEVPLLPYIAQAANLHLLLRDASIFGKWEGLSSSEISTFVNRVERAGDYSYHCVKWS	240
Qy	241	TGLNLRGTNAESWVRYNQFRDRTLMLVDLVALFPSTQMPYPIKTTAQLTREYVTDAI	300
Db	241	TGLNLRGTNAESWVRYNQFRDRTLMLVDLVALFPSTQMPYPIKTTAQLTREYVTDAI	300
Qy	301	GTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTTIYSLSRWSNTQYMNW	360
Db	301	GTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTTIYSLSRWSNTQYMNW	360
Qy	361	GGHLEPRTIGTGLNISTQGSTNTSINPVTLPFTSRDYRTESLAGLNLFLTOPVN-VPR	419
Db	361	GGHLEPRTIGTGLNISTQGSTNTSINPVTLPFTSRDYRTESLAGLNLFLTOPVNGVPR	420
Qy	420	VDHFKFVTHPIASDNFYYPGAGIGTQDSENELPPEATGQPNYESYSHRSLSHIGLIS	479
Db	421	VDHFKFVTHPIASDNFYYPGAGIGTQDSENELPPEATGQPNYESYSHRSLSHIGLIS	480
Qy	480	ASHVKALVSWTHRSADRTNTEPNSTIQIPLVKAFNLSSGAAVVRGPGFTGGDILARTN	539
Db	481	ASHVKALVSWTHRSADRTNTEPNSTIQIPLVKAFNLSSGAAVVRGPGFTGGDILARTN	540
Qy	540	TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATWNRGEDLDYK	599
Db	541	TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATWNRGEDLDYK	600
Qy	600	TFXTVGFTTPFSLLDVQSTFTTGAMNFGSGNEVYIDRIEFVFPVEVTEAEYDFEKAQEKV	659
Db	601	TFRTVGFTTPFSLDVQSTFTTGAMNFGSGNEVYIDRIEFVFPVEVTEAEYDFEKAQEKV	660
Qy	660	TALFTSTNPRGLKTDVKDHYHDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM	718
Db	661	TALFTSTNPRGLKTDVKDHYHDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM	719
RESULT 5			
Id	O85796	PRELIMINARY;	PRT; 719 AA.
AC	O85796;		
DT	01-NOV-1998 (TREMBLrel. 08, Created)		
DT	01-NOV-1998 (TREMBLrel. 08, Last sequence update)		
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)		
DE	Insecticidal protein.		
GN	Name=cry101;		
OS	Bacillus thuringiensis (subsp. kurstaki).		
OG	Plasmid large plasmid.		
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.		
OX	NCBI_TaxID=29339;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=S101;		
RA	Zhong Q., Deng R., Long Q., Yuan M., Pang Y., Wang X.;		
RL	Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF076953; AAC26910.1; -		
DR	HSSP; P02985; ICIV.		
DR	GO; GO:0005102; Fireceptor binding; IEA.		
DR	GO; GO:0005952; P:defense response; IEA.		
DR	GO; GO:0009405; P:pathogenesis; IEA.		
DR	InterPro; IPR001178; Endotoxin.		
DR	InterPro; IPR005638; endotoxin C.		
DR	InterPro; IPR005639; endotoxin N.		
DR	InterPro; IPR008979; Gal bind like.		
DR	Pfam; PF03944; Endotoxin_C; 1.		
DR	Pfam; PF00555; Endotoxin_M; 1.		
DR	Pfam; PF03945; Endotoxin_N; 1.		

KW	Plasmid.		
SQ	SEQUENCE	719 AA; 81230 MW; 42746D478359BBA7 CRC64;	
Query Match			
Best Local Similarity 99.1%; Score 3716.5; DB 2; Length 719;			
Matches 714; Conservative 0; Mismatches 4; Indels 1; Gaps 1;			
Qy	1	MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNIHEDCLKXSEYENVEPFVASTI	60
Db	1	MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNIHEDCLKXSEYENVEPFVASTI	60
Qy	61	QTGIGIAGKILGTLGVPPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA	120
Db	61	QTGIGIAGKILGTLGVPPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA	120
Qy	121	RNKALTDLKGGLDALAVYHDSLEWGNRNTRARSVVKSQYIALELMFVQKLPSPFAVSG	180
Db	121	RNKALTDLKGGLDALAVYHDSLEWGNRNTRARSVVKSQYIALELMFVQKLPSPFAVSG	180
Qy	181	BEVPLLPYIAQAANLHLLLRDASIFGKWEGLSSSEISTFVNRVERAGDYSYHCVKWS	240
Db	181	BEVPLLPYIAQAANLHLLLRDASIFGKWEGLSSSEISTFVNRVERAGDYSYHCVKWS	240
Qy	241	TGLNLRGTNAESWVRYNQFRDRTLMLVDLVALFPSTQMPYPIKTTAQLTREYVTDAI	300
Db	241	TGLNLRGTNAESWVRYNQFRDRTLMLVDLVALFPSTQMPYPIKTTAQLTREYVTDAI	300
Qy	301	GTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTTIYSLSRWSNTQYMNW	360
Db	301	GTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTTIYSLSRWSNTQYMNW	360
Qy	361	GGHLEPRTIGTGLNISTQGSTNTSINPVTLPFTSRDYRTESLAGLNLFLTOPVN-VPR	419
Db	361	GGHLEPRTIGTGLNISTQGSTNTSINPVTLPFTSRDYRTESLAGLNLFLTOPVNGVPR	420
Qy	420	VDHFKFVTHPIASDNFYYPGAGIGTQDSENELPPEATGQPNYESYSHRSLSHIGLIS	479
Db	421	VDHFKFVTHPIASDNFYYPGAGIGTQDSENELPPEATGQPNYESYSHRSLSHIGLIS	480
Qy	480	ASHVKALVSWTHRSADRTNTEPNSTIQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN	539
Db	481	ASHVKALVSWTHRSADRTNTEPNSTIQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN	540
Qy	540	TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATWNRGEDLDYK	599
Db	541	TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATWNRGEDLDYK	600
Qy	600	TFXTVGFTTPFSLLDVQSTFTTGAMNFGSGNEVYIDRIEFVFPVEVTEAEYDFEKAQEKV	659
Db	601	TFRTVGFTTPFSLDVQSTFTTGAMNFGSGNEVYIDRIEFVFPVEVTEAEYDFEKAQEKV	660
Qy	660	TALFTSTNPRGLKTDVKDHYHDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM	718
Db	661	TALFTSTNPRGLKTDVKDHYHDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM	719
RESULT 6			
Id	CAC85964	PRELIMINARY;	PRT; 719 AA.
AC	CAC85964;		
DT	02-MAR-2004 (TREMBLrel. 27, Created)		
DT	02-MAR-2004 (TREMBLrel. 27, Last sequence update)		
DT	02-MAR-2004 (TREMBLrel. 27, Last annotation update)		
DE	Delta-endotoxin.		
GN	CRY11A.		
OS	Bacillus thuringiensis (subsp. kurstaki).		
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;		
OC	Bacillus cereus group; Bacillus thuringiensis.		
OX	NCBI_TaxID=29339;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=BNS3;		
RA	Tounsi S., Zouari N., Jaoua S.;		

RT "Cloning and study of the expression of a novel cryIIa-type gene from  
 RT *Bacillus thuringiensis* subsp. *kurstaki*.";  
 RL J. Appl. Microbiol. 95:23-28(2003).  
 DR EMBL; AJ315121; CAC85964.1; --  
 SQ SEQUENCE 719 AA; 81203 MW; 8676E5A6C25DAF88 CRC64;

Query Match 99.1%; Score 3714.5; DB 2; Length 719;  
 Best Local Similarity 99.2%; Pred. No. 4.2e-251;  
 Matches 713; Conservative 1; Mismatches 4; Indels 1; Gaps 1;

Qy 1 M K L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y E N V E P F V S A S T I 60  
 Db 1 M K L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y E N V E P F V S A S T I 60

Qy 61 Q T G I G I A G K I L G T L G V P F A G Q V A S L Y S F I L G E L W P K G N Q W E I F M E H V E E I I N Q K I S T Y A 120  
 Db 61 Q T G I G I A G K I L G T L G V P F A G Q V A S L Y S F I L G E L W P K G N Q W E I F M E H V E E I I N Q K I S T Y A 120

Qy 121 R N K A L T D L K G L D A L A V Y H D S L E S W G N R N T R A S V V K S Q Y I A L E M F V K L P S F A V S G 180  
 Db 121 R N K A L T D L K G L D A L A V Y H D S L E S W G N R N T R A S V V K S Q Y I A L E M F V K L P S F A V S G 180

Qy 181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S E I S T F Y N Q R V E R A G D Y S Y H C V K W Y S 240  
 Db 181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S E I S T F Y N Q R V E R A G D Y S Y H C V K W Y S 240

Qy 241 T G L N N L R G T N A E S W R Y N Q R F R D M T L M V L D L V A L F P S Y D T Q M Y P I K T T A Q L T R E V Y T D A I 300  
 Db 241 T G L N N L R G T N A E S W R Y N Q R F R D M T L M V L D L V A L F P S Y D T Q M Y P I K T T A Q L T R E V Y T D A I 300

Qy 301 G T V H P H S F T S T T W Y N N N A P S F S A E A A V V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N W 360  
 Db 301 G T V H P H S F T S T T W Y N N N A P S F S A E A A V V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N W 360

Qy 361 G C H K L E P T T I G G L N I S T Q S T N T S I N P V L P T S R D V Y R T E S L A G L N L F L T Q P V N - V P R 419  
 Db 361 G C H K L E P T T I G G L N I S T Q S T N T S I N P V L P T S R D V Y R T E S L A G L N L F L T Q P V N G V P R 420

Qy 420 V D F H K W F T H P I A S D N F Y P G Y A G I G T Q L O D S E N E L P P E A T G O P N Y E S Y S H R L S H I G L I S 479  
 Db 420 V D F H K W F T H P I A S D N F Y P G Y A G I G T Q L O D S E N E L P P E A T G O P N Y E S Y S H R L S H I G L I S 480

Qy 480 A S H V K A L Y V S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G G D I L R R T N 539  
 Db 480 A S H V K A L Y V S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G G D I L R R T N 540

Qy 540 T G T F G D I R V N I N P P F A Q R Y R I R Y A S T T D L Q P H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 599  
 Db 540 T G T F G D I R V N I N P P F A Q R Y R I R Y A S T T D L Q P H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 600

Qy 600 T F X T V G F T T P F S L D V Q S T T F T I G A W N F S S G N E V Y I D R I E F V P V E V T Y E A E Y D F E K A Q E K V 659  
 Db 600 T F R T V G F T T P F S D V Q S T T F T I G A W N F S S G N E V Y I D R I E F V P V E V T Y E A E Y D F E K A Q E K V 660

Qy 660 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K Y A Q L H T G R N M 718  
 Db 661 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K Y A Q L H T G R N M 719

RESULT 7  
 Q8KY61 PRELIMINARY; PRT; 719 AA.  
 AC Q8KY61  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE C-  
 OS *Bacillus thuringiensis*.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1426;  
 RN [1]  
 RP Porcar M., Martinez C., Caballero P.;  
 RA SEQUENCE FROM N.A.

RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF278797; AAM73516.1; --  
 DR PIR; B42459; B42459.  
 DR HSSP; P02965; 1C1Y.  
 DR GO; GO:0005102; P:receptor binding; IEA.  
 DR GO; GO:0008952; P:defense response; IEA.  
 DR GO; GO:0009405; P:pathogenesis; IEA.  
 DR InterPro; IPR001178; Endotoxin.  
 DR InterPro; IPR005638; endotoxin C.  
 DR InterPro; IPR005639; endotoxin N.  
 DR InterPro; IPR008979; Gal bind like.  
 DR Pfam; PF03944; Endotoxin C; 1-like.  
 DR Pfam; PF00555; Endotoxin M; 1.  
 DR Pfam; PF03945; Endotoxin N; 1.  
 SQ SEQUENCE 719 AA; 80984 MW; 84F1287246264473 CRC64;

Query Match 95.7%; Score 3587.5; DB 2; Length 719;  
 Best Local Similarity 95.7%; Pred. No. 3.3e-242;  
 Matches 688; Conservative 12; Mismatches 18; Indels 1; Gaps 1;

Qy 1 M K L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y E N V E P F V S A S T I 60  
 Db 1 M K L K N P D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K I S E Y E N V E P F V S A S T I 60

Qy 61 Q T G I G I A G K I L G T L G V P F A G Q V A S L Y S F I L G E L W P K G N Q W E I F M E H V E E I I N Q K I S T Y A 120  
 Db 61 Q T G I S I A G K I L G T L G V P F A G Q V A S L Y S F I L G E L W P K G N Q W E I F M E H V E E I I N Q K I S T Y A 120

Qy 121 R N K A L T D L K G L D A L A V Y H D S L E S W G N R N T R A S V V K S Q Y I A L E M F V K L P S F A V S G 180  
 Db 121 R N K A L T D L K G L D A L A V Y H S L E S W G N R K N T R A S V V K S Q Y I A L E M F V K L P S F A V S G 180

Qy 181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S E I S T F Y N Q R V E R A G D Y S Y H C V K W Y S 240  
 Db 181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S E I S T F Y N Q R V E R A G D Y S D H C V K W Y S 240

Qy 241 T G L N N L R G T N A E S W R Y N Q R F R D M T L M V L D L V A L F P S Y D T Q M Y P I K T T A Q L T R E V Y T D A I 300  
 Db 241 T G L N N L R G T N A E S W R Y N Q R F R D M T L M V L D L V A L F P S Y D T L V Y P I K T T A Q L T R E V Y T D A I 300

Qy 301 G T V H P H S F T S T T W Y N N N A P S F S A E A A V V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N W 360  
 Db 301 G T V H P N A S F A S T T W Y N N N A P S F T I E S A V V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N W 360

Qy 361 G C H K L E P T T I G G L N I S T Q S T N T S I N P V L P T S R D V Y R T E S L A G L N L F L T Q P V N - V P R 419  
 Db 361 G C H R L E P T T I G G L N T S T Q S T N T S I N P V L P T S R D V Y R T E S L A G L N L F L T Q P V N G V P R 420

Qy 420 V D F H K W F T H P I A S D N F Y P G Y A G I G T Q L O D S E N E L P P E A T G O P N Y E S Y S H R L S H I G L I S 479  
 Db 421 V D F H K W F T H P I A S D N F Y P G Y A G I G T Q L O D S E N E L P P E T T G O P N Y E S Y S H R L S H I G L I S 480

Qy 480 A S H V K A L Y V S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G G D I L R R T N 539  
 Db 481 A S H V K A L Y S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G G D I L R R T N 540

Qy 540 T G T F G D I R V N I N P P F A Q R Y R I R Y A S T T D L Q P H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 599  
 Db 541 T G T F G D I R V N I N P P F A Q R Y R I R Y A S T T D I Q P H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 600

Qy 600 T F X T V G F T T P F S L D V Q S T T F T I G A W N F S S G N E V Y I D R I E F V P V E V T Y E A E Y D F E K A Q E K V 659  
 Db 601 T F R T V G F T T P F S D V Q S T T F T I G A W N F S S G N E V Y I D R I E F V P V E V T Y E A E Y D F E K A Q E K V 660

Qy 660 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K Y A Q L H T G R N M 718  
 Db 661 T A L F T S T N P G L K T N V T E Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K Y A Q L H T G R N M 719

RESULT 8  
 Q9F0P8 PRELIMINARY; PRT; 719 AA.  
 ID Q9F0P8  
 AC Q9F0P8;



Db 1 MKLNKPDKHQSLSNAKVDKIATDSLKNETDIELKNNMNEYLRNHEHESIDPFVSASTI 60  
 Qy 61 QTGIGIAGKILGTGVFPAGQVSLYSFILGELWPKGNQWEIFMEHVEEIIINOKISTYA 120  
 Db 61 QTGIGIAGKILGTGVFPAGQVSLYSFILGELWPKGNQWEIFMEHVEEIIINOKISTYA 120  
 Qy 121 RNKALTDKGLDALAVYHDSLVSGVGNRNNTARSVVKSYQYIALELMFVKQLPSFAVSG 180  
 Db 121 RNKALSDRLGLDALAVYHDSLVSGVGNRNNTARSVVKSYQYIALELMFVKQLPSFAVSG 180  
 Qy 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTEYFNQVRERAGDYSVHCVKWYS 240  
 Db 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTEYFNQVRERAGDYSVHCVKWYS 240  
 Qy 241 TGLNLEGTAESVWRVYNQFRDMLMVLVDLVALFSPSYDQYPIKTTAQLTREVYTDAI 300  
 Db 241 TGLNLEGTAESVWRVYNQFRDMLMVLVDLVALFSPSYDQYPIKTTAQLTREVYTDAI 300  
 Qy 301 GTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTTYSLLSRWSNTQYNNMW 360  
 Db 301 GTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTTYSLLSRWSNTQYNNMW 360  
 Qy 361 GGHKLEFRTIGTNTISQGSTNTSINPVLPTSRDVRTESLAGLNFLTQPVN-VPR 419  
 Db 361 GGHKLEFRTIGTNTISQGSTNTSINPVLPTSRDVRTESLAGLNFLTQPVN-VPR 419  
 Qy 419 GGHKLEFRTIGTNTISQGSTNTSINPVLPTSRDVRTESLAGLNFLTQPVN-VPR 419  
 Db 419 GGHKLEFRTIGTNTISQGSTNTSINPVLPTSRDVRTESLAGLNFLTQPVN-VPR 419  
 Qy 420 VDFHWKFTVTHPIASDNFYYPGAGIGTQLQDSENELPPEATQPNYESYSHRLSHIGLIS 479  
 Db 420 VDFHWKFTVTHPIASDNFYYPGAGIGTQLQDSENELPPEATQPNYESYSHRLSHIGLIS 479  
 Qy 479 VDFHWKFTVTHPIASDNFYYPGAGIGTQLQDSENELPPEATQPNYESYSHRLSHIGLIS 479  
 Db 479 VDFHWKFTVTHPIASDNFYYPGAGIGTQLQDSENELPPEATQPNYESYSHRLSHIGLIS 479  
 Qy 480 ASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRTN 539  
 Db 480 ASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRTN 539  
 Qy 539 ASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRTN 539  
 Db 539 ASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRTN 539  
 Qy 540 TGFEGDIRVNNPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSGATNWRGDDLYK 600  
 Db 540 TGFEGDIRVNNPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSGATNWRGDDLYK 600  
 Qy 600 TGFEGDIRVNNPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSGATNWRGDDLYK 600  
 Db 600 TGFEGDIRVNNPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSGATNWRGDDLYK 600  
 Qy 601 AFRVTGFTTPFSFNAQSTFTIGAMNFSGLNEVDRIEFVPEVTEAEYDFEKAQEKV 659  
 Db 601 AFRVTGFTTPFSFNAQSTFTIGAMNFSGLNEVDRIEFVPEVTEAEYDFEKAQEKV 659  
 Qy 659 AFRVTGFTTPFSFNAQSTFTIGAMNFSGLNEVDRIEFVPEVTEAEYDFEKAQEKV 659  
 Db 659 AFRVTGFTTPFSFNAQSTFTIGAMNFSGLNEVDRIEFVPEVTEAEYDFEKAQEKV 659

RESULT 10  
 ClID BACTU STANDARD; PRT; 719 AA.  
 AC Q9XDL1;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Pesticidal crystal protein cryII (insecticidal delta-endotoxin)  
 DE CryII(d) (Crystalline entomocidal protoxin) (81 kDa crystal protein).  
 GN Name=cryIId; Synonym=cryII(d), NrcryV;  
 OS Bacillus thuringiensis.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1428;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BR30;  
 RA MEDLINE=20374042; PubMed=10919402;  
 RA Choi S.-K., Shin B.-S., Kong E.-M., Rho H.M., Park S.-H.;  
 RT "Cloning of a new Bacillus thuringiensis cryII-type crystal protein  
 gene".  
 RL Curr. Microbiol. 41:65-69(2000).  
 CC -!- FUNCTION: Promotes colloid osmotic lysis by binding to the midgut  
 CC epithelial cells of many lepidopteran larvae. Active on Plutella  
 CC xylostella and on Bombyx mori.  
 CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during  
 CC sporulation and is accumulated both as an inclusion and as part of

CC the spore coat.  
 CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-  
 CC terminus.  
 CC -!- SIMILARITY: Belongs to the delta endotoxin family.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
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 CC or send an email to license@isb-sib.ch)  
 CC  
 CC EMBL; AF047579; AAD4366.1; -;  
 DR HSP; P02965; ICYI.  
 DR InterPro; IPR001178; Endotoxin.  
 DR InterPro; IPR005638; endotoxin C.  
 DR InterPro; IPR005639; endotoxin N.  
 DR InterPro; IPR008979; Gal bind Like.  
 DR Pfam; PF03944; Endotoxin\_C; 1.  
 DR Pfam; PF03955; Endotoxin\_M; 1.  
 DR Pfam; PF03945; Endotoxin\_N; 1.  
 KW Sporulation; Toxin.  
 SQ SEQUENCE 719 AA; 81403 MW; F335F5689D380C45 CRC64;  
 Query Match 89.6%; Score 3359.5; DB 1; Length 719;  
 Best Local Similarity 89.3%; Pred. No. 3e-226;  
 Matches 642; Conservative 35; Mismatches 41; Indels 1; Gaps 1;  
 Qy 1 MKLNKQDQHQSFSSNAKVDKIATDSLKNETDIELQNNHEDCLKXSEYENYEPFVSASTI 60  
 Db 1 MKLNKQDQHQSFSSNAKVDKIATDSLKNETDIELQNNHEDCLKXSEYENYEPFVSASTI 60  
 Qy 61 QTGIGIAGKILGTGVFPAGQVSLYSFILGELWPKGNQWEIFMEHVEEIIINOKISTYA 120  
 Db 61 QTGIGIAGKILGTGVFPAGQVSLYSFILGELWPKGNQWEIFMEHVEEIIINOKISTYA 120  
 Qy 121 RNKALTDKGLDALAVYHDSLVSGVGNRNNTARSVVKSYQYIALELMFVKQLPSFAVSG 180  
 Db 121 RNKALTDKGLDALAVYHDSLVSGVGNRNNTARSVVKSYQYIALELMFVKQLPSFAVSG 180  
 Qy 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTEYFNQVRERAGDYSVHCVKWYS 240  
 Db 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTEYFNQVRERAGDYSVHCVKWYS 240  
 Qy 241 TGLNLEGTAESVWRVYNQFRDMLMVLVDLVALFSPSYDQYPIKTTAQLTREVYTDAI 300  
 Db 241 TGLNLEGTAESVWRVYNQFRDMLMVLVDLVALFSPSYDQYPIKTTAQLTREVYTDAI 300  
 Qy 301 GTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTTYSLLSRWSNTQYNNMW 360  
 Db 301 GTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTTYSLLSRWSNTQYNNMW 360  
 Qy 361 GGHKLEFRTIGTNTISQGSTNTSINPVLPTSRDVRTESLAGLNFLTQPVN-VPR 419  
 Db 361 GGHKLEFRTIGTNTISQGSTNTSINPVLPTSRDVRTESLAGLNFLTQPVN-VPR 419  
 Qy 420 VDFHWKFTVTHPIASDNFYYPGAGIGTQLQDSENELPPEATQPNYESYSHRLSHIGLIS 479  
 Db 420 VDFHWKFTVTHPIASDNFYYPGAGIGTQLQDSENELPPEATQPNYESYSHRLSHIGLIS 479  
 Qy 479 VDFHWKFTVTHPIASDNFYYPGAGIGTQLQDSENELPPEATQPNYESYSHRLSHIGLIS 479  
 Db 479 VDFHWKFTVTHPIASDNFYYPGAGIGTQLQDSENELPPEATQPNYESYSHRLSHIGLIS 479  
 Qy 480 ASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRTN 539  
 Db 480 ASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRTN 539  
 Qy 539 ASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRTN 539  
 Db 539 ASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRTN 539  
 Qy 540 TGFEGDIRVNNPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSGATNWRGDDLYK 600  
 Db 540 TGFEGDIRVNNPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSGATNWRGDDLYK 600  
 Qy 600 TGFEGDIRVNNPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSGATNWRGDDLYK 600  
 Db 600 TGFEGDIRVNNPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSGATNWRGDDLYK 600  
 Qy 601 AFRVTGFTTPFSFNAQSTFTIGAMNFSGLNEVDRIEFVPEVTEAEYDFEKAQEKV 659  
 Db 601 AFRVTGFTTPFSFNAQSTFTIGAMNFSGLNEVDRIEFVPEVTEAEYDFEKAQEKV 659  
 Qy 659 AFRVTGFTTPFSFNAQSTFTIGAMNFSGLNEVDRIEFVPEVTEAEYDFEKAQEKV 659  
 Db 659 AFRVTGFTTPFSFNAQSTFTIGAMNFSGLNEVDRIEFVPEVTEAEYDFEKAQEKV 659

QY 660 TALFTSTNPRGLKTDVVDYHIDQVSNLVESLSDFFYLDEKRELFEIVKYAKQLHIERNM 718  
 DB 661 TAMFTSTNRLKTNVTCHIDQVSNLVESLSDFFYLDEKRELFEIVKYAKQLHIERNM 719

RESULT 11  
 ID CLIC\_BACTU STANDARD; PRT; 719 AA.  
 AC 087404;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Pesticidal crystal protein cryIIc (insecticidal delta-endotoxin  
 DE CryII(c) (Crystalline entomocidal protoxin) (81 kDa crystal protein).  
 GN Name=cryIIc; Synonyms=cryII(c);  
 OS Bacillus thuringiensis.  
 OG Plasmid.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1428;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=c18 / Egypt;  
 RA Osman Y.A., Makkour M.A., Bulla L.A. Jr.;  
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut  
 CC epithelial cells of insects.  
 CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during  
 CC sporulation and is accumulated both as an inclusion and as part of  
 CC the spore coat.  
 CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-  
 CC terminus.  
 CC -!- SIMILARITY: Belongs to the delta endotoxin family.

QY 1 MKLKNQDKHQSPSSNAKVDKLSLKNETDIELQINNHEDCLAKSEYENVEPVSASTI 60  
 DB 1 MKLKNPDKHQTLSSNAKVDKLSLKNETDIELQINNHEDCLAKSEYENVEPVSASTI 60

QY 61 QTGIGIAGKILGTLGVPAGQVASYLSFILGELPKGNQWEIFMEHVEEIIINQKISTYA 120  
 DB 61 QTGIGIAGKILGTLGVPAGQVASYLSFILGELPKGNQWEIFMEHVEEIIINQKISTYA 120

QY 121 RNKALTDLKGGDALAVHDSLEWGNVGNNTNRSVVKQYIALELMFVKQLPSPFAVSG 180  
 DB 121 RNKALTDLKGGDALAVHDSLEWGNVGNNTNRSVVKQYIALELMFVKQLPSPFAVSG 180

QY 181 BEVPLLPPIYAQAANLHLLLRDASIFGKMWGLSSSEISTFFYNQROVERAGDYSYHCVKWS 240  
 DB 181 BEVPLLPPIYAQAANLHLLLRDASIFGKMWGLSSSEISTFFYNQROVERAGDYSYHCVKWS 240

Query Match 89.6%; Score 3358.5; DB 1; Length 719;  
 Best Local Similarity 89.6%; Pred. No. 3.5e-226;  
 Matches 644; Conservative 33; Mismatches 41; Indels 1; Gaps 1;

QY 241 TGLNNLRGTNAESWVRYNQFRDMTLMVLVDLVALPSSYDTOMYPIKTTAQTRREYTDAL 300  
 DB 241 TGLNNLRATNGSWVRYNQFRKDIELMWLDLVRVFPSTYDVLVPIKTTSQLTREYTDAL 300

QY 301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMW 360  
 DB 301 GTVDNQLRSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMW 360

QY 361 GGHKLEFRITIGTLNISTOGSNTNTSINPVTLPFTSRDVRTESLAGLNLFTQPVN-VPR 419  
 DB 361 GGHLESRPFGALNTSTOGSNTNTSINPVTLOFTSRDVRTESWAGLNLFTQPVNGVPR 420

QY 420 VDFHMKFVTHPIASDNFYYPGAGTQLQDSNELPPEATQPNYSESRLSHIGLIS 479  
 DB 421 VDFHMKFPTLPASDNFYYPGAGTQLQDSNELPPEATQPNYSESRLSHIGLIS 480

QY 480 ASHKVALVYSWTHRSADRNTTIEPNSITQIPLVKAFNLSGGAUVRGPGFTGGDILRETN 539  
 DB 481 GSHVKALVYSWTHRSADRNTTIEPNSITQIPLVKAFNLSGGAUVRGPGFTGGHILRETK 540

QY 540 TGTFGDIRVNIINPPFAQRYRVRIRYASTTDLOFHTSINGKAINQGNFSATMNRGDLDYK 599  
 DB 541 SGTFGHIRVNIINPPFAQRYRVRIRYASTTDLOFHTSINGKAINQGNFSATMNRGDLDYK 600

QY 600 TPTXVGTFTPFSLLDVOSTFTIGANFSGNEVYIDRIEFVPEVYTYEAEYDFEKAQEKV 659  
 DB 601 TPTXVGTFTPFSDVOSTFTIGANFSGNEVYIGRIEFVPEVYTYEAEYDFEKAQEKV 660

QY 660 TALFTSTNPRGLKTDVVDYHIDQVSNLVESLSDFFYLDEKRELFEIVKYAKQLHIERNM 718  
 DB 661 TALFTSTNPRGLKTDVVDYHIDQVSNLVESLSDFFYLDEKRELFEIVKYAKQLHIERNM 719

RESULT 12  
 C1BB\_BACTU STANDARD; PRT; 1229 AA.  
 ID C1BB\_BACTU STANDARD; PRT; 1229 AA.  
 AC Q45739;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Pesticidal crystal protein cryIbB (insecticidal delta-endotoxin  
 DE CryIb(b) (Crystalline entomocidal protoxin) (140 kDa crystal protein).  
 GN Name=cryIbB; Synonyms=cryIb(b), cryET5;  
 OS Bacillus thuringiensis.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1428;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NRRL B-21110 / EG5847;  
 RA Donovan W.P., Tan Y., Jany C.S., Gonzalez J.M. Jr.;  
 RT "Bacillus thuringiensis cryet4 and cryet5 toxin genes and proteins  
 RT toxic to lepidopteran insects";  
 RL Patent number US5322687, 21-JUN-1994.  
 CC -!- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut  
 CC epithelial cells of many lepidopteran larvae.  
 CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during  
 CC sporulation and is accumulated both as an inclusion and as part of  
 CC the spore coat.  
 CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-  
 CC terminus.  
 CC -!- SIMILARITY: Belongs to the delta endotoxin family.

QY 61 QTGIGIAGKILGTLGVPAGQVASYLSFILGELPKGNQWEIFMEHVEEIIINQKISTYA 120  
 DB 61 QTGIGIAGKILGTLGVPAGQVASYLSFILGELPKGNQWEIFMEHVEEIIINQKISTYA 120

QY 121 RNKALTDLKGGDALAVHDSLEWGNVGNNTNRSVVKQYIALELMFVKQLPSPFAVSG 180  
 DB 121 RNKALTDLKGGDALAVHDSLEWGNVGNNTNRSVVKQYIALELMFVKQLPSPFAVSG 180

QY 181 BEVPLLPPIYAQAANLHLLLRDASIFGKMWGLSSSEISTFFYNQROVERAGDYSYHCVKWS 240  
 DB 181 BEVPLLPPIYAQAANLHLLLRDASIFGKMWGLSSSEISTFFYNQROVERAGDYSYHCVKWS 240

InterPro; IPR001178; Endotoxin.  
 HSSP; P02965; 1CIY.  
 EMBL; L32020; AAA22344.1;  
 HSSP; P02965; 1CIY.  
 InterPro; IPR001178; Endotoxin.



DR InterPro: IPR005638; endotoxin\_C.  
DR InterPro: IPR005639; endotoxin\_N.  
DR InterPro: IPR008979; Gal\_bind\_like.  
DR Pfam: PF03944; Endotoxin\_C; 1.  
DR Pfam: PF00555; Endotoxin\_M; 1.  
DR Pfam: PF03945; Endotoxin\_N; 1.  
KW Sporulation; Toxin.  
SQ SEQUENCE 1229 AA; 139769 MW; A4C949DB675C3269 CRC64;

Query Match 64.4%; Score 2415; DB 1; Length 1229;  
Best Local Similarity 65.1%; Pred. No. 8.2e-160;  
Matches 467; Conservative 91; Mismatches 141; Indels 18; Gaps 7;

QY 13 SSNAKVDKISTDLSKN-ETDIELQ-NINHEDECLMSEVENPEFVSASTIQTGIGTAGKI 70  
DB 7 NENEIINALSPTVSNSTQWNLSPDARIEDSLCAEVNNDIPVSAVSTQGTGINAGRI 66

QY 71 LGTLGVFPAGQVASYLFIIGELWPKGNQWEIFMEHVEEIIINQKISTYARNKALDILKG 130  
DB 67 LGVLGVFPAGQLASFYSFLVGLWPSGRDPWEIFLHVQLIRQQVTENTRTAARLEG 126

QY 131 LGDALAVYHDSLESVWGNNTTRARSVVKQYIALELMFVKLPSPFVSGEEVPLPIYA 190  
DB 127 LGRGYRYSQALFTWLDNRDARSIIILERYVALELDITTAIPFLRINEEVPPLMVA 186

QY 191 QAANLHLLLRDASIFGKWLGSSEISTFYNRQVERAGDYSYHCVKWYSTGLNNLRGTN 250  
DB 187 QAANLHLLLRDASLFGSEWGMASDVNQYQEIRYTEESYHNCVQWYNTGLNNLRGTN 246

QY 251 AESWRYNQPRDMLVLDLVALPSPYDTQMPKTKTAQLTRVYTDGATGVHPHPSFT 310  
DB 247 AESWLRYNQPRDMLVLDLVALPSPYDTQMPKTKTAQLTRVYTDGATGVHPHPSFT 306

QY 311 STTWNNNAPSFAIAEAAVVRNPHLLDFLEQVITYSLLSRWSTNTQYMMWGHKLEFRTI 370  
DB 307 STTWNNNAPSFAIAEAAVVRNPHLLDFLEQVITYSLLSRWSTNTQYMMWGHKLEFRTI 366

QY 371 GGTNLISQTGST-NTSINPVTLPFTSRDVRVYTESLAGNLFLTPQVN-VPVRVDFHMKFVT 428  
DB 367 GGTNLISQTGST-NTSINPVTLPFTSRDVRVYTESLAGNLFLTPQVN-VPVRVDFHMKFVT 422

QY 429 HPIASDNFYPG-----YAGIGTQLODSNELPPEATGQPNYSESHRSLHIGLISAS 481  
DB 423 --INPQNIYERGATYTSQYQGVGLDSETELPETTERPNTYSESHRSLHIGLIGN 480

QY 482 HVKALVYSWTHRSADRTNTIENSTIQTPLVKAFNLSSGAAVVRGPGFTGGDILRNTG 541

RESULT 13  
C1BC\_BACTM STANDARD; PRT; 1233 AA.  
AC Q45774;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Peptidicidal crystal protein cryIbC (Insecticidal delta-endotoxin  
DE CryIbC) (Crystalline entomocidal protoxin) (140 kDa crystal protein).  
GN Name=cryIbC; Synonyms=cryIb(C), cryIbC;  
OS Bacillus thuringiensis (subsp. morrisoni).

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=1441;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Bishop A.H., Bone E.J., Ellar D.J.;  
RT "Cloning of novel Bacillus thuringiensis delta-endotoxin.";  
RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: Promotes colloid osmotic lysis by binding to the midgut  
epithelial cells of insects.  
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during  
sporulation and is accumulated both as an inclusion and as part of  
the spore coat.  
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-  
terminus.  
CC -!- SIMILARITY: Belongs to the delta endotoxin family.  
CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; Z46442; CAAB6568.1; -.  
DR HSSP; P02965; 1CIY.  
DR InterPro: IPR001178; Endotoxin.  
DR InterPro: IPR005638; endotoxin\_C.  
DR InterPro: IPR005639; endotoxin\_N.  
DR InterPro: IPR008979; Gal\_bind\_like.  
DR Pfam; PF03944; Endotoxin\_C; 1.  
DR Pfam; PF00555; Endotoxin\_M; 1.  
DR Pfam; PF03945; Endotoxin\_N; 1.  
KW Sporulation; Toxin.  
SQ SEQUENCE 1233 AA; 140451 MW; 7318382413529F21 CRC64;

Query Match 64.4%; Score 2415; DB 1; Length 1233;  
Best Local Similarity 65.1%; Pred. No. 8.2e-160;  
Matches 467; Conservative 91; Mismatches 141; Indels 18; Gaps 7;

QY 13 SSNAKVDKISTDLSKN-ETDIELQ-NINHEDECLMSEVENPEFVSASTIQTGIGTAGKI 70  
DB 7 NENEIINALSPTVSNSTQWNLSPDARIEDSLCAEVNNDIPVSAVSTQGTGINAGRI 66

QY 71 LGTLGVFPAGQVASYLFIIGELWPKGNQWEIFMEHVEEIIINQKISTYARNKALDILKG 130  
DB 67 LGVLGVFPAGQLASFYSFLVGLWPSGRDPWEIFLHVQLIRQQVTENTRTAARLEG 126

QY 131 LGDALAVYHDSLESVWGNNTTRARSVVKQYIALELMFVKLPSPFVSGEEVPLPIYA 190  
DB 127 LGRGYRYSQALFTWLDNRDARSIIILERYVALELDITTAIPFLRINEEVPPLMVA 186

QY 191 QAANLHLLLRDASIFGKWLGSSEISTFYNRQVERAGDYSYHCVKWYSTGLNNLRGTN 250  
DB 187 QAANLHLLLRDASLFGSEWGMASDVNQYQEIRYTEESYHNCVQWYNTGLNNLRGTN 246

QY 251 AESWRYNQPRDMLVLDLVALPSPYDTQMPKTKTAQLTRVYTDGATGVHPHPSFT 310  
DB 247 AESWLRYNQPRDMLVLDLVALPSPYDTQMPKTKTAQLTRVYTDGATGVHPHPSFT 306

QY 311 STTWNNNAPSFAIAEAAVVRNPHLLDFLEQVITYSLLSRWSTNTQYMMWGHKLEFRTI 370  
DB 307 STTWNNNAPSFAIAEAAVVRNPHLLDFLEQVITYSLLSRWSTNTQYMMWGHKLEFRTI 366

QY 371 GGTNLISQTGST-NTSINPVTLPFTSRDVRVYTESLAGNLFLTPQVN-VPVRVDFHMKFVT 428  
DB 367 GGTNLISQTGST-NTSINPVTLPFTSRDVRVYTESLAGNLFLTPQVN-VPVRVDFHMKFVT 422

QY 429 HPIASDNFYPG-----YAGIGTQLODSNELPPEATGQPNYSESHRSLHIGLISAS 481  
DB 423 --INPQNIYERGATYTSQYQGVGLDSETELPETTERPNTYSESHRSLHIGLIGN 480

QY 482 HVKALVYSWTHRSADRTNTIENSTIQTPLVKAFNLSSGAAVVRGPGFTGGDILRNTG 541  
DB 481 TLAPVYSWTHRSADRTNTIENSTIQTPLVKAFNLSSGAAVVRGPGFTGGDILRNTG 540

QY 542 TFGDIRVNIAPPAAQRYRVRIRVASTTDLPHTSINGKAINQGNFSAATWNRGDDLYKTF 601  
DB 541 TFGDIRVNIAPPAAQRYRVRIRVASTTDLPHTSINGKAINQGNFSAATWNRGDDLYKTF 600

QY 602 XTGVFTTFFSILDVQSTFTIGANFSSGNEVYIDRIEFVPEVITYAEYDFEKAQEKVTA 661  
DB 601 RTAGSFSPFNLAQSFTILGAQSFN-QEYVIDRVEFVPAEYTFEAYDLERAQAVNA 659

QY 662 LFTSTNPRGLKTDVQYHIDQVSNVLSLSDSEFLVDEKRELFEIVYAKOLHITRM 718  
DB 660 LFTSTNPRGLKTDVQYHIDQVSNVLSLSDSEFLVDEKRELFEIVYAKOLHITRM 716

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Db 481 TLAPVSWTHRSADRTNTIGNRIITQIPLVKNLHSGVTVCGPFTGGDILRRNTG 540
QY 542 TFGDIRVNINPPFAQVRVIRYASTTDLQPHSTSGKAINQGNFSAATMNGEDLDYKTF 601
Db 541 TFGDIRLNVNPLSQVRVIRYASTTDLQPHSTSGKAINQGNFSAATMNGEDLDYKTF 600
QY 602 XTGFTTSPFLDQSTFTICAMNFGSSGNEVYIDRIEFVPEVVEYAEYDFEKAQKVTA 661
Db 601 RTAGFTSPFNLAQSTFTLGAQFSN-QEYIDRVFVPAEVTFAEYDLEKRAQKAVNA 659
QY 662 LFTSTNPRGLKTDVYDHIDQVSNLVESLSEDFYLDKRELFEIVKYAKQLHIERNM 718
Db 660 LFTSTNPRGLKTDVYDHIDQVSNLVESLSEDFYLDKRELFEIVKYAKQLHIERNM 716

RESULT 14
Q93T75 PRELIMINARY; PRT; 1228 AA.
AC Q93T75;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Delta-endotoxin CryIb2.
GN Name=cryIb2;
OS Bacillus thuringiensis (subsp. entomocidus).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1436;
RN [1];
RP SEQUENCE FROM N.A.
RC STRAIN=HD-9;
RA Mat Isa M.N., Abdullah M.A.F., Mahadi N.M.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF036302; AAKS1084.1; -.
DR HSP; P07130; 1DLC.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin C.
DR InterPro; IPR005639; endotoxin N.
DR InterPro; IPR008979; Gal bind like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF03945; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
SQ SEQUENCE 1228 AA; 139620 MW; 3DA2A4DBF59C95C3 CRC64;

Query Match 60.0%; Score 2249; DB 2; Length 1228;
Best Local Similarity 62.3%; Pred. No. 3.4e-148;
Matches 446; Conservative 80; Mismatches 164; Indels 26; Gaps 7;

QY 23 TDSLKNEDIELQNIH-----ECLMKSEYENVEPVFVASTIQTGTGIAGKI 70
Db 2 TSNRXNENETINAVSNHSAQMDLLPDAIEDSLCIAEGNIDPPVFASTVQTGINIAGRI 61
QY 71 LGTLGVFPAGVAVSYSTIGELPKGNQWEIFMEHVEEIIINOKISYARNAKALTDLKG 130
Db 62 LGVLGVFPAGVAVSYSTIGELPKGNQWEIFMEHVEEIIINOKISYARNAKALTDLKG 121
QY 131 LGDALAVYHDSLESVGNRNNTARSPVKSQVIALELMFVOKLSPFVSGEVEPLLIYA 190
Db 122 LGDSFRAYCQSLDLEWLRDARTSVLHTQVIALELDLFLNMPFAIRNOEVEPLLMVYA 181
QY 191 QAAHLHLLLRDASTFGKWLGSSEISTFYNNRVERAGDYSYHCVKWSYGLANLRTGN 250
Db 182 QAAHLHLLLRDASTFGKWLGSSEISTFYNNRVERAGDYSYHCVKWSYGLANLRTGN 241
QY 251 AESWRYNQFRDMTLMVLDLVALPSPYDTQYPIKTTAQLTRVYDTAIVTHPHSPFT 310
Db 242 AASWRYNQFRDMTLMVLDLVALPSPYDTQYPIKTTAQLTRVYDTAIVTHPHSPFT 299
QY 311 STTWNNNAPSATAEAAVVRNPHLLDEQLQITFSASSRWSNTRHMTYWRGHTIQSRPI 359

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Db 300 SMWYNNNAPSATAEAAVVRNPHLLDEQLQITFSASSRWSNTRHMTYWRGHTIQSRPI 359
QY 371 GCTLNISCGSTNTNTINPVTLPFTSRDYVRTESLAGNLF--LTQPVN-VRVDFHMKFV 427
Db 360 GGGLNTSHGATNTSINPVTLPFTSRDYVRTESLAGNLF--LTQPVN-VRVDFHMKFV 416
QY 428 THP-----IASDNFYPGYAGTGTQDSENELPPEATGQPNYESYSHRLSHIGLISASH 482
Db 417 TNPQISDRGTANYQSP--YESPGLQKDSLETLPETTERPNYESYSHRLSHIGLISASH 475
QY 483 VVALVYSWTHRSADRTNTIGNRIITQIPLVKNLHSGVTVCGPFTGGDILRRNTG 542
Db 476 VNPVYVSWTHRSADRTNTIGNRIITQIPLVKNLHSGVTVCGPFTGGDILRRNTG 535
QY 543 FGDIRVNINPPFAQVRVIRYASTTDLQPHSTSGKAINQGNFSAATMNGEDLDYKTFX 602
Db 536 FGPDIRVNINPPFAQVRVIRYASTTDLQPHSTSGKAINQGNFSAATMNGEDLDYKTFX 595
QY 603 TVGFTTTPSLDQSTFTICAMNFGSSGNEVYIDRIEFVPEVVEYAEYDFEKAQKVTA 662
Db 596 REAFTTPTFTQIQTIRTSIQGLSGNGEYIDRIEFVPEVVEYAEYDFEKAQKVTA 655
QY 663 FTSTNPRGLKTDVYDHIDQVSNLVESLSEDFYLDKRELFEIVKYAKQLHIERNM 718
Db 656 FTSTNPRGLKTDVYDHIDQVSNLVESLSEDFYLDKRELFEIVKYAKQLHIERNM 711

RESULT 15
C1BA_BACTK STANDARD; PRT; 1228 AA.
AC P05517; Q45731;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pesticidal crystal protein cryIbA (insecticidal delta-endotoxin
DE CryIb(a)) (crystalline entomocidal protoxin) (140 kDa crystal protein).
GN Name=cryIbA; Synonyms=cryIb(a), cryA4;
OS Bacillus thuringiensis (subsp. kurstaki), and
OS Bacillus thuringiensis (subsp. entomocidus).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=29339, 1436;
RN [1];
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.kurstaki; STRAIN=HD-2;
RX MEDLINE=88203216; PubMed=3362680;
RA Brizzard B.L., Whiteley H.R.;
RT "Nucleotide sequence of an additional crystal protein gene cloned from
RT Bacillus thuringiensis subsp. thuringiensis."
RL Nucleic Acids Res. 16:2723-2723(1988).
RN [2];
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.entomocidus; STRAIN=HD-110;
RA Soetaert P.;
CC -1- FUNCTION: Promotes colloid osmotic lysis by binding to the midgut
CC epithelial cells of insects.
CC -1- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -1- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -1- SIMILARITY: Belongs to the delta endotoxin family.
CC
CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X06711; CAA29898.1; -.
CC EMBL; X95704; CAA65003.1; -.
DR

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DR PIR; S00873; S00873.
DR HSP; P07130; 1DLC.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal_bind_like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
KW Sporulation; Toxin.
FT VARIANT 150 150 Y->H (in strain HD-110).
SQ SEQUENCE 1228 AA; 139647 MW; C8E3A19F5D99575 CRC64;

Query Match      60.0%; Score 2248; DB 1; Length 1228;
Best Local Similarity 62.3%; Pred. No. 4e-148;
Matches 446; Conservative 80; Mismatches 164; Indels 26; Gaps 7;

QY 23 TDSLKNETDIELQNIH-----EDCLKMEYENVEPVSVASITQIGIAGKI 70
Db 2 TNRKKNENEIINAVSNESAQMDLLPDARIEDSLCIAEGNNIDPFVSASTVQTGINIAGRI 61

QY 71 LGTLGVFPAGQVASLYFILGELMPKGNQWEIFMEHVEEIIINQKISTYARNKALTDLKG 130
Db 62 LGVLGVFPAGQASLYFYLNGELMPGRDQWEIFLEHVEQLINQQTENARNALARIQG 121

QY 131 LGDALAVYHDSLSWGNRNNTARSVVKSQYTALELMFVKQLPSPAVSGEEVPLPIYA 190
Db 122 LGDSFRAYQOSLEDMLNRODARTSVLYTQYTALELDFLNAFLFAIRNQEVPLLVYA 181

QY 191 QANLHLLLRDASIFKKEGLSSSEISTFYNQVERAGDSYHCVKWSYSTGLNNLRGTN 250
Db 182 QANLHLLLRDASLFGSEFGLTSQELQRYERYQVERTRDYSYCVENYNTGLNSLRGTN 241

QY 251 AESWRYNQPRDNTLMVLDLVALFPSTYDQMPYIKTTAQLTREVTYDAIGTVHPHSFT 310
Db 242 AASWRYNQPRDITLGVLDLVALFPSTYDRTYPTINTSAQLTREVTYDAIGAT--GVNMA 299

QY 311 STTWYNNAPSFSAIEAAVVRNHLDFLEQVITYLLSEWSNTQYMMWGGHKLFRIT 370
Db 300 SMWYNNAPSFSAIEAARSPELLDFLEQLTIFSSASWSNRHTYWRGHTIQSRPI 359

QY 371 GGTINISGTSTNTSINPVTLPFTSRDVRTESLAGLNF--LTQPVN-VPRVDFHWKFV 427
Db 360 GGLTNTSTHCAATNTSINPVTLRPASRDVYRTESYAGVLLWGIYLEPIHGVTVRNF-- 416

QY 428 THP-----IASDFYPCYAGIGTQLODSNELPPEATGQPNYESYSHRSLHIGLISASH 482
Db 417 TNPQNTSDRGATANYQP-YESPGLQKDSLETLPETTERPNYESYSHLSHIGIILQSR 475

QY 483 VKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDIILRRNTGT 542
Db 476 VNPVVISWTHRSADRTNTIGPNRIITQIPMKASELPQGTIVVAGPGFTGGDIILRRNTGG 535

QY 543 FGIIRVNNPPFQRYAVRIRYASTTDLQPHTSINGKAINQGNFSATMNRGDLDYKTFX 602
Db 536 FGIIRVTVNGPLTQRYAIGRYASTVDFFVSRGGTTVNNPFRLTMTNSGDELKYCNFV 595

QY 603 TVGFTTPEFLDVCSTETTCAMNFFSGNEVYIDRIFVPVVEVTEAEYDEKAEKVVAL 662
Db 596 RRAFTTEPTTQDIIRTSIQLSNGEVEYIDKIEIIPVATFEAEYDLERAQEAVAL 655

QY 663 FTSTNPRLKTDVKDHIDQVSNLVESLSDSEFYLDKRELFYVKAKQLHIERNM 718
Db 656 FTNTNPRRLKTDVTDYHIDQVSNLVACLSDSEFCLEKRELEKVKYAKRLSDERNL 711

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Search completed: October 28, 2004, 18:29:48  
Job time : 102.442 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 28, 2004, 18:05:43 ; Search time 19.191 Seconds

(without alignments)  
3604.811 Million cell updates/sec

Title: US-10-019-823B-56

Perfect score: 3762

Sequence: 1 MKLKNQDKHQSFSSNAKVDK.....KRELFEIVKYANELHIERNM 719

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:\*

1: Pir1:\*

2: Pir2:\*

3: Pir3:\*

4: Pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3762	100.0	719	2 I39814	Insecticidal prote
2	3753	99.8	719	2 S25383	parasporal crystal
3	3743	99.5	719	2 I39815	insecticidal prote
4	3503	93.1	719	2 I40590	crv465 protein -
5	2262	5	60.1	2 S00873	parasporal crystal
6	1891	50.3	380	2 B42459	hypothetical prote
7	1483	39.4	1157	1 S49247	parasporal crystal
8	1467	39.0	1166	2 S32645	parasporal crystal
9	1461	38.8	1174	2 S32649	parasporal crystal
10	1459	38.8	1155	2 A26513	parasporal crystal
11	1452	38.6	1155	2 JD0002	parasporal crystal
12	1452	38.6	1155	2 A29125	parasporal crystal
13	1443	38.4	1155	2 I39838	parasporal crystal
14	1439	38.3	934	2 J20247	parasporal crystal
15	1438	38.2	1176	2 JT0241	parasporal crystal
16	1435	38.1	1155	2 S02134	parasporal crystal
17	1434	38.1	1181	2 A41052	parasporal crystal
18	1432	38.1	1176	2 JC2102	parasporal crystal
19	1428	38.0	1176	2 A22617	parasporal crystal
20	1428	38.0	1176	2 S02215	parasporal crystal
21	1353	36.0	1174	2 A42459	parasporal crystal
22	1338	35.6	1138	2 A48944	parasporal crystal
23	1324	35.2	1156	2 A29838	parasporal crystal
24	1316	35.0	823	2 S04191	parasporal crystal
25	1307	34.8	1189	2 S00944	parasporal crystal
26	1301	34.6	1154	2 S39536	parasporal crystal
27	1257	33.4	1171	2 I40572	parasporal crystal
28	1257	33.4	1171	2 A37829	parasporal crystal
29	1254	33.3	1176	2 A48970	parasporal crystal

RESULT 1

I39814

Insecticidal protein cryVI - Bacillus thuringiensis

C/Species: Bacillus thuringiensis

C/Date: 19-Jul-1996 #sequence revision 19-Jul-1996 #text change 25-Aug-1999

C/Accession: I39814

R/Shin, B.S.; Park, S.H.; Choi, S.K.; Koo, B.T.; Lee, S.T.; Kim, J.I.

Adol. Environ. Microbiol. 61: 2402-2407, 1995

A/Title: Distribution of cryV-type insecticidal protein genes in Bacillus thuringiensis

tomocidus.

A/Reference number: I39814; MUID:95314293; PMID:7793960

A/Accession: I39814

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-719 <RES>

A/Cross-references: GB:I36338; NID:g540281; PIDN:AAC36999.1; PID:g540282

C/Genetics:

C/Gene: cryVI

C/Superfamily: parasporal crystal protein

Query Match 100.0%; Score 3762; DB 2; Length 719;

Best Local Similarity 100.0%; Pred. No. 1.3e-251; Indels 0; Gaps 0;

Matches 719; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKNSEYENVEPPFVSASTI 60

Db 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKNSEYENVEPPFVSASTI 60

QY 61 QTGIGIAGKILGTGVPFAGQVASYLSYFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120

Db 61 QTGIGIAGKILGTGVPFAGQVASYLSYFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120

QY 121 RNKALTDLKGDLAVYHDSLESWGNRNNTNRASVVKVSOYIALELMFVKLPFVAVSG 180

Db 121 RNKALTDLKGDLAVYHDSLESWGNRNNTNRASVVKVSOYIALELMFVKLPFVAVSG 180

QY 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNRQVERAGDYSYHCWKYS 240

Db 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNRQVERAGDYSYHCWKYS 240

QY 241 TGLNNLRGNASWRYNQFRDMLMWLDLVALFPSTDYDQMYPIKTTAQLTREYVTDAT 300

Db 241 TGLNNLRGNASWRYNQFRDMLMWLDLVALFPSTDYDQMYPIKTTAQLTREYVTDAT 300

QY 301 GTVHPHPSFTSTWYNNNAPSFAEAAVVRNPHLLDLEQVITYSLSRVNSNTQYMMNW 360

Db 301 GTVHPHPSFTSTWYNNNAPSFAEAAVVRNPHLLDLEQVITYSLSRVNSNTQYMMNW 360

QY 361 GGHKLEFRITGGTLANITSGGSTNTSINPVTLPFTSRDVRTESLAGLFLFTQPVNGVPR 420

Db 361 GGHKLEFRITGGTLANITSGGSTNTSINPVTLPFTSRDVRTESLAGLFLFTQPVNGVPR 420

ALIGNMENTS

QY 421 VDFHWKFTVTHPIASDNFYYPGAGIGTQLQDSENELPPEATQPNYSYSHRLSHIGLIS 480  
 DB 421 VDFHWKFTVTHPIASDNFYYPGAGIGTQLQDSENELPPEATQPNYSYSHRLSHIGLIS 480  
 QY 481 ASHVKALVYSWTHRSADRNTIENPSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 540  
 DB 481 ASHVKALVYSWTHRSADRNTIENPSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 540  
 QY 541 TGTFGDIRVNNPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATNRGCDLDYK 600  
 DB 541 TGTFGDIRVNNPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATNRGCDLDYK 600  
 QY 601 TERTVGTTPPSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVVPVEVYEAEDFKAQEKV 660  
 DB 601 TERTVGTTPPSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVVPVEVYEAEDFKAQEKV 660  
 QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKEKELFEIVKYANELHIERNM 719  
 DB 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKEKELFEIVKYANELHIERNM 719

## RESULT 2

S25383  
 parasporal crystal protein cryIIal - Bacillus thuringiensis  
 N:Alternate names: delta-endotoxin; parasporal crystal protein cryV  
 C:Species: Bacillus thuringiensis  
 C>Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 09-Jul-2004  
 C:Accession: S25383  
 R:Tailor, R.; Tippet, J.; Gibb, G.; Pells, S.; Pike, D.; Jordan, L.; Bly, S.  
 Mol. Microbiol. 6, 1211-1217, 1992  
 A:Title: Identification and characterization of a novel Bacillus thuringiensis delta-end  
 A:Reference number: S25383; MUID:92269582; PMID:1588820  
 A:Accession: S25383  
 A:Molecule type: DNA  
 A:Residues: 1-719 <TAI>  
 A:Cross-references: UNIPROT:Q45752; EMBL:X62821; NID:940289; PIDN:CAA44633.1; PID:940290  
 C:Genetics:  
 A:Gene: cryV  
 C:Superfamily: parasporal crystal protein  
 C:Keywords: delta-endotoxin

Query Match 99.8%; Score 3753; DB 2; Length 719;  
 Best Local Similarity 99.7%; Pred. No. 5.2e-251;  
 Matches 717; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKXSEYENVEPVSASTI 60  
 DB 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKXSEYENVEPVSASTI 60  
 QY 61 QTGIGIAGKILGTLGVPPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINOKISTYA 120  
 DB 61 QTGIGIAGKILGTLGVPPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINOKISTYA 120  
 QY 121 RNKALTDLKGGLDALAVYHDSLESWVGNNRTRASVVKSOYIALELMFVKQLSPFAVSG 180  
 DB 121 RNKALTDLKGGLDALAVYHDSLESWVGNNRTRASVVKSOYIALELMFVKQLSPFAVSG 180  
 QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFFNROVERAGDYSYHCVKWYS 240  
 DB 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFFNROVERAGDYSYHCVKWYS 240  
 QY 241 TGLNLRGNAESWRYNQFRDNTLMVLDLVALFPSYDTOMYPIKTTAQLTREYVTDAL 300  
 DB 241 TGLNLRGNAESWRYNQFRDNTLMVLDLVALFPSYDTOMYPIKTTAQLTREYVTDAL 300  
 QY 301 GTVHPHPSFTSTTWNNNAPSFAIAEAAVVRNPHLLDFLEQVTIYSLLSRSNTOYMMNW 360  
 DB 301 GTVHPHPSFTSTTWNNNAPSFAIAEAAVVRNPHLLDFLEQVTIYSLLSRSNTOYMMNW 360  
 QY 361 GGHKLEFRITIGTLNISTCGSTNTSINPVTLPTSDRVYRTESLAGLNLFLTQPVNGVPR 420  
 DB 361 GGHKLEFRITIGTLNISTCGSTNTSINPVTLPTSDRVYRTESLAGLNLFLTQPVNGVPR 420

QY 421 VDFHWKFTVTHPIASDNFYYPGAGIGTQLQDSENELPPEATQPNYSYSHRLSHIGLIS 480  
 DB 421 VDFHWKFTVTHPIASDNFYYPGAGIGTQLQDSENELPPEATQPNYSYSHRLSHIGLIS 480  
 QY 481 ASHVKALVYSWTHRSADRNTIENPSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 540  
 DB 481 ASHVKALVYSWTHRSADRNTIENPSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 540  
 QY 541 TGTFGDIRVNNPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATNRGCDLDYK 600  
 DB 541 TGTFGDIRVNNPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATNRGCDLDYK 600  
 QY 601 TERTVGTTPPSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVVPVEVYEAEDFKAQEKV 660  
 DB 601 TERTVGTTPPSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVVPVEVYEAEDFKAQEKV 660  
 QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKEKELFEIVKYANELHIERNM 719  
 DB 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKEKELFEIVKYANELHIERNM 719

## RESULT 3

I39815  
 insecticidal protein cryV - Bacillus thuringiensis  
 C:Species: Bacillus thuringiensis  
 C>Date: 19-Jul-1996 #sequence\_revision 19-Jul-1996 #text\_change 09-Jul-2004  
 C:Accession: I39815  
 R:Gleaves, A.P.; Williams, R.; Hedges, R.J.  
 Appl. Environ. Microbiol. 59, 1683-1687, 1993  
 A:Title: Screening by polymerase chain reaction of Bacillus thuringiensis serotypes for t  
 iensis subsp. kurstaki.  
 A:Reference number: I39815; MUID:93298009; PMID:8517758  
 A:Accession: I39815  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-719 <RES>  
 A:Cross-references: UNIPROT:Q45752; GB:M98544; NID:9142767; PIDN:AAA22354.1; PID:9142768  
 C:Genetics:  
 A:Gene: cryV  
 C:Superfamily: parasporal crystal protein

Query Match 99.5%; Score 3743; DB 2; Length 719;  
 Best Local Similarity 99.6%; Pred. No. 2.6e-250;  
 Matches 716; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKXSEYENVEPVSASTI 60  
 DB 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKXSEYENVEPVSASTI 60  
 QY 61 QTGIGIAGKILGTLGVPPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINOKISTYA 120  
 DB 61 QTGIGIAGKILGTLGVPPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINOKISTYA 120  
 QY 121 RNKALTDLKGGLDALAVYHDSLESWVGNNRTRASVVKSOYIALELMFVKQLSPFAVSG 180  
 DB 121 RNKALTDLKGGLDALAVYHDSLESWVGNNRTRASVVKSOYIALELMFVKQLSPFAVSG 180  
 QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFFNROVERAGDYSYHCVKWYS 240  
 DB 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFFNROVERAGDYSYHCVKWYS 240  
 QY 241 TGLNLRGNAESWRYNQFRDNTLMVLDLVALFPSYDTOMYPIKTTAQLTREYVTDAL 300  
 DB 241 TGLNLRGNAESWRYNQFRDNTLMVLDLVALFPSYDTOMYPIKTTAQLTREYVTDAL 300  
 QY 301 GTVHPHPSFTSTTWNNNAPSFAIAEAAVVRNPHLLDFLEQVTIYSLLSRSNTOYMMNW 360  
 DB 301 GTVHPHPSFTSTTWNNNAPSFAIAEAAVVRNPHLLDFLEQVTIYSLLSRSNTOYMMNW 360  
 QY 361 GGHKLEFRITIGTLNISTCGSTNTSINPVTLPTSDRVYRTESLAGLNLFLTQPVNGVPR 420  
 DB 361 GGHKLEFRITIGTLNISTCGSTNTSINPVTLPTSDRVYRTESLAGLNLFLTQPVNGVPR 420

QY 421 VDFHKKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGPNVYESYSHRLSHIGLIS 480  
DB 421 VDFHKKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGPNVYESYSHRLSHIGLIS 480  
QY 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
DB 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
QY 541 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAFMNREGDLDYK 600  
DB 541 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAFMNREGDLDYK 600  
QY 601 TERTVGTFTTSPFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPVEVTEAEYDPEKAQEKV 660  
DB 601 TERTVGTFTTSPFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPVEVTEAEYDPEKAQEKV 660  
QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719  
DB 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719

RESULT 4  
I40590  
cryv465 protein - Bacillus thuringiensis  
C/Species: Bacillus thuringiensis  
C/Date: 12-Aug-1996 #sequence\_revision 12-Aug-1996 #text\_change 09-Jul-2004  
C/Accession: I40590  
R/Shin, B.S.; Choi, S.K.; Koo, B.T.; Lee, S.T.; Kim, J.I.  
Appl. Environ. Microbiol. 61, 2402-2407, 1995  
A/Title: Distribution of cryV-type insecticidal protein genes in Bacillus thuringiensis  
comocidus.  
A/Reference number: I39814; MUID: 95314293; PMID: 7793960  
A/Accession: I40590  
A/Status: preliminary; translated from GS/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-719 <RES>  
A/Cross-references: UNIPROT:Q45709; EMBL:U07642; NID:g467234; PIDN:AAA82114.1; PID:g4672  
C/Genetics:  
A/Gene: cryv465  
C/Superfamily: parasporal crystal protein

Query Match 93.1%; Score 3503; DB 2; Length 719;  
Best Local Similarity 92.5%; Pred. No. 9.5e-234;  
Matches 665; Conservative 32; Mismatches 22; Indels 0; Gaps 0;

QY 1 M LKLNQDKHQSNAKVDKISTDSLKNETDIELQNIHEDCLKMSEYENVEPVSASTI 60  
DB 1 M LKLNQDKHQSNAKVDKISTDSLKNETDIELQNIHEDCLKMSEYENVEPVSASTI 60  
QY 61 QTGGIAGKILGTLGVPPAGQVASYLFIIGELWPKGNQWEI FMEHVEEII NOKISTYA 120  
DB 61 QTGGIAGKILGTLGVPPAGQVASYLFIIGELWPKGNQWEI FMEHVEEII NOKILTVA 120  
QY 121 RNKALTDLKGIDALAVYHDSLESWGNRNNTARSVVKVQYIALELMFVQKLPSPAVSG 180  
DB 121 RNKALSDRLGIDALAVYHDSLESWGNRNNTARSVVKVQYIALELMFVQKLPSPAVSG 180  
QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSEISTFTYNQVERAGDYSYHCVKWYS 240  
DB 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSEISTFTYNQVERAGDYSYHCVKWYN 240  
QY 241 TGLNLRGNTAESWVRVYNQFRDMLMVLIDLVALFPSYDTOMYPIKTTAQLTREVYTDAL 300  
DB 241 TGLNLRGNTAESWVRVYNQFRDMLMVLIDLVALFPSYDTOMYPIKTTAQLTREVYTDAL 300  
QY 301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW 360  
DB 301 GTVHPNQAFASTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW 360  
QY 361 GGHLKLPRTTGGTLNISTQGSTNTSINPVTLPFTSRDVRVETESLAGNLPLTQPVNGVPR 420  
DB 361 GGHLKLPRTTGGTLNISTQGSTNTSINPVTLPFTSRDVRVETESLAGNLPLTQPVNGVPR 420

QY 421 VDFHKKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGPNVYESYSHRLSHIGLIS 480  
DB 421 VDFHKKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGPNVYESYSHRLSHIGLIS 480  
QY 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
DB 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
QY 541 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAFMNREGDLDYK 600  
DB 541 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAFMNREGDLDYK 600  
QY 601 TERTVGTFTTSPFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPVEVTEAEYDPEKAQEKV 660  
DB 601 TERTVGTFTTSPFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPVEVTEAEYDPEKAQEKV 660  
QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719  
DB 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719

RESULT 5  
S00873  
parasporal crystal protein cryBa1 - Bacillus thuringiensis subsp. thuringiensis  
N/Alternate names: parasporal crystal protein cryA4  
C/Species: Bacillus thuringiensis subsp. thuringiensis  
C/Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 09-Jul-2004  
C/Accession: S00873  
R/Brizard, B.L.; Whiteley, H.R.  
Nucleic Acids Res. 16, 2723-2724, 1988  
A/Title: Nucleotide sequence of an additional crystal protein gene cloned from Bacillus t  
A/Reference number: S00873; MUID: 88203216; PMID: 3362680  
A/Accession: S00873  
A/Molecule type: DNA  
A/Residues: 1-1228 <BRI>  
A/Cross-references: UNIPROT:P05517; EMBL:X06711; NID:g40264; PIDN:CAA29898.1; PID:g58094  
C/Genetics:  
A/Gene: cryA4  
A/Start codon: TTG  
C/Superfamily: parasporal crystal protein  
C/Keywords: delta-endotoxin

Query Match 60.1%; Score 2262.5; DB 2; Length 1228;  
Best Local Similarity 62.4%; Pred. No. 9.6e-148;  
Matches 447; Conservative 79; Mismatches 163; Indels 25; Gaps 6;

QY 23 TDSLKNETDIELQNIH-----EDCLKMSEYENVEPVSASTIQTGGIAGKI 70  
DB 2 TSNRNKNEEII NAVSNHSAQMDLLPDARIEDSLCIAEGNIDPPVSASTVQTGINIAGRI 61  
QY 71 LGTLGVPPAGQVASYLFIIGELWPKGNQWEI FMEHVEEII NOKISTYARNKALTDLKG 130  
DB 62 LGVLGVPPAGQVASYLFIIGELWPKGRDQWEI FLEHVEQLINQOITENARNTALRIQGG 121  
QY 131 LGDALAVYHDSLESWGNRNNTARSVVKVQYIALELMFVQKLPSPAVSGEVPPLPIYA 190  
DB 122 LGDSFRAVQCSLEDWLENRDARTSVLYQYIALELDLFLNAPLFAIRNCEVPLMUYA 181  
QY 191 QAANLHLLLRDASIFGKEWGLSSEISTFTYNQVERAGDYSYHCVKWYSYGLNNLRGTN 250  
DB 182 QAANLHLLLRDASIFGSEFGLTSOEIQRYRQVERTRDYSYDCEVWYNTGLNSLRGTN 241  
QY 251 AESWVRVYNQFRDMLMVLIDLVALFPSYDTOMYPIKTTAQLTREVYTDALGVHHPHPSFT 310  
DB 242 AASWVRVYNQFRDMLMVLIDLVALFPSYDTOMYPIKTTAQLTREVYTDALGVHHPHPSFT 299  
QY 311 STTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNWGGHKLKLPRTI 370  
DB 300 SMWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNWGGHKLKLPRTI 359  
QY 371 GGTINISTQGSTNTSINPVTLPFTSRDVRVETESLAGNLPLTQPVNGVPRVDFHKEFV 428  
DB 360 GGGLNTSTHGATNTSINPVTLPFTSRDVRVETESLAGNLPLTQPVNGVPRVDFHKEFV 416

429 QY THP-----IASNFYPGYAGIGTQLODSENELPPEATQOPNYESYSHRLSHIGLISASH 483  
 Db INPQNISDRGTANYQSP-YESPGQLKDSLETLPETTERPNYESYSHRLSHIGLISASH 475  
 QY 484 VKALVYSHRSADRTNIENPSITQILPKAFNLSSGAAVVRPGPTGGDILRRITNGT 543  
 Db 476 VNVFYVSHRSADRTNIGRNRIQIPMWKASLPQGTIVVRPGPTGGDILRRITNGG 535  
 QY 544 FQDIRVNIIPPAQRYRRIYASTTDLQFHTSINGKAINOCNFSATNRGDEDLDYKTF 603  
 Db 536 FQPIRVTVNGPLTQRYRIGFRYASIVDFDFVSRGGTTVNNFRRLRTNWSGDELKYNFV 595  
 QY 604 TVGFTPTPSFLDVQSTFTIGAWNFSNGNEVDIRIEFVVPVEVTVBAEYDFEKAQKVTAL 663  
 Db 596 RRAFTPTPTFTQIQDIIRTS:QGLSGNGEVYDKIEIIPVATPEAEYDLERAQAYNAL 655  
 QY 664 FTSTNPRGLKTDVKDHYDQVSNLVESLDSFYLDKRELFEIVKYANELHIERNM 719  
 Db 656 FINTNPRKLKTDVTDYHIDQVSNLVACLSDFCLDKRELLEKVKYAKLSDERNL 711

RESULT 6  
 B42459  
 hypothetical protein 2 (cryIF 3' region) - Bacillus thuringiensis (strain aizawai) (frag  
 C:Species: Bacillus thuringiensis  
 C:Date: 10-Jul-1992 #sequence\_revision 10-Jul-1992 #text\_change 09-Jul-2004  
 C:Accession: B42459  
 R:Chambers, J.A.; Jelen, A.; Gilbert, M.P.; Jany, C.S.; Johnson, T.B.; Gawron-Burke, C.  
 J. Bacteriol. 173, 3966-3976, 1991  
 A:Title: Isolation and characterization of a novel insecticidal crystal protein gene fr  
 A:Reference number: A42459; MUID:91286178; PMID:2061280  
 A:Accession: B42459  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-380 <CHA>  
 A:Cross-references: UNIPROT:Q8K561; UNIPROT:Q45740; GB:M63897  
 C:Superfamily: parasporal crystal protein

Query Match 50.3%; Score 1891; DB 2; Length 380;  
 Best Local Similarity 95.3%; Pred. No. 6.7e-123; Indels 0; Gaps 0;  
 Matches 362; Conservative 8; Mismatches 10

QY 1 MKLKNQDQHQSFSSNAKVDKISTDSLKNETDIELQNIHEDCLKXSEYENVEPVSASTI 60  
 Db 1 MKLKNPDQHQSFSSNAKVDKISTDSLKNETDIELQNIHEDCLKISTEYENVEPVSASTI 60  
 QY 61 QTGIGIAGKILGTGVPPAGQVASYLSYILGELMPKGNQWEIEMEHVEEIIINOKISTYA 120  
 Db 61 QTGIGIAGKILGTGVPPAGQVASYLSYILGELMPKGNQWEIEMEHVEEIIINOKISTYA 120  
 QY 121 RNKALTDLKLGDALAVYHDSLESWGNRNNTARSVVKSVYIALELMFVKLPSFAVSG 180  
 Db 121 RNKALTDLKLGDALAVYHDSLESWGNRNNTARSVVKSVYIALELMFVKLPSFAVSG 180  
 QY 181 EBPVLLPIYAQANLHLLLRDASIFGKEWGLSSSEISTFTNROVERAGDYSHCVKWS 240  
 Db 181 EBPVLLPIYAQANLHLLLRDASIFGKEWGLSSSEISTFTNROVERAGDYSDCVKWS 240  
 QY 241 TGLNLRGNTNABSWRYNQFRDMLTMVLDLVALPSPYDTQMPYIKTTAQTREVVYDAI 300  
 Db 241 TGLNLRGNTNABSWRYNQFRDMLTMVLDLVALPSPYDTQMPYIKTTAQTREVVYDAI 300  
 QY 301 GTVHPHPSFTSTYNNAPSPAEEAAVVRNPHLLDFLEQVTIYSLLSRWNSQYNNMW 360  
 Db 301 GTVHPNAPSPATYNNAPSPSTIESAVVRNPHLLDFLEQVTIYSLLSRWNSQYNNMW 360  
 QY 361 GGHKLEERTIGGLNISTQG 380  
 Db 361 GGHRLFEFTIGGLNLTSTQG 380

RESULT 7

S49247  
 parasporal crystal protein cry9Ca1 [validated] - Bacillus thuringiensis  
 N;Alternate names: parasporal crystal protein cryIH  
 C:Species: Bacillus thuringiensis  
 C:Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 09-Jul-2004  
 C:Accession: A59350; S49247  
 R:Lambert, B.; Buysse, L.; Decock, C.; Janssens, S.; Piens, C.; Saey, B.; Seurinck, J.; V  
 Appl. Environ. Microbiol. 62, 80-86, 1996  
 A:Title: A Bacillus thuringiensis insecticidal crystal protein with a high activity agai  
 A:Reference number: A59350; MUID:96141404; PMID:8572715  
 A:Accession: A59350  
 A:Molecule type: DNA  
 A:Residues: 1-1157 <LAM>  
 A:Cross-references: UNIPROT:Q45733; EMBL:Z37527; NID:G547554; PIDN:CAA85764.1; PID:G5475  
 A:Experimental source: serovar tolworthi  
 C:Comment: This parasporal crystal protein, active against corn borer and other insects,  
 C:Superfamily: parasporal crystal protein  
 C:Keywords: delta-endotoxin

Query Match 39.4%; Score 1483; DB 1; Length 1157;  
 Best Local Similarity 43.1%; Pred. No. 5.7e-94;  
 Matches 321; Conservative 113; Mismatches 220; Indels 90; Gaps 15;

QY 26 LKNETDIELQNIHEDCLKXSEYENVEPVSAS-----TIQTGIGIAGKILGTLPVFP 78  
 Db 29 LASDPNALQNNYKDYLTQMTDEDYDTSYNPSLSISGRDAVQTALTVVGRILGALGVFP 88  
 QY 79 ACQVASLYSFIIGELMPKGNQ-WEIEMEHVEEIIINOKISTYARNKALTDLKLGDALAV 137  
 Db 89 SGQVSYFYFLNTLWPNVNDTAINAFMRQVELVNNQITFEARNQALARLOGLSDSFV 148  
 QY 138 YHDSLESWGNRNNTARSVVKASQVIALELMFVKLPSFAVSGEVEPVLPIYAQANLH 197  
 Db 149 YQRSIQNLADRNDTNTLSVVRQAQFIALDLDVFNALPLFAVNGQQVLLSVYQAQVNLH 208  
 QY 198 LLRDASIFGKEWGLSSSEISTFTNROVERAGDYSHCVKWSYTGNNLRGNTNABSWRY 257  
 Db 209 LLLKDSALFEGEGVGTQGEISTYDRQLELTAKYNYCETWYNTGLDLRGNTESWJRY 268  
 QY 258 NQFRDMLTMVLDLVALPSPYDTQMPYIKTTAQLREVVYDAIGTVHPHPSFTSTYNN 317  
 Db 269 HQERRENTLVLDVALFPYDVLRYPTGSNPQLREVYDPIVFNPAVGLCRWGTN 328  
 QY 318 NAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWNS-NTQYNNWNGHLE----- 366  
 Db 329 PYNTFSELENAFIRPHEFLDRNLSTISS--NRFPVSGNFMNDYWSGHTLRRSYLNDSAVQ 386  
 QY 367 -----FRITGGTLMISTOGSTNTSINPVTLPTFDVYRTESLAGLNLFLTPQVNGVPR 420  
 Db 387 EDSYGLITTRATINPGVDGTRN--IESTAVDFRS-----ALIG-----IYGNR 429  
 QY 421 VDFHKEVTHPIASDNFYYPGAGIGT-----QLQDSENELPP-EATQPIVYESYS 470  
 Db 430 ASP-----VPGGIFNGTTPANGGCRDLTYDNDLPPDESG-----SST 469  
 QY 471 HRLSHIGLIS-----ASHVKALVSWTHRSADRTNTEIPNSITQILPKAFNLSSG 521  
 Db 470 HRLSHVTFPSFQTNQAGSIANAGSVPTVYWRDVLNNTITFNRIQTQLPKVASAPVSG 529  
 QY 522 AAVVRGFGTGGDILRRITNGTFGDIRVINNPFPFAQRVVRIRYASTTDLQPHHTSINKA 581  
 Db 530 TTVLKPGFGTGGGILLRRTNGTFTGLRVTVNSPLTQQYRLRVRFASFTGNFIRVLRGGVS 589  
 QY 582 INQGNFSAFMNRGEDLDYKTFRTVGFTT-----PESFLDVQSTFTIGAWNFSNGEVI 635  
 Db 590 IGVRLGSTMNRGQELTYESFTTRFTTTGPNPPTFTTQAOEILTVNABGVSTGEYII 649  
 QY 636 DRIEFVPEVTVYAEYDFEKAQKVTALFTSTNPRGLKTDVVDKDYHIDQVSNLVESLSD 695  
 Db 650 DRIEIVPVNPAEAEEDLEAKKAVASLFRTRD-GLQVNVTDYQVDQAANLVSLSD 708  
 QY 696 YLDEKRELFEIVKYANELHIERNM 719



Db 709 YGDKKMLLEAVRAAKRLSRERNL 732

RESULT 8  
S32645  
parasporal crystal protein cryIga1 - Bacillus thuringiensis  
C:Species: Bacillus thuringiensis  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
C:Accession: S32645  
R:Lambert, B.  
submitted to the EMBL Data Library, April 1993  
A:Reference number: S32645  
A:Accession: S32645  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1166 <LAM>  
A:Cross-references: UNIPROT:Q45746; EMBL:Z22510; NID:G295861; PIDN:CAA80233.1; PID:G295861  
C:Superfamily: parasporal crystal protein  
C:Keywords: delta-endotoxin

Query Match 39.0%; Score 1467.5; DB 2; Length 1166;  
Best Local Similarity 45.8%; Pred. No. 6.8e-93;  
Matches 323; Conservative 100; Mismatches 207; Indels 75; Gaps 17;

Qy 41 DCLRVSEYE---NVPEFVSASTIQTGTIGIAGKILGTLPVAGQVAVSLYSFILGELWPK 96  
Db 13 NCLNPESEIFNARNSNFGLVSQVSSGL---TRFLLEAAVPEAGFALGLFDIHWGL--- 66  
Qy 97 GKQWEIFMEHVEEIIINOKISTYARNKALTDLKGDLALAVHDSLESWVGNNTRARS 156  
Db 67 GVDQMSFLRQIEQLRQIEITELERNRATALLTGLSSSYNLVEALREWENDENPEASQE 126  
Qy 157 VKSOYTALELMFVOKLPSPAVSGEEVPLPIYAQAANLHLLLRDASIFGKWSGLSSSE 216  
Db 127 RVTRFRPLTDAAVTGLPTLAIRNLEVNLSVTQAANLHLLLRDASIFGKWSGLSSSE 186  
Qy 217 ISTFYNQVERAGDYSHYCKVYSTGLNNLRGTNAESWRYNQFRDMDLMLVLDLVALFP 276  
Db 187 IEDLYTRLTSGNIQYSDHCARWYNOGLNEIGGISR---RYLDFQDLTISLVDIVALFP 242  
Qy 277 SYDQWYPIKTAQLTREVYTDAL--CTVHPHSPSTTWNNAEVSFSAIEAAVNRPH 334  
Db 243 NYDIRTPITQSQLTREIYTSVPVAGNI-----NFGLSIANVLRAPH 285  
Qy 335 LLDPLEQVITYLSLRWSNTQYMMMGCHKLEFRTIG--GTLN-----ISTQGSTNTS 385  
Db 286 LMDPDIRIVLYTNSR--STPY---WAGHEVISRRTGQGGQGNIRPPLYGVAANAEPVYT 340  
Qy 386 INPVLTPFTSRDVIYTES-----LACNLFLTPQVNGVPRVDFHWKFTVHTPIASDNFY 439  
Db 341 IRPTGFTDEORQWYRARSRVVSRSGQDFSLDVAVG-----FLT-IPSAVSIVR 389  
Qy 440 PGVAGIGTQDQGENELPPEATQPNYESYSHRLSHGLISAS-----HVKALVYSWTHR 494  
Db 390 NGF--GNT---DIIDEIPLEGTP--FTGSHRLCHVGFLASSPFFISQVAPADIFSWTHR 443  
Qy 495 SADRNTIENSITQIPLKAFNLSSGAAVVRGPGTGGDILRRTNTGTFGDIRVNNIPP 554  
Db 444 SATLTNTIAPDVITQIPLKAFNLHSGATVKGPGTGGDILRRTNVGSGFDMRVNITAP 503  
Qy 555 FAQRYRIRIYASTDLOFHTSINGKAINQGNFSAWNEGEDLDYKTERVTGFTTPEPSFL 614  
Db 504 LSGRYRIRIYASTDLOFHTSINGKAINQGNFSAWNEGEDLDYKTERVTGFTTPEPSFL 563  
Qy 615 DVOSTFTIGAWNFSNGNEVYDRIEFVPEVVEYAEYDFEKAQKVTALTFTSTNPRGLKT 674  
Db 564 DANSTFTIGAFGSPNNEVYDRIEFVPAEVTPEAEVDLEKAQKAVNALFTSSNQIGLKT 623  
Qy 675 DVKDYHIDQVSNLVSLSDEFYLDKRELEFPIVVKYANELHIERNM 719  
Db 624 DVTDIYHIDKVNLSVECLSDSEFCDEKREUSEKVKHAKRLSDERNL 668

RESULT 9  
S32649

parasporal crystal protein cryIpa3 - Bacillus thuringiensis  
C:Species: Bacillus thuringiensis  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
C:Accession: S32649  
R:Lambert, B.  
submitted to the EMBL Data Library, April 1993  
A:Reference number: S32645  
A:Accession: S32649  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1174 <LAM>  
A:Cross-references: UNIPROT:Q45749; EMBL:Z22512; NID:G295865; PIDN:CAA80235.1; PID:G295865  
C:Superfamily: parasporal crystal protein  
C:Keywords: delta-endotoxin

Query Match 38.8%; Score 1461; DB 2; Length 1174;  
Best Local Similarity 44.6%; Pred. No. 1.9e-92;  
Matches 324; Conservative 101; Mismatches 205; Indels 96; Gaps 17;

Qy 36 NINHE----DCLKMEYENVEPVFSASTIQTGTIGIA--GKILGTLPVAGQVAVSLYSFIL 90  
Db 4 NIONQCPVYNCLSNPEVEILSEERSTGRLPDLISLSTRFLLSSEFVPGVGVAFGLFDLIW 63  
Qy 91 GELWPKGNQWEIFMEHVEEIIINOKISTYARNKALTDLKGDLALAVHDSLESWVGNNR 150  
Db 64 GPITP---SESLFLQLQIEQLRQIEITELERNRATITLGLADSYEVLEALREWEENPN 120  
Qy 151 NTRARSVVKSOYTALELMFVOKLPSPAVSGEEVPLPIYAQAANLHLLLRDASIFGKEW 210  
Db 121 NLAQLREDVIRIPANTDDALITAINNFTLSFEIPLLSVYVQAANLHLLLRDASVFGQGW 180  
Qy 211 GLSSSEISTFYNQVERAGDYSHYCKVYSTGLNNLRGTNAESWRYNQFRDMDLMLVLD 270  
Db 181 GUDIATVANNHNLINLHRYTEHCLDTYNOGLENLRTNQWSERFQFRELTLTVLD 240  
Qy 271 LVALPSPYDQWYPIKTAQLTREVYTDALGTVHPHSPSTTWNNAEVSFSAIEAAV 329  
Db 241 IVALPSPYDQWYPIKTAQLTREVYTDALGTVHPHSPSTTWNNAEVSFSAIEAAV 290  
Qy 330 VNNPHLLDPLEQVITYLSLRWSNTQYMMMGCHKLEFRTIGTTLNISTQGSTNTSINPV 389  
Db 291 VRPPLHMDFMN---SLFVTAETVRSQTVNGCHLV-----SSRNTAGNPI 331  
Qy 390 TLPPF-----TSRDVYRTESLAGLNLFLTPQVNGVPRVDFHWKFTVHTPIAS 434  
Db 332 NPFIYGINPGGAIWIAEDPRPFYRT-----LSDPV-----FVRGGFGN 371  
Qy 435 DNFFYPGVAGIGTQIQ-----DSENELPPEATQPNYESYSHRLSHI----- 476  
Db 372 PH-YVLGLRGVAFQQTGNHTRTFNSGCTIDSLDEIPQDNGSGAPWNDYSHVLAHVTVR 430  
Qy 477 --GLISASHV-KALVYSWTHRSADRNTIENSITQIPLKAFNLSSGAAVVRGPGTGG 533  
Db 431 WFEIAGSDWRAPMFWSWTHRSADRNTIENSITQIPLKAFNLSSGAAVVRGPGTGG 490  
Qy 534 DILRRTNTGTFGDIRVNNIPPFAQRYRIRIYASTDLOFHTSINGKAINQGNFSAWNE 593  
Db 491 DLLRRTNTGTFADIRVNTIGPLSQRYRIRIYASTDLOFHTSINGKAINQGNFSAWNE 550  
Qy 594 GEDLDYKTERVTGFTTPEPSFLDVOSTFTIGAWNFSNGNEVYDRIEFVPEVVEYAEYDF 653  
Db 551 GGNLESGNFRTAGFSTPFSFNAQSTFTLTGTAQFSN--QEVYDRIEFVPAEVTPEAESDL 609  
Qy 654 EKAQKVTALTFTSTNPRGLKTDVNDYHIDQVSNLVSLSDEFYLDKRELEFPIVVKYANEL 713  
Db 610 ERAQKAVNALFTSSISQLGKNTNVTGYHLDQVSNLVSLSDEFYLDKRELEFPIVVKYANEL 669  
Qy 714 HIERNM 719  
Db 670 SDKRNL 675

JD00002  
paraaporal crystal protein cryIIAb3 - Bacillus thuringiensis  
N:Alternate names: delta-endotoxin-2; entomocidal protoxin; entomopathogenic crystal prot  
C:Species: Bacillus thuringiensis  
C:Date: 28-Dec-1987 #sequence revision 28-Dec-1987 #text change 09-Jul-2004  
C:Accession: A90025; A91560; A90955; S14555; A26461; A24172; A29043; JD00002  
R:Kondo, S.; Tamura, N.; Kunitake, A.; Hattori, M.; Akashi, A.; Ohmori, I.  
Agric. Biol. Chem. 51, 455-463, 1987  
A:Title: Cloning and nucleotide sequencing of two insecticidal delta-endotoxin genes from  
A:Reference number: A90025  
A:Accession: A90025  
A:Molecule type: mRNA  
A:Residues: 1-1155 <CON>  
A:Cross-references: UNIPROT:P06578  
A:Experimental source: subsp. kurstaki  
R:Geiser, M.; Schweitzer, S.; Grimm, C.  
Gene 48, 109-118, 1986  
A:Title: The hypervariable region in the genes coding for entomopathogenic crystal protei  
A:Reference number: A91560; MUID:87163505; PMID:3557124  
A:Accession: A91560  
A:Molecule type: DNA  
A:Residues: 1-1155 <GEI>  
A:Cross-references: PIDN:AAA22551.1; PID:g143124  
A:Experimental source: subsp. kurstaki  
R:Wabiko, H.; Raymond, K.C.; Bulla Jr., L.A.  
DNA 5, 305-314, 1986  
A:Title: Bacillus thuringiensis entomocidal protoxin gene sequence and gene product anal  
A:Reference number: A90955; MUID:86300092; PMID:3743328  
A:Accession: A90955  
A:Molecule type: DNA  
A:Residues: 1-1155 <WAB>  
A:Cross-references: NID:G142719; PIDN:AAA22330.1; PID:g142720  
A:Experimental source: subsp. berliner  
R:Chak, K.F.; Jen, J.C.  
Submitted to the EMBL Data Library, October 1990  
A:Description: Complete nucleotide sequence and expression in Escherichia coli of a cry  
A:Reference number: S14555  
A:Accession: S14555  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1155 <CHA>  
A:Cross-references: EMBL:X54939; NID:G40272; PIDN:CAA38701.1; PID:g40273  
R:Hofte, H.; de Greve, H.; Seurinck, J.; Janssens, S.; Mahillon, J.; Ampe, C.; Vandekerck  
Eur. J. Biochem. 161, 273-280, 1986  
A:Title: Structural and functional analysis of a cloned delta endotoxin of Bacillus thuri  
A:Reference number: A26461; MUID:87054026; PMID:3023091  
A:Accession: A26461  
A:Molecule type: DNA  
A:Residues: 1-730, 'L', 732-784, 'R', 786-1155 <HOP>  
A:Cross-references: GB:X04698; NID:G40254; PIDN:CAA28405.1; PID:g40255  
A:Experimental source: strain berliner 1715  
C:Comment: This toxin is lethal to the larvae of lepidopterans and dipterans.  
C:Genetics:  
A:Gene: cry-1-2; bt2  
C:Superfamily: parasporal crystal protein  
C:Keywords: Delta-endotoxin  
F:82-586/Product: toxic peptide #status predicted <TYP>  
F:82-300/Region: toxic #status predicted  
F:300-586/Region: insecticidal #status predicted  
Query Match 38.6%; Score 1452; DB 2; Length 1155;  
Best Local Similarity 44.1%; Pred. No. 7.8e-92;  
Matches 313; Conservative 111; Mismatches 229; Indels 56; Gaps 13;  
36 NINHEDECLMSEYENVE-PFVSASTIQG-----IGIAGKILGTGLVPPAGQVASLYS 87  
4 NPNINECIPYNCNPEVEVLGGERIETGTPIDISLSTQFLSEF-VPGAGFVLGLVD 62  
88 FILGELWPKGNQWEIFMEHVEEIIINOKISTYARNKALTDLKGDLALAVYHDSLESWVG 147  
63 IIWGIF---GPSQWDAFLVQIQLNQRIEFAFNQAIISRLGSLNLYQIYAESFREWEA 119  
148 NRNNTRASVVKVSYQYIAELMFLVQKLPFAVSSEGVPELPIYQAQANLHLLLDASIFG 719  
635 GLKTDVTDYHIDQVSNLVBLSDEFYLDKRLBELFIYKYVANELHILERNM 719  
635 GLKTDVTDYHIDQVSNLVBLSDEFYLDKRLBELFIYKYVANELHILERNM 683  
RESULT 11

Db	120	DPTNPALEMR:QFVNDMSALTAIPI:PAVQNYQVPLLSVYQAANLHLVSURDVSFG	179
Qy	208	KEWGLSSSEISTFYNQOVERAGDYSVHCWKVYSTGLNLRCTNAESWVRYNQRRDWTLM	267
Db	180	QRWGFAAATINSYNDLTRELIGNYTDHAWRYNTGLERVWGPDRDMIRYNQFRRELTLT	239
Qy	268	VLDLVALFSPYQPMYPIKTTAQLTRVYVTDATGVHEHPHSFTTWNNAESP-----S	323
Db	240	VLDIVSUFNYDSRTPIVNTVSQLTREIYTPNV-----LENFDSFRGSAQ	285
Qy	324	AIEAAVVRPHLLDFLEQVIYSLLSR-----WSNTQYANM--WGGHKLFRRTIGTGLNI	376
Db	286	GIEGS-IRSPHLMILNSITIYDAHRGEYWSGHQIWASPVGSGSEFPFPI:GTMGNA	344
Qy	377	STOGSTNTSNPVTLPFTSERYRTESLAGNLFLTQPVNGVPRVDPHFWKVTHTPIASON	436
Db	345	APQORIVAGLGQGYRTLSTLYRPPFNIGIN--NQQLSLVDGTEPAYG-----TSSN	395
Qy	437	FYPGPGVAGTGLQDSENELPPEATQPNYSYSHRLSHLGLI-----SASHVKALVY	489
Db	396	LPNAVVRKSGT--VUSDLEIPQNNVPRQGFSHRLSHVMSFRSGFSNSVSIIIRAPM	453
Qy	490	SWTHRSADRNTTIEPNSITQIPLVKAFNLSCGAAVRPGPGTGGDILRRNTTCTFGDIDV	549
Db	454	SWTHRGAEPNNIIPSSQITQIPLTKSTNLGSGTSVVKPGPTGGDILRRISPOQISTLAV	513
Qy	550	NINPPAQRYRRIYASTDLOPHTSINGKALINQGNFSAFMARGEDLDYKTRTIVGFTT	609
Db	514	NITAPUSQRYRRIYASTNLQPHTSIDGRPINQGNFSAFMSSGNSLQSGSPRTVGFTT	573
Qy	610	PFSELDVQGTFTIGAWNFSSNGEVYDRIEFPVPEVTEYAEYDFEKAQKVTAFLTSTNP	669
Db	574	PFNFSGSSVFTLSAHVFNSGNEVYDRIEFPVPAEVTFEAEYDLERAQKAVNELFTSSNQ	633
Qy	670	RLGKTDVKDYHIDQVSNLVESLSDBFYLDKRELFETVKYANELHIERNM	719
Db	634	IGLKTDVTDYHIDQVSNLVECLSDBFCDKELSELVKYAKRLSDFRNI	683

RESULT 12  
A29125  
parasporal crystal protein Bt2 - *Bacillus thuringiensis* subsp. *kurstaki* (strain HD-1)  
C:Species: *Bacillus thuringiensis* subsp. *kurstaki*  
C:Date: 15-Dec-1988 #sequence\_revision 15-Dec-1988 #text\_change 09-Jul-2004  
C:Accession: A29125  
R:Fischhoff, D.A.; Bowdish, K.S.; Perlak, F.J.; Marrone, P.G.; McCormick, S.M.; Niedermere  
Bio/Technology 5, 807-813, 1987  
A:Title: Insect tolerant transgenic tomato plants.  
A:Reference number: A29125  
A:Accession: A29125  
A:Status: not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-1156 <FIS>  
A:Cross-references: UNIPROT:Q9F296; UNIPROT:Q93R21  
C:Superfamily: parasporal crystal protein  
C:Keywords: delta-endotoxin

Query Match	38.6%	Score 1452;	DB 2;	Length 1156;
Best Local Similarity	44.2%;	Pred. No. 7.8e-92;		
Matches 314;	Conservative 111;	Mismatches 229;	Indels 56;	Gaps 13
QY	36	NINHEDCLQWSEYENVE-PFVSASTIQG-----IGIAGKILGTGLVPPFAGQVASLYS	87	
		:           :           :		
Db	4	NNINECIPYNCLSPEVEVGGRIETGYTPDISLSTQFLLSSEF-VPGAGFVLGLVD	62	
		:           :           :		
QY	88	FILGELWPKRGKQWEIFMHEVVEEINOKISTPYARNKALTDLKGGLDALAVYHDSLESWVG	147	
		:           :           :		
Db	63	IIWGIF--GPSQWDAFLVQIEQLINQRIEFARNOAISLEGLSNLYQIYAESPWEA	119	
		:           :           :		
QY	148	NRNNTARSVVKSVQIALELMFVKLSPSPAVSGEEVPLPIYAQAANLHLILLRDASIFG	207	
		:           :           :		
Db	120	DTNPALREEMRIQNDMNSALTATLEFVQNYQVPELLSVYQQAANLHSLVLRDSVFG	179	
		:           :           :		

Qy	208	KEWGLSSSEISFYNRQVERACDYSYHCVKYVSTGLNNLRGTNAESWVRYNQRPDRMTLM	267
Db	180	QRWGFDAAATYNSRNGYNDLTRELCNVTDHAVRYNTGLERWGPDSRDWIRYNQRPRELTLT	239
Qy	268	VLDLVALFSPDYOMYPKTTAAQLTREYVTDAGTVHHPSPFTSTWYNNNAPSF---S	323
Db	240	VLDIVSLFFNYSRYPPIRTVSQLTRELYNPV-----LENFDSFRGSAQ	285
Qy	324	ATBAAVRNPHLLDFLEOVTTYSLLSR-----WSNTQYMMN---WGHKLEFRTIGTGLNI	376
Db	286	GIEGS-IRSPHLMDLINSITTYDAHRGEYWSGHQMASPVGSPETFPPLGYTMGNA	344
Qy	377	STQSGSNTSINPVTLPFTRSDRYATESIAGLNLFLOPVNGVPRVPDHKEVTHPTASDN	436
Db	345	APQORVACLGQGVYRTLSYLRRPFGIN---NOQLSVLDGTBFAYG-----TSSN	395
Qy	437	FYPGVAGIGTQDSENELPEATGPNVESYSHRLSHIGLI-----SASHVKALYV	489
Db	396	LPSAVYRKSGT--VDSLDEIPQNNVNPVPRQGFSHRLSHVSMFSGFSNSSVSIIRAPMF	453
Qy	490	SWTHRSADRTNIEBNSITQIPLKAKNLSGAAVVRGPGFTGGDILRTNTCTGCDIRV	549
Db	454	SWIHSASFNIIIPSSQITQIPLKSNLGSSTVVKPGPFTGGDILRTISPGQISTLRV	513
Qy	550	NINPPAQRYRYRYASTDLOFHTSINGKAINQGNFSAATMRGDDLYKTFRTVGFMT	609
Db	514	NITAPLSQRYRYRYASTTNLQFHTSIDGRPINQGNFSAATMSGGNLQSGSFRVGFMT	573
Qy	610	RPSELDVQSTFTIGAWPSSGNEYVIDRIEFVPVYTYEAYDFEAKQKVALTFTSTNP	669
Db	574	PNFNGSGSVFTLSAHVNSGNEYVIDRIEFVPAEVTFEAYDLEAKAVNELFTSSNQ	633
Qy	670	RLGKTDVRKDYHIDQVSNLAVESLSDEFYLDKRELFBIKVYANELHTERNM	719
Db	634	IGLKTDVTDYHIDQVSNLVECLSEFCLDSKXSELSEKVKHAKELSPERNL	7683

RESULT 13

I39838  
parasporal crystal protein - *Bacillus thuringiensis*  
C/Species: *Bacillus thuringiensis*  
C/Date: 19-Jul-1996 #sequence\_revision 19-Jul-1996  
C/Accession: I39838  
R/Hefford, M.A.; Brousseau, R.; Prefontaine, G.; Hanson, J.  
J. Biotechnol. 6, 307-322, 1987  
A/Rittle: Sequence of a lepidopteran toxin gene of *Bacillus thuringiensis*  
A/Reference number: I39838  
A/Accession: I39838  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-1155 <RES>  
A/Cross/relations: UNIPROT:P06578; GB:M37263; NID:900000000  
C/Superfamily: parasporal crystal protein  
C/Keywords: delta-endotoxin

Query Match	38.4%	Score 1443;	DB 2;	Length 1155;
Best Local Similarity	44.1%;	Pred. No. 3.3e-91;		
Matches 313;	Conservative 111;	Mismatches 230;	Indels 56;	Gaps 13
QY	36	NINHEDCLKSEYNVE-PFVSASTQTG-----IGIAGKILGTGVPPAGQVASIYS	87	
		::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::		
Db	4	NNINECIPYNCLSNPEVVLGGERTGTPTIDLSLUTQLLSEF-VFGAGFVLGLAVD	62	
QY	88	FILGELWPKGNQWEIEFWHEVEIIINQKISTYARNKALTDLKGLGDALVAHDSLESWVG	147	
		::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::		
Db	63	IIWGIF---GPSQDAFLVQIELINQRLTEEFARNQAIISLEGLSNLYQIYAESFREWA	119	
QY	148	NNNNTRASRVVKSYIALEMFLVQKI.PSPFAVSGEEVFLLPITYAQANHLHLILLRDAITFG	207	
		::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::		
Db	120	DFTNPALREEMRIQFNDMNSALTATPLFAVQNYQVPILLSVTVOAANHLHSVLRDVSVFG	179	
QY	208	KEWGLSSSEISTFYNRQVERAGDYSVHCVKWYSTGNNIRGTNARSWTYRNQPRDDWTIM	267	

Db 180 QWGFDAATINSRNDLTRLCNTDVAWRVNTGLERWGPDSRDWIRNQFRRLTLT 239  
 QY 268 VLDLVALFPSSYDTQWYPIKTTAQLTREYVYDAIGTVHPHPSFTSTTYNNNAPSFALEA 327  
 Db 240 VLDLVALFPSSYDTQWYPIKTTAQLTREYVYDAIGTVHPHPSFTSTTYNNNAPSFALEA 285  
 QY 328 AV---VRNPHLLDFLEQVTHYLLSRNWKNTQYMMWGGHKLFRITGTT---LAINSTOGS 381  
 Db 286 RIEQNIQPHLMIDILNRIITVDVHRG-----FNWWSGHQITASPVGSGGEFAPFLPGN 340  
 QY 382 TMTSINPVLPTSDVYRTESL-----AGLNLELTQFVNGVPRVDVPHKVFTHPI 432  
 Db 341 AGNAPPPVLVSLTGLIFRTLLSSPLRYRIILGSGPN---NQELFVLDTGTEFSPASLTNL 397  
 QY 433 ASDNPPYAGIGTQLODSENELPPEATQPNYESYSHRLSHIGLISAS-----HVKAL 487  
 Db 398 PSTIYRQGTV-----DSLVDIIPPQNSVPPRAGFSHRLSHVSHVTLMSQAAGAVVTLRAP 450  
 QY 488 VYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVRGPGFTGDIILRTNTGTGDI 547  
 Db 451 TFSWQHSRSEFNIIIPSSQITQIPLTKSTNLGSGTSVVKGPGFTGDIILRTSPQISTL 510  
 QY 548 RVNINPPFAQRYRVRIRYASTTDLQHTSINGKAINQGNFSATMNRGDDLYKTRTVGF 607  
 Db 511 RVNITAPLSQRYRVRIRYASTTDLQHTSINGKAINQGNFSATMNRGDDLYKTRTVGF 570  
 QY 608 TTPFSLDVQSTFTIGAWNFSSGNEVYDRIEFVPEVVEYAEYDEFAEYDRAQKAVNELFTSS 667  
 Db 571 TTPFNSGSSVFTLSAHVFNSGNEVYDRIEFVPEVVEYAEYDEFAEYDRAQKAVNELFTSS 630  
 QY 668 NPGRLKTDVKYHIDQVSNLVECLSEDFCLDEKQELSEKVKHAKLSDERNL 719  
 Db 631 NQIGLKTVDYHIDQVSNLVECLSEDFCLDEKQELSEKVKHAKLSDERNL 682  
 RESULT 15  
 JT0241  
 parasporal crystal protein - Bacillus thuringiensis (strain aizawai IPL7)  
 N;Alternate names: 135K insecticidal protein  
 C;Species: Bacillus thuringiensis  
 C;Date: 23-Aug-1987 #sequence\_revision 23-Aug-1987 #text\_change 09-Jul-2004  
 C;Accession: A22798  
 R;Shibano, Y.; Yamagata, A.; Nakamura, N.; Iizuka, T.; Sugisaki, H.; Takanami, M.  
 Gene 34, 243-251, 1985  
 A;Title: Nucleotide sequence coding for the insecticidal fragment of the Bacillus thurin  
 A;Reference number: A22798; MUID:85232070; PMID:2989108  
 A;Accession: A22798  
 A;Molecule type: DNA  
 A;Residues: 1-934 <SHI>  
 A;Cross-references: UNIPROT:Q9SSV8; GB:M10917; NID:g143100; PIDN:AAA22552.1; PID:g551713  
 C;Comment: The authors translated the codon ACA for residue 264 as Ser.  
 C;Superfamily: parasporal crystal protein  
 C;Keywords: delta-endotoxin  
 Query Match 38.3%; Score 1439.5; DB 2; Length 934;  
 Best Local Similarity 43.3%; Pred. No. 4.1e-91;  
 Matches 308; Conservative 118; Mismatches 22; Indels 61; Gaps 12;  
 QY 36 NINHEDECLMSEYENVE-PFVSASTIQG-----IGIAGKILGTGLVFPAGQVASYLS 87  
 Db 4 NPNINECIPNCLSNPEVEVLGGERIETGYTPIDISLSTQFLSEF-VPGAGFVLGLVD 62  
 QY 88 FILGELWPKGKQWEIFMEHVEEINQKISTYARNKALTDLKGLGDALAVYHDSLESVWG 147  
 Db 63 IIWGIF---GPSQWDAFLVQIQLNRIEENQARQAISRLGLSNLYQIYAESFREWEA 119  
 QY 148 NRNNTARSVKSQVIALELMFVKQLPSFVSGEVEPILPIYAQANLHLLLRDASTFG 207  
 Db 120 DPTNPALREEMRIQFNDMNSALTTPAIPFAVQNYQVPLLSVYVQAANLHLSLRDVSFVG 179  
 QY 208 KEWGLSSSEISTFYNRQVERAGDYSYHCVKYSTGLNLRGTNAESWRYNQFRDMLTM 267  
 Db 180 QWGFDAATINSRNDLTRLCNTDVAWRVNTGLERWGPDSRDWIRNQFRRLTLT 239

QY 268 VLDLVALFPSSYDTQWYPIKTTAQLTREYVYDAIGTVHPHPSFTSTTYNNNAPSFALEA 327  
 Db 240 VLDLVALFPSSYDTQWYPIKTTAQLTREYVYDAIGTVHPHPSFTSTTYNNNAPSFALEA 285  
 QY 328 AV---VRNPHLLDFLEQVTHYLLSRNWKNTQYMMWGGHKLFRITGTT---LAINSTOGS 381  
 Db 286 RIEQNIQPHLMIDILNRIITVDVHRG-----FNWWSGHQITASPVGSGGEFAPFLPGN 340  
 QY 382 TMTSINPVLPTSDVYRTESL-----AGLNLELTQFVNGVPRVDVPHKVFTHPI 432  
 Db 341 AGNAPPPVLVSLTGLIFRTLLSSPLRYRIILGSGPN---NQELFVLDTGTEFSPASLTNL 397  
 QY 433 ASDNPPYAGIGTQLODSENELPPEATQPNYESYSHRLSHIGLISAS-----HVKAL 487  
 Db 398 PSTIYRQGTV-----DSLVDIIPPQNSVPPRAGFSHRLSHVSHVTLMSQAAGAVVTLRAP 450  
 QY 488 VYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVRGPGFTGDIILRTNTGTGDI 547  
 Db 451 TFSWQHSRSEFNIIIPSSQITQIPLTKSTNLGSGTSVVKGPGFTGDIILRTSPQISTL 510  
 QY 548 RVNINPPFAQRYRVRIRYASTTDLQHTSINGKAINQGNFSATMNRGDDLYKTRTVGF 607  
 Db 511 RVNITAPLSQRYRVRIRYASTTDLQHTSINGKAINQGNFSATMNRGDDLYKTRTVGF 570  
 QY 608 TTPFSLDVQSTFTIGAWNFSSGNEVYDRIEFVPEVVEYAEYDEFAEYDRAQKAVNELFTSS 667  
 Db 571 TTPFNSGSSVFTLSAHVFNSGNEVYDRIEFVPEVVEYAEYDEFAEYDRAQKAVNELFTSS 630  
 QY 668 NPGRLKTDVKYHIDQVSNLVECLSEDFCLDEKQELSEKVKHAKLSDERNL 719  
 Db 631 NQIGLKTVDYHIDQVSNLVECLSEDFCLDEKQELSEKVKHAKLSDERNL 682  
 RESULT 15  
 JT0241  
 parasporal crystal protein - Bacillus thuringiensis (strain aizawai IPL7)  
 N;Alternate names: 135K insecticidal protein  
 C;Species: Bacillus thuringiensis  
 C;Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 09-Jul-2004  
 C;Accession: JT0241  
 R;Shimizu, M.; Oshite, K.; Nakamura, K.; Takada, Y.; Oeda, K.; Ohkawa, H.  
 Agric. Biol. Chem. 52, 1565-1573, 1988  
 A;Title: Cloning and expression in Escherichia coli of the 135-kDa insecticidal protein c  
 A;Reference number: JT0241  
 A;Accession: JT0241  
 A;Molecule type: DNA  
 A;Residues: 1-1176 <SHI>  
 A;Cross-references: UNIPROT:P02965  
 A;Note: b. thuringiensis aizawai IPL7 produces similar 130K and 135K insecticidal proteir  
 C;Comment: The 135K protein has insecticidal activity against Plutella xylostella larvae.  
 C;Superfamily: parasporal crystal protein  
 C;Keywords: delta-endotoxin  
 Query Match 38.2%; Score 1438.5; DB 2; Length 1176;  
 Best Local Similarity 43.3%; Pred. No. 6.9e-91;  
 Matches 308; Conservative 117; Mismatches 226; Indels 61; Gaps 12;  
 QY 36 NINHEDECLMSEYENVE-PFVSASTIQG-----IGIAGKILGTGLVFPAGQVASYLS 87  
 Db 4 NPNINECIPNCLSNPEVEVLGGERIETGYTPIDISLSTQFLSEF-VPGAGFVLGLVD 62  
 QY 88 FILGELWPKGKQWEIFMEHVEEINQKISTYARNKALTDLKGLGDALAVYHDSLESVWG 147  
 Db 63 IIWGIF---GPSQWDAFLVQIQLNRIEENQARQAISRLGLSNLYQIYAESFREWEA 119  
 QY 148 NRNNTARSVKSQVIALELMFVKQLPSFVSGEVEPILPIYAQANLHLLLRDASTFG 207  
 Db 120 DPTNPALREEMRIQFNDMNSALTTPAIPFAVQNYQVPLLSVYVQAANLHLSLRDVSFVG 179  
 QY 208 KEWGLSSSEISTFYNRQVERAGDYSYHCVKYSTGLNLRGTNAESWRYNQFRDMLTM 267  
 Db 180 QWGFDAATINSRNDLTRLCNTDVAWRVNTGLERWGPDSRDWIRNQFRRLTLT 239

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Qy 268 VLDLVALPSPYDQMYPIKTTAQLTREYVYDAIGTVHHPSPFTSTWYNNAPSFSAIEA 327
Db 240 VLDLVALPSPYDQMYPIKTTAQLTREYVYDAIGTVHHPSPFTSTWYNNAPSFSAIEA 327
Qy 328 AV---VRNPHLLDLEQVYIYLLSRWSNTQYMMWGHKLEFRTIGT---LNISTQGS 381
Db 286 RIEQNIQPHLMIDLINSITITVDHRG-----FNYSGHQITASPVGSGPEFAFPLFGN 340
Qy 392 TNSINPVTLPTSRDVRTESL-----AGLNLFLTQPVNGVPRVDFHWKFTVTHPI 432
Db 341 AGNAAPPVVLVSLTGLGIFRLLSSPLVRRILILGSPN---NOELFVLDGTEFSPASLTNLT 397
Qy 433 ASDNFPYGVAGIGTQLQDSNELPPEATQGPNYESYSHRLSHIGLISAS-----HYKAL 487
Db 398 PSTIYRQRTV-----DSLVDIFPQDQNSVPPRAGFSHRLSHVMTLSQAAGAVYTLRAP 450
Qy 488 VYSWTHRSADRNTIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRNTGTGFDI 547
Db 451 TFSQWCHRSAEFNNILPSSQITQIPLTKSTNLGSGTSVVRGPGFTGGDILRRNTGTGFDI 510
Qy 548 RVNINPFAORYRIRIYASTDLQFHTSINGKAINQNFSAIINQNGEDLDYKTFRTVGF 607
Db 511 RVNITAPLSORYRIRIYASTNLQFHTSIDGRFINQNFSAIINQNGEDLDYKTFRTVGF 570
Qy 608 TTPESFLDVOSTFTIGAWNFSSGNEVYIDRIEFVVPVETVYEAEDPEKAEKVTAFTST 667
Db 571 TTPNFNGSGSVFTLSAHVFNNGNEVYIDRIEFVPAEVTPEAEYDLERAQKAVNELFTSS 630
Qy 668 NPGKLTVDKVDYHIDQVSNLVESLSDEFYLDKRELFPEIVKYANELHIERNM 719
Db 631 NOIGLKTVDYHIDQVSNLVESLSDEFYLDKRELFPEIVKYANELHIERNM 719

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Search completed: October 28, 2004, 18:31:52  
 Job time : 21.191 secs





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Query Match      99.4%; Score 3739; DB 3; Length 719;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 715; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MKLNQDKHQFSSNAKVDKISTDSLNKNETDIELQNHEDCLKMSYENVEPVSASTI 60
DB 1 MKLNQDKHQFSSNAKVDKISTDSLNKNETDIELQNHEDCLKMSYENVEPVSASTI 60

QY 61 QTGIGIAGKILGTLGVPFAGQVASYLSFILGELWPKGNQWEIEMHVEELINQKISTYA 120
DB 61 QTGIGIAGKILGTLGVPFAGQVASYLSFILGELWPKGNQWEIEMHVEELINQKISTYA 120

QY 121 RNKALTDLKGDLAVYHDSLESWGNRNTRARSVVKSQYIALELMFVQKLSFVAVSG 180
DB 121 RNKALTDLKGDLAVYHDSLESWGNRNTRARSVVKSQYIALELMFVQKLSFVAVSG 180

QY 181 BEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWS 240
DB 181 BEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWS 240

QY 241 TGLNLRGTNABSWRVYRQFRDMLMVLDLVALFPSYDTQWPIKTTAQLTREYVYDAI 300
DB 241 TGLNLRGTNABSWRVYRQFRDMLMVLDLVALFPSYDTQWPIKTTAQLTREYVYDAI 300

QY 301 GTVHPHPSFTSTWYNNAPSSAIEAAVVRNPHLLDLEQVTTIYSLLSRWSNTQYNNMW 360
DB 301 GTVHPHPSFTSTWYNNAPSSAIEAAVVRNPHLLDLEQVTTIYSLLSRWSNTQYNNMW 360

QY 361 GGHKLEFRITGTLNISTCGSNTSINPVTLPFTSRDVRTESLAGLNLFLTQPVNGVPR 420
DB 361 GGHKLEFRITGTLNISTCGSNTSINPVTLPFTSRDVRTESLAGLNLFLTQPVNGVPR 420

QY 421 VDFHMKFVTHPIASDNFYYPGAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLIS 480
DB 421 VDFHMKFVTHPIASDNFYYPGAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLIS 480

QY 481 ASHVKALVSWTHRSADRNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
DB 481 ASHVKALVSWTHRSADRNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540

QY 541 TGTFGDIRVNIAPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATNWRGEDLDYK 600
DB 541 TGTFGDIRVNIAPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATNWRGEDLDYK 600

QY 601 TPTVGTFTPPFSLDVQSTFTIGAMNFSNGNEVIYDRIEFVPEVTEAEYDFEKAQEKV 660
DB 601 TPTVGTFTPPFSLDVQSTFTIGAMNFSNGNEVIYDRIEFVPEVTEAEYDFEKAQEKV 660

QY 661 TALFTSTNPRGLKTDVQYHIDQVSNLVESLSDEFLDEKRELFEIVKYANELHIERNM 719
DB 661 TALFTSTNPRGLKTDVQYHIDQVSNLVESLSDEFLDEKRELFEIVKYANELHIERNM 719

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RESULT 2
US-09-661-322A-42
; Sequence 42, Application US/09661322A
; Patent No. 6593293
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Chu, Chih-Rei
; APPLICANT: Donovan, William P.
; APPLICANT: Gilmer, Amy J.
; APPLICANT: Ruper, Mark J.
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin Compo
; FILE REFERENCE: MECO201
; CURRENT APPLICATION NUMBER: US/09/661,322A
; CURRENT FILING DATE: 2000-09-13
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 42
; LENGTH: 710
; TYPE: PRI

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; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (200)...(200)
; OTHER INFORMATION: No. 6593293-Coding
US-09-661-322A-42

Query Match      92.0%; Score 3459.5; DB 4; Length 710;
Best Local Similarity 92.1%; Pred. No. 2.2e-301;
Matches 662; Conservative 16; Mismatches 32; Indels 9; Gaps 1;

QY 1 MKLNQDKHQFSSNAKVDKISTDSLNKNETDIELQNHEDCLKSEYENVEPVSASTI 60
DB 1 MKLNQDKHQFSSNAKVDKISTDSLNKNETDIELQNHEDCLKSEYENVEPVSASTI 51

QY 61 QTGIGIAGKILGTLGVPFAGQVASYLSFILGELWPKGNQWEIEMHVEELINQKISTYA 120
DB 61 QTGIGIAGKILGTLGVPFAGQVASYLSFILGELWPKGNQWEIEMHVEELINQKISTYA 111

QY 121 RNKALTDLKGDLAVYHDSLESWGNRNTRARSVVKSQYIALELMFVQKLSFVAVSG 180
DB 121 RNKALTDLKGDLAVYHDSLESWGNRNTRARSVVKSQYIALELMFVQKLSFVAVSG 171

QY 181 BEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWS 240
DB 181 BEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWS 231

QY 241 TGLNLRGTNABSWRVYRQFRDMLMVLDLVALFPSYDTQWPIKTTAQLTREYVYDAI 300
DB 241 TGLNLRGTNABSWRVYRQFRDMLMVLDLVALFPSYDTQWPIKTTAQLTREYVYDAI 291

QY 301 GTVHPHPSFTSTWYNNAPSSAIEAAVVRNPHLLDLEQVTTIYSLLSRWSNTQYNNMW 360
DB 301 GTVHPHPSFTSTWYNNAPSSAIEAAVVRNPHLLDLEQVTTIYSLLSRWSNTQYNNMW 351

QY 361 GGHKLEFRITGTLNISTCGSNTSINPVTLPFTSRDVRTESLAGLNLFLTQPVNGVPR 420
DB 361 GGHKLEFRITGTLNISTCGSNTSINPVTLPFTSRDVRTESLAGLNLFLTQPVNGVPR 411

QY 421 VDFHMKFVTHPIASDNFYYPGAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLIS 480
DB 421 VDFHMKFVTHPIASDNFYYPGAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLIS 471

QY 481 ASHVKALVSWTHRSADRNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
DB 481 ASHVKALVSWTHRSADRNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 531

QY 541 TGTFGDIRVNIAPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATNWRGEDLDYK 600
DB 541 TGTFGDIRVNIAPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATNWRGEDLDYK 591

QY 601 TPTVGTFTPPFSLDVQSTFTIGAMNFSNGNEVIYDRIEFVPEVTEAEYDFEKAQEKV 660
DB 601 TPTVGTFTPPFSLDVQSTFTIGAMNFSNGNEVIYDRIEFVPEVTEAEYDFEKAQEKV 651

QY 661 TALFTSTNPRGLKTDVQYHIDQVSNLVESLSDEFLDEKRELFEIVKYANELHIERNM 719
DB 661 TALFTSTNPRGLKTDVQYHIDQVSNLVESLSDEFLDEKRELFEIVKYANELHIERNM 710

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RESULT 3
US-08-286-870A-4
; Sequence 4, Application US/08286870A
; Patent No. 6063605
; GENERAL INFORMATION:
; APPLICANT: ELY, S
; APPLICANT: TAILOR, RH
; APPLICANT: TIPPETT, JM
; APPLICANT: BLENN, RG
; TITLE OF INVENTION: BACTERIAL GENES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DABRY & CUSHMAN

```



ADDRESSEE: Intellectual Property Group of  
ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP  
STREET: 1100 New York Avenue, N.W.  
City: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3918  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/286,870A  
FILING DATE: 05-AUG-1994  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/520228  
FILING DATE: 09-MAY-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 8910624.9  
FILING DATE: 09-MAY-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: PAUL N. KOKULIS  
REGISTRATION NUMBER: 16,773  
REFERENCE/DOCKET NUMBER: 70608/220720  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 861-3000  
TELEFAX: (202) 822-0944  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 648 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-286-870A-4

Query Match 90.1%; Score 3389; DB 3; Length 648;  
Best Local Similarity 99.8%; Pred. No. 4.1e-255;  
Matches 647; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRLKQDKHQSFSNAKVDKISTSLKNETDIELONINHEDECLKMSYENVEPVSASTI 60  
DB 1 MRLKQDKHQSFSNAKVDKISTSLKNETDIELONINHEDECLKMSYENVEPVSASTI 60  
QY 61 QTGIGIAGKILGTGVFPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
DB 61 QTGIGIAGKILGTGVFPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
QY 121 RNKALTDLKGIDALAVYHDSLESWGVRNNTARSVVKSQYIALELMFVKLPSPAVSG 180  
DB 121 RNKALTDLKGIDALAVYHDSLESWGVRNNTARSVVKSQYIALELMFVKLPSPAVSG 180  
QY 181 BEVPLLPYIAQAANLHLLILDASIFGKWLGLSSSEISTFYNQVERAGDYSYHCVKWTYS 240  
DB 181 BEVPLLPYIAQAANLHLLILDASIFGKWLGLSSSEISTFYNQVERAGDYSYHCVKWTYS 240  
QY 241 TGLNLRGNTNAESWVRNQFRDMLVLDLVALFPSYDTQMPYIKTTAOLREVYTDAL 300  
DB 241 TGLNLRGNTNAESWVRNQFRDMLVLDLVALFPSYDTQMPYIKTTAOLREVYTDAL 300  
QY 301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSWSNTQYNNW 360  
DB 301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSWSNTQYNNW 360  
QY 361 GGHKLEPRTTGGTUNISTQSTNTSINPVLPTFSRDVYTESLAGINLFLTOPVNGVR 420  
DB 361 GGHKLEPRTTGGTUNISTQSTNTSINPVLPTFSRDVYTESLAGINLFLTOPVNGVR 420  
QY 421 VDFHWKVTPIASDNFYPGYAGIGTQLODSENELPPEATGPQNYESYSHRLSHIGLIS 480  
DB 421 VDFHWKVTPIASDNFYPGYAGIGTQLODSENELPPEATGPQNYESYSHRLSHIGLIS 480

QY 481 ASHVKALVSWTHRSADRNTTIEPNSITQIPLVKAFNLSSGAAVVRGPGTGDILRRTN 540  
DB 481 ASHVKALVSWTHRSADRNTTIEPNSITQIPLVKAFNLSSGAAVVRGPGTGDILRRTN 540  
QY 541 TGTFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAWMRGEDLDYK 600  
DB 541 TGTFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAWMRGEDLDYK 600  
QY 601 TFRVTGFTTFFSFLDVQSTFTIGANFSSGNEVYIDRIEFVPEVYIE 648  
DB 601 TFRVTGFTTFFSFLDVQSTFTIGANFSSGNEVYIDRIEFVPEVYIE 648

## RESULT 4

US-09-003-217-2  
Sequence 2, Application US/09003217  
Patent No. 5986177  
GENERAL INFORMATION:  
APPLICANT: Osman, Yehia A.  
APPLICANT: Madkour, Magdy A.  
APPLICANT: Bulla, Lee A.  
TITLE OF INVENTION: BACILLUS THURINGIENSIS ISOLATES WITH  
TITLE OF INVENTION: BROAD SPECTRUM ACTIVITY  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: W. Murray Spruill (Alston & Bird, LLP)  
STREET: 3605 Glenwood Ave. Suite 310  
CITY: Raleigh  
STATE: NC  
COUNTRY: US  
ZIP: 27622  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/003,217  
FILING DATE:  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Spruill, W. Murray  
REGISTRATION NUMBER: 32,943  
REFERENCE/DOCKET NUMBER: 5718-3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 919 420 2202  
TELEFAX: 919 881 3175  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 719 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-003-217-2

Query Match 89.8%; Score 3379; DB 2; Length 719;  
Best Local Similarity 89.7%; Pred. No. 3.8e-294;  
Matches 645; Conservative 34; Mismatches 40; Indels 0; Gaps 0;

QY 1 MRLKQDKHQSFSNAKVDKISTSLKNETDIELONINHEDECLKMSYENVEPVSASTI 60  
DB 1 MRLKQDKHQSFSNAKVDKISTSLKNETDIELONINHEDECLKMSYENVEPVSASTI 60  
QY 61 QTGIGIAGKILGTGVFPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
DB 61 QTGIGIAGKILGTGVFPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
QY 121 RNKALTDLKGIDALAVYHDSLESWGVRNNTARSVVKSQYIALELMFVKLPSPAVSG 180  
DB 121 RNKALTDLKGIDALAVYHDSLESWGVRNNTARSVVKSQYIALELMFVKLPSPAVSG 180  
QY 181 BEVPLLPYIAQAANLHLLILDASIFGKWLGLSSSEISTFYNQVERAGDYSYHCVKWTYS 240  
DB 181 BEVPLLPYIAQAANLHLLILDASIFGKWLGLSSSEISTFYNQVERAGDYSYHCVKWTYS 240

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Db 181 BEVPLLPYQAANLHLLLRDASIFKKNGLSASEISTFYNRQVERTRDYSYHCVKWNN 240
QY 241 TGLNNLRGTNAESWRYNQFRDMTLMVLDAVALFPGVDQMYPIKTTAQTREVTYDAI 300
Db 241 TGLNNLRGTNAESWRYNQFRDMTLMVLDAVALFPGVDQMYPIKTTAQTREVTYDAI 300
QY 301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVITYSLLSRWSTQYNNMW 360
Db 301 GTVDPNQALRSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVITYSLLSRWSTQYNNMW 360
QY 361 GGHKLEFRTIGTINISSTQGSTNTSINPVTLPFTSRDVRYSAGLNLFLTOPVNGVPR 420
Db 361 GGHKLEFRTIGTINISSTQGSTNTSINPVTLPFTSRDVRYSAGLNLFLTOPVNGVPR 420
QY 421 VDFHMKFVTHPIASDNFYYPGAGIGTOLQDSENELPPEATGQPNYESYSHRLSHIGLIS 480
Db 421 VDFHMKFVTHPIASDNFYYPGAGIGTOLQDSENELPPEATGQPNYESYSHRLSHIGLIS 480
QY 481 ASHVKALVYSWTHRSADRTNTEPNISITQIPLVKAFNLSGAAVVRGPGFTGGDILRTN 540
Db 481 GSHVKALVYSWTHRSADRTNTEPNISITQIPLVKAFNLSGAAVVRGPGFTGGDILRTK 540
QY 541 TGTGFGDIRVNIWPPPAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDDLYK 600
Db 541 SGTFGHIRVNIWPPPAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDDLYK 600
QY 601 TFRTVGFTTPFSFSDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVVEYAEYDFEKAQEKV 660
Db 601 TFRTVGFTTPFSFSDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVVEYAEYDFEKAQEKV 660
QY 661 TALFTSTNPRGLKTDVKYHIDQVSNLVSDEFLYDEKELFEIVKAYANELHIERNM 719
Db 661 TALFTSTNPRGLKTDVKYHIDQVSNLVSDEFLYDEKELFEIVKAYANELHIERNM 719

RESULT 5
US-09-218-942-2
; Sequence 2, Application US/09218942
; Patent No. 6232439
; GENERAL INFORMATION:
; APPLICANT: Osman, Yehia
; TITLE OF INVENTION: Bacillus Thuringiensis Isolates with Broad Spectrum
; FILE REFERENCE: Cxvli
; CURRENT APPLICATION NUMBER: US/09/218,942
; CURRENT FILING DATE: 1998-12-22
; EARLIER APPLICATION NUMBER: 60/035,361
; EARLIER FILING DATE: 1997-01-10
; EARLIER APPLICATION NUMBER: 09/003,217
; EARLIER FILING DATE: 1998-01-06
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 719
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-09-218-942-2

Query Match 89.7%; Score 3374; DB 3; Length 719;
Best Local Similarity 89.7%; Pred. No. 1,1e-293;
Matches 645; Conservative 34; Mismatches 40; Indels 0; Gaps 0;

QY 1 MKLKNQDQKHQSFSSNAKVDKISTDSLKNETDIELQNIHEDCLKMSYENVPEVFSASTI 60
Db 1 MKLKNQDQKHQSFSSNAKVDKISTDSLKNETDIELQNIHEDCLKMSYENVPEVFSASTI 60
QY 61 QTGIGIAGKILGTGLVPPAGQVASYLSFTLSEKLPKGNQWEIEMHVEEIIINOKISTYA 120
Db 61 QTGIGIAGKILGTGLVPPAGQVASYLSFTLSEKLPKGNQWEIEMHVEEIIINOKISTYA 120
QY 121 RNKALTDLKLGDALAVHDSLESVGNRNNTNRASVVKVQSYIALELMFVKLPFSFVSG 180
Db 121 RNKALTDLKLGDALAVHDSLESVGNRNNTNRASVVKVQSYIALELMFVKLPFSFVSG 180

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## RESULT 6

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US-08-286-870A-6
; Sequence 6, Application US/08286870A
; Patent No. 603605
; GENERAL INFORMATION:
; APPLICANT: ELY, S
; APPLICANT: TAILOR, RH
; APPLICANT: TIPPETT, JM
; APPLICANT: BLENK, RG
; TITLE OF INVENTION: BACTERIAL GENES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DABY & CUSHMAN
; ADDRESSEE: Intellectual Property Group of
; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMEUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/286,870A
; FILING DATE: 05-AUG-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/520228
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 8910624.9
; FILING DATE: 09-MAY-1989

```

ATTORNEY/AGENT INFORMATION:  
NAME: PAUL N. KOKULIS  
REGISTRATION NUMBER: 16,773  
REFERENCE/DOCKET NUMBER: 70608/220720  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 861-3000  
TELEFAX: (202) 822-0944  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 535 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-286-870A-6

Query Match 74.3%; Score 2795; DB 3; Length 535;  
Best Local Similarity 99.8%; Pred. No. 6e-242;  
Matches 534; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MKLNQKHQSFSSNAKVDKISTDSLNKEDIELQINHHEDCLKMSYENVEPVSASTI 60  
Db 1 MKLNQKHQSFSSNAKVDKISTDSLNKEDIELQINHHEDCLKMSYENVEPVSASTI 60  
Qy 61 QTGIGIAGKILGTGVFPAGQVASYLFIIGELWPKGNQWEIEMHEVEEIIINOKISTYA 120  
Db 61 QTGIGIAGKILGTGVFPAGQVASYLFIIGELWPKGNQWEIEMHEVEEIIINOKISTYA 120  
Qy 121 RNKALTDKLGDAVYHDSLESWGNNRNNTRARSVVKSYQYIALELMFVKLPSPAVSG 180  
Db 121 RNKALTDKLGDAVYHDSLESWGNNRNNTRARSVVKSYQYIALELMFVKLPSPAVSG 180  
Qy 181 EEPVLLPIYQAANLHLLRDASIFGKWLSSSEISTFYNQVERAGDYSHCVKWKYS 240  
Db 181 EEPVLLPIYQAANLHLLRDASIFGKWLSSSEISTFYNQVERAGDYSHCVKWKYS 240  
Qy 241 TGLNLRGTNAESWVRVYNQFRDMLTMDLVALFPSSYDQMPYIKTTAQLTREVTDAI 300  
Db 241 TGLNLRGTNAESWVRVYNQFRDMLTMDLVALFPSSYDQMPYIKTTAQLTREVTDAI 300  
Qy 301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYLLSRWSNTQYNNMW 360  
Db 301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYLLSRWSNTQYNNMW 360  
Qy 361 GGHKLEPRTTGGTLNISTQSTNTSINPVTLPFTSRDVRVYTESLAGNLFLTOPVNGVPR 420  
Db 361 GGHKLEPRTTGGTLNISTQSTNTSINPVTLPFTSRDVRVYTESLAGNLFLTOPVNGVPR 420  
Qy 421 VDFHWKVTTHPIASDNFYPCYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
Db 421 VDFHWKVTTHPIASDNFYPCYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
Qy 481 ASHVKALVYSWTHRSADRTNTIBPNSITQPLVKAFLNLSGAAVVRGPGFTGGDI 535  
Db 481 ASHVKALVYSWTHRSADRTNTIBPNSITQPLVKAFLNLSGAAVVRGPGFTGGDI 535

RESULT 7  
US-08-100-709-4  
Sequence 4, Application US/08100709  
Patent No. 532687  
GENERAL INFORMATION:  
APPLICANT: Donovan, William P.  
APPLICANT: Tan, Yiping  
APPLICANT: Jany, Christine S.  
APPLICANT: Gonzalez Jr., Jose M.  
TITLE OF INVENTION: BACILLUS THURINGIENSIS CRYET4 AND CRYET5  
TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.  
ADDRESSEE: Nadel  
STREET: 1601 Market Street, 36th Floor  
CITY: Philadelphia

STATE: Pennsylvania  
COUNTRY: U.S.A.  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/100,709  
FILING DATE: 19930729  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Egolf, Christopher  
REGISTRATION NUMBER: 27633  
REFERENCE/DOCKET NUMBER: 7205-49  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-757-1590  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1229 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-100-709-4

Query Match 64.8%; Score 2437.5; DB 1; Length 1229;  
Best Local Similarity 65.4%; Pred. No. 2.8e-209;  
Matches 469; Conservative 90; Mismatches 141; Indels 17; Gaps 6;

Qy 13 SSNAKVDKISTDSLNK-ETDIELQ-NHHEDCLKMSYENVEPVSASTIQTGIGIAGKI 70  
Db 7 NENEINALSIFTVSNPSTQMNLSPDARIEDSLCAEVNNDIPFVSASTVQTGGINIAGRI 66  
Qy 71 LGTLGVFPAGQVASYLFIIGELWPKGNQWEIEMHEVEEIIINOKISTYARNKALTDLKG 130  
Db 67 LGVLGVFPAGQVASYLFIIGELWPKGNQWEIEMHEVEEIIINOKISTYARNKALTDLKG 126  
Qy 131 LGDALAVYHDSLESWGNNRNNTRARSVVKSYQYIALELMFVKLPSPAVSGEVPILPIYA 190  
Db 127 LGRGYSYQQALETWLDNRNDARSIIERYVALELDITTAIPLFRIRNEBEPVLLMVYA 186  
Qy 191 QAANLHLLLRDASIFGKWLSSSEISTFYNQVERAGDYSHCVKWSYGLNLRGTN 250  
Db 187 QAANLHLLLRDASIFGKWLSSSEISTFYNQVERAGDYSHCVKWSYGLNLRGTN 246  
Qy 251 AESWYRNQFRDMLTMDLVALFPSSYDQMPYIKTTAQLTREVTDAIQTGTHPHPSFT 310  
Db 247 AESWLRVYNQFRDMLTMDLVALFPSSYDQMPYIKTTAQLTREVTDAIQTGTHPHPSFT 306  
Qy 311 STTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYLLSRWSNTQYNNMWGKLEPRTI 370  
Db 307 STTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYLLSRWSNTQYNNMWGKLEPRTI 366  
Qy 371 GGTALNISTQSTNTSINPVTLPFTSRDVRVYTESLAGNLFLTOPVNGVPRVDFHWKFT 429  
Db 367 GGTALNISTQSTNTSINPVTLPFTSRDVRVYTESLAGNLFLTOPVNGVPRVDFHWKFT 422  
Qy 430 HPIASDNFYPCYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 482  
Db 423 --INPQNTYERGATTYSQYQGVIGLDFSETLPETTERPNTYESYSHRLSHIGLIS 480  
Qy 483 HVKALVYSWTHRSADRTNTIBPNSITQPLVKAFLNLSGAAVVRGPGFTGGDILRRNTG 542  
Db 481 TLRAVYSWTHRSADRTNTIBPNSITQPLVKAFLNLSGAAVVRGPGFTGGDILRRNTG 540  
Qy 543 TFGDIRVNNPPFAQRVRYRYASTTDLQFHTSINGKAINCGNPFSAFMMRGEGLDYKTF 602  
Db 541 TFGDIRLNNVPLSQRVRYRYASTTDLQFHTSINGKAINCGNPFSAFMMRGEGLDYKTF 600  
Qy 603 RTVGFTTTPSFIDVOSTETIGAMFSSCNVEYIDRIEFPVPEVTEYAEYDEKAEKVTA 662  
Db 601 RTAGFTTFNLAQSTITLGAQSFSN-QEYIIDRVEFPVPAEYFEAYIDLERAKAVNA 659

QY 663 LFTSTNPRGLKTDVNDYHIDQVSNLVSLSDEFYLDKRELFEIVKYANELHIERNM 719  
 DB 660 LFTSTNPRGLKTDVNDYHIDQVSNVACLSDFCDEKRELFEIVKYAKLSDERNL 716

RESULT 8  
 US-08-176-865-4  
 ; Sequence 4, Application US/08176865  
 ; Patent No. 5616319  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Donovan, William P.  
 ; APPLICANT: Tan, Yiping  
 ; APPLICANT: Jany, Christine S.  
 ; APPLICANT: Gonzalez Jr., Jose M.  
 ; TITLE OF INVENTION: BACILLUS THURINGIENSIS cryET4 AND cryET5  
 ; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS  
 ; NUMBER OF SEQUENCES: 5  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.  
 ; ADDRESS: Nadel  
 ; STREET: 1601 Market Street, 36th Floor  
 ; CITY: Philadelphia  
 ; STATE: Pennsylvania  
 ; COUNTRY: U.S.A.  
 ; ZIP: 19103  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent in Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/176,865  
 ; FILING DATE: 30-DEC-1993  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/100,709  
 ; FILING DATE: 29-JUL-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Egoif, Christopher  
 ; REGISTRATION NUMBER: 27633  
 ; REFERENCE/DOCKET NUMBER: 7205-49  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 215-757-1590  
 ; INFORMATION FOR SEQ ID NO: 4:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1229 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-176-865-4

Query Match 64.8%; Score 2437.5; DB 1; Length 1229;  
 Best Local Similarity 65.4%; Pred No. 2.8e-209;  
 Matches 469; Conservative 90; Mismatches 141; Indels 17; Gaps 6;

QY 13 SSNAKVDKISTDSLKN-ETDIELQ-NINHEBCLQXSEYENVEPFFVASTIQTGIGAKI 70  
 DB 7 NENEINALSIPTVSNPSTQMLSPDARIEDSLCVAEVNNDPPFVASTVQTGINIAGRI 66

QY 71 LGTLGVPRAGVASYSLTGLWPKGNQWEIEMHVEELINOKISTYARKALTDLKG 130  
 DB 67 LGVLGVPPAGVQASYSFLVGLWPSGRDPWEIFLHVQIRQVNTENTAIARLEG 126

QY 131 LGDALAVHDSLESVWGNRNTTRARSVVKQSYIALELMFVQKLPSPFAVSGEVELLPYIA 190  
 DB 127 LCGYRSYQQALETWLDNENDARSIIILRYVALELOITTAIPLFRIRNEVEVLLMYVA 186

QY 191 QANLHLLLRDASTFGKWLGSLSSEISTFFYNQVERAGDYSHCVKYSTGLNNLRGTN 250  
 DB 187 QANLHLLLRDASLFGSEWGSASSDVNQYQEQEIRYITEYSNHCVMQNTGLNNLRGTN 246

QY 251 AESSWRYNQFRDMLVLWDLVALFPSTQMPYIKTTAQLTREYVYTDALGTVHPHPSFT 310

DB 247 AESSWRYNQFRDMLVLWDLVALFPSTQMPYIKTTAQLTREYVYTDALGTVHPHPSFT 306  
 QY 311 STTWNNNAPSFAIEAAVVRNPHLLDFLEQVITYSLLSRWSNTQYMMWGGHKLFEFTI 370  
 DB 307 STWNNNAPSFAIEAAIFRPPHLLDFPEQLTIYSASSRWSSTQHMNYVWGHRLNPRPI 366

QY 371 GGTLMISTQGST-NTSINPVLPTSRDYYRTESLAGLNLFTQPVNGVPRVDHKKVFT 429  
 DB 367 GGTLMISTQGST-NTSINPVLPTSRDYYRTESLAGLNLFTQPVNGVPRVDHKKVFT 422

QY 430 HPIASDNFYPG-----YAGIGTQLQDSENEPPEATGQPNYESYSHRLSHIGLISAS 482  
 DB 423 --INQNIYERGATYTSQPYQGVGLQDFDSETELPETTERPNYESYSHRLSHIGLIIGN 480

QY 483 HVKALVYSWTHRSADRTNTIENSITQPLVKAFNLSSGAAVVPGPGTGGDILRRNTG 542  
 DB 481 TLRAPVYSWTHRSADRTNTIGENRITQPLVKALNLHSGVTYVGGPGTGGDILRRNTG 540

QY 543 TFGDIRVNINPPFAQRYRVIRYASTTDLQPHTSINGKAINQGNESATWNRGDEDLYKTF 602  
 DB 541 TFGDIRVNINPVSQRYRVIRYASTTDLQPHTSINGKAINQGNESATWNRGDNLEYRSP 600

QY 603 RTVGFTTSPFLDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVITYEAYDDEKAEKYTA 662  
 DB 601 RTAGFTSPFLNQAQSTFTLGAQSPSN-QEVYIDRVFVPAEVTFEASYDLERAKAYNA 659

QY 663 LFTSTNPRGLKTDVNDYHIDQVSNLVSLSDEFYLDKRELFEIVKYANELHIERNM 719  
 DB 660 LFTSTNPRGLKTDVNDYHIDQVSNVACLSDFCDEKRELFEIVKYAKLSDERNL 716

RESULT 9  
 US-08-474-038-4  
 ; Sequence 4, Application US/08474038  
 ; Patent No. 5679343  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Donovan, William P.  
 ; APPLICANT: Tan, Yiping  
 ; APPLICANT: Jany, Christine S.  
 ; APPLICANT: Gonzalez Jr., Jose M.  
 ; TITLE OF INVENTION: BACILLUS THURINGIENSIS cryET4 AND cryET5  
 ; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS  
 ; NUMBER OF SEQUENCES: 5  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.  
 ; ADDRESS: Nadel  
 ; STREET: 1601 Market Street, 36th Floor  
 ; CITY: Philadelphia  
 ; STATE: Pennsylvania  
 ; COUNTRY: U.S.A.  
 ; ZIP: 19103  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent in Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/474,038  
 ; FILING DATE: 07-JUN-1995  
 ; CLASSIFICATION: 514  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/176,865  
 ; FILING DATE: 30-DEC-1993  
 ; APPLICATION NUMBER: US 08/100,709  
 ; FILING DATE: 29-JUL-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Egoif, Christopher  
 ; REGISTRATION NUMBER: 27633  
 ; REFERENCE/DOCKET NUMBER: 7205-49  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 215-757-1590  
 ; INFORMATION FOR SEQ ID NO: 4:

```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 1229 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-474-038-4

Query Match      64.8%; Score 2437.5; DB 1; Length 1229;
Best Local Similarity 65.4%; Pred. No. 2.8e-209;
Matches 469; Conservative 90; Mismatches 141; Indels 17; Gaps 6;

QY 13 SSNAKVDKISDLSKN-ETDIQLQ-NINHEDCLMKSEYENVEPFVSASTIQTGIGIAGKI 70
DB 7 NENEIINALSIPTVSNPSTQNLSPDARIEDSLCVAEVNNDIPFVSASTVTGTGINIAGRI 66
QY 71 LGTLGVPPAGVASLYSIFILGELWPKGNQWEIFMEHVBEIINQKISTYARNKALTDLKG 130
DB 67 LGLVLGVPPAGQASFYSLFGELWPGRDPWEIFLEHVEQLIRQQVTTENTRTAIARLEG 126
QY 131 LGDALAVYHDSLESWGNNRNRARSVKQSQAIALELMFVKLPSPFAVGSEVPLLPIYA 190
DB 127 LGRYSYQOALETWLDNRDARSIIILERYVALELDITTAIPLFRIRNEEVPMLMVA 186
QY 191 QAAHLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSHCVKWYSTGLNNLRGTN 250
DB 187 QAAHLHLLLRDASIFGSEWGMASSDVNQYYQEQIRYTEESNHCVQWYNTGLNNLRGTN 246
QY 251 AESWRYNOFRDMTLMVLIDLVALFPSYDTOMYPKITTAQLTRVYTDAIGTVHPHSFT 310
DB 247 AESWLRYNOFRDLTGVLIDLVALFPSYDTRTPINTSAQLTREIYTDPIGRTNAPSGA 306
QY 311 STTWYNNAFSAIEAAYVRNPRLDLEQVTIYSLSRWSNTQYMMNGGHKLEFRTI 370
DB 307 STNWENNAPSFSAIEAAIFRPPLLDDPEQLTIYSASSRWSSQHWMNYVGHLENERPI 366
QY 371 GGTNLNSTOGST-NTSINPVLTFTSDRVYRTESLAGNLFLTQPVGNGVRPDRPHWKFTV 429
DB 367 GGTNLNSTOGLTNNTSINPVLTFTSDRVYRTESLAGNLFLTQPVGNGVRPDRPHWKFTV 422
QY 430 HPIASDNFFYPG-----YAGIGTOLQODSENELPPEATGOPNVESYSHRLSHIGLISAS 482
DB 423 --INPNIVYERATTYSQPYQGVIQLFSETLPPETERPNVESYSHRLSHIGLIIGN 480
QY 483 HVKALVSWTHRSADRTNIETPSITQIPLVKAFNLSSGAAYVRPGPFTGGDILLRRTNTG 542
DB 481 TLRAPVYSWTHRSADRTNITGNRTIQIPLVKALNLHSGVTYVVGPGFTGGDILLRRTNTG 540
QY 543 TEGDIRVNLPFAQRVRYRIRYASTTDLQPHTSINGKAINGNFSAHWARGEDLDYKTF 602
DB 541 TEGDIRLNINVLPSORVRYRIRYASTTDLQPHTRINGTNVIGNFSFWARGDNLEYRSF 600
QY 603 RTVGFTPTPSFLDVOSTFTIGAMFNSSGNEVVDIRIEFPVVEVYAEYDFPERAQEKVTA 662
DB 601 RTAGFSTPENFLNAOSTFTPLGAQSFN-QEYVIDRVEFPVAEYDFEAEDLERAKAVNA 659
QY 663 LTSNTNPRGLKTVDKYHDIDQSVNLVESLSDEFPYLDEKRELFEIKYVANELLHERNM 719
DB 660 LFTSTNPRELKTVDYHDIDQSVNMVACLSEDFCLDEKRELFEXKVYAKRLSDERNL 716

RESULT 10
US-08-779-046-4
; Sequence 4, Application US/08779046
; Patent No. 5854053
; GENERAL INFORMATION:
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yiping
; APPLICANT: Jany, Christine S.
; APPLICANT: Gonzalez Jr., Jose M.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS cryET4 AND cryET5
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:

```

543 TFGDIRVNINPPAQRVIRYASTTDLQFHTSINGKAINOGNFSATMREGDLDYKTF 602  
 541 TFGDIRVNINPPAQRVIRYASTTDLQFHTSINGKAINOGNFSATMREGDLDYKTF 600  
 603 RTVGFTTFFSFLDVOSTTIGAMFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKVTA 662  
 601 RTAGFSTFPELNAQSTFLLGAQFSN-QEYVIDRVEFVPAEVTFEAEYDLERAQKAVNA 659  
 663 LFTSTNPRGLTKVDYHIDQVSNVACLSDFCLDEKRELFEVKYAKRLSDERNL 716  
 660 LFTSTNPRGLTKVDYHIDQVSNVACLSDFCLDEKRELFEVKYAKRLSDERNL 716

RESULT 11  
 US-08-881-340-4  
 ; Sequence 4, Application US/08881340  
 ; Patent No. 5942658  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Donovan, William P.  
 ; APPLICANT: Tan, Yiping  
 ; APPLICANT: Gan, Christine S.  
 ; APPLICANT: Gonzalez Jr., Jose M.  
 ; TITLE OF INVENTION: BACILLUS THURINGIENSIS CRYET4 AND CRYET5  
 ; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS  
 ; NUMBER OF SEQUENCES: 5  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.  
 ; STREET: 1601 Market Street, 36th Floor  
 ; CITY: Philadelphia  
 ; STATE: Pennsylvania  
 ; COUNTRY: U.S.A.  
 ; ZIP: 19103  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent in Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/881,340  
 ; FILING DATE: 24-JUN-1997  
 ; CLASSIFICATION: 424  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/100,709  
 ; FILING DATE: 29-JUL-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Egolf, Christopher  
 ; REGISTRATION NUMBER: 27633  
 ; REFERENCE/DOCKET NUMBER: 7205-49  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 215-757-1590  
 ; INFORMATION FOR SEQ ID NO: 4:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1229 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: Protein  
 ; US-08-881-340-4

Query Match 64.8%; Score 2437.5; DB 2; Length 1229;  
 Best Local Similarity 65.4%; Pred. NO. 2.8e-209;  
 Matches 469; Conservative 90; Mismatches 141; Indels 17; Gaps 6;

13 SSNAVKDKISTDLN-KETDIELQ-NINHECLKMSVENVEPVFVSASTIOTGIGAKGI 70  
 7 NENEINLSIPTVSNPSTQWLSDPARIEDSLCAEVNNDPFFVSASTVOTGINIAGRI 66  
 71 LGTLGVPPAGQVASTYFELGELWPKGNQWEIFMEHVEEIIINQIKSTYAPNKALTDLKG 130  
 67 LGVLGVPPAGQLASFSYFLVGLWPSGRDPWEIFLEHVEQLIROQVTRNTAARLEG 126  
 131 LGDALAVHDSLESVWGNRNTARSPVSKVSQVIAELMFVQKLPSFAVSGEEVPLPIYA 190

127 LCGYRSYQQALETWLDNRNDARSRIILERYVALELDITTAIPLFIRIRNEBVPILMYA 186  
 191 QANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCWKWYSTGLNNLRGTN 250  
 187 QANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCWKWYSTGLNNLRGTN 246  
 251 AESSVRYNQFRDMLTMLVLDLVALFPSTDTQWPIKTTAQLTREYVTDALQVHPHPST 310  
 247 AESSVRYNQFRDMLTMLVLDLVALFPSTDTQWPIKTTAQLTREYVTDALQVHPHPST 306  
 311 STTWNNAPPSAIEAAVVRNPHLLDLEQVYIYSLSRNSNTQYMMWGGHKLERTI 370  
 307 STWNNAPPSAIEAAVVRNPHLLDLEQVYIYSLSRNSNTQYMMWGGHKLERTI 366  
 371 GGTLMISTQGST-NTSINPVTLPFTSRDVRTESLAGNLFLTPQVNGVPRVDFHWKFTV 429  
 367 GGTLMISTQGST-NTSINPVTLPFTSRDVRTESLAGNLFLTPQVNGVPRVDFHWKFTV 422  
 430 HPIASDNFYYPG-----YAGIGLOQDSSENLPEATGQPNYESYSHRSLSHGLISAS 482  
 423 --INPONIYERGATTYSQFYQVGIQDFDSETELPETTERPNYESYSHRSLSHGLIIGN 480  
 483 HVKALVSWTHESADRTNIBNSITQPLVKAFNLSCAAVVRGPGTGGDILRRNTG 542  
 481 TURAPVSWTHESADRTNIBNSITQPLVKAFNLSCAAVVRGPGTGGDILRRNTG 540  
 543 TFGDIRVNINPPAQRVIRYASTTDLQFHTSINGKAINOGNFSATMREGDLDYKTF 602  
 541 TFGDIRVNINPPAQRVIRYASTTDLQFHTSINGKAINOGNFSATMREGDLDYKTF 600  
 603 RTVGFTTFFSFLDVOSTTIGAMFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKVTA 662  
 601 RTAGFSTFPELNAQSTFLLGAQFSN-QEYVIDRVEFVPAEVTFEAEYDLERAQKAVNA 659  
 663 LFTSTNPRGLTKVDYHIDQVSNVACLSDFCLDEKRELFEVKYAKRLSDERNL 716  
 660 LFTSTNPRGLTKVDYHIDQVSNVACLSDFCLDEKRELFEVKYAKRLSDERNL 716

RESULT 12  
 US-08-448-170-10  
 ; Sequence 10, Application US/08448170  
 ; Patent No. 5723758  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Payne, Jewel  
 ; APPLICANT: Cummings, David A.  
 ; APPLICANT: Cannon, Raymond J.C.  
 ; APPLICANT: Narva, Kenneth E.  
 ; APPLICANT: Stelman, Steve  
 ; TITLE OF INVENTION: No. 5723758el Bacillus thuringiensis Isolate Denoted  
 ; TITLE OF INVENTION: B.t. PS158C2, Active Against Lepidopteran Pests, and Genes  
 ; TITLE OF INVENTION: Encoding Lepidopteran-Active Toxins  
 ; NUMBER OF SEQUENCES: 10  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: David R. Saliwanchik  
 ; STREET: 2421 N.W. 41st Street, Suite A-1  
 ; CITY: Gainesville  
 ; STATE: Florida  
 ; COUNTRY: USA  
 ; ZIP: 32606  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent in Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/448,170  
 ; FILING DATE:  
 ; CLASSIFICATION: 424  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/069,902  
 ; FILING DATE: 01-JUNE-1993  
 ; CLASSIFICATION: 424

```
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/759,247
; FILING DATE: 13-SEPT-1991
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: M/S 102D.C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 488 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-448-170-10

Query Match 62.1%; Score 2335.5; DB 1; Length 488;
Best Local Similarity 89.5%; Pred. No. 8.9e-201;
Matches 445; Conservative 13; Mismatches 30; Indels 9; Gaps 1;

Qy 1 MKLNQDKHQSFSNAKVDKISTSLKNETDIELONINHEDECLKMSYENVEPVSASTI 60
Db 1 MKSKQNNHQSLSNNATVDKNTGSLNNTNTELFNFH-----EGIEPFPVSSTI 51
Qy 61 QTGIGIAGKILGTGVFPAGQVASYLSFILGELMPKGNQWEIFMEHVEEIIINQKISTYA 120
Db 52 QTGIGIVGKILGNLGVFPAGQVASYLSFILGELMPKGSQWEIFMEHVEELINQKISTYA 111
Qy 121 RNKALTDLKGDLALAVYHDSLESWGNRNNTARSVVKSOYIALELMFVQKLPSPAVSG 180
Db 112 RNKALADLKGDLALAVYHDSLESWNIENRNNTARSVVKSOYITLMLFVQSLPSPAVSG 171
Qy 181 EEVPLLPYQAANLHLLLRDASIFGKWLGSSEISTFYNQVRSAGDYSYHCVKWS 240
Db 172 EEVPLLPYQAANLHLLLRDASIFGKWLGSSEISTFYNQVRSAGDYSYHCVKWS 231
Qy 241 TGLNLRGTNAESWRYNQFRDMLMVLVDLVALFPSPYDTQMYPIKTTAQLTREYITDAI 300
Db 232 TGLNLRGMNNAESWRYNQFRDMLMVLVDLVALFPSPYDTQMYPIKTTAQLTREYITDAI 291
Qy 301 GTVHPHPSFTSTTWNNAEAEAVVRNPHLLDLEQVTIYSLLSWSNTQYNNMW 360
Db 292 GTVHPHPSFTSTTWNNAEAEAVVRNPHLLDLEQVTIYSLLSWSNTQYNNMW 351

; TITLE OF INVENTION: Encoding Lepidopteran-Active Toxins
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jay M. Sanders
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,803
; FILING DATE: 31-OCT-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/069,902
; FILING DATE: 01-JUNE-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/759,247
; FILING DATE: 13-SEPT-1991
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/448,170
; FILING DATE: 23-MAY-1995
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Sanders, Jay M.
; REGISTRATION NUMBER: 39,355
; REFERENCE/DOCKET NUMBER: M/S 102DCD1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 488 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-961-803-10

Query Match 62.1%; Score 2335.5; DB 3; Length 488;
Best Local Similarity 89.5%; Pred. No. 8.9e-201;
Matches 445; Conservative 13; Mismatches 30; Indels 9; Gaps 1;

Qy 1 MKLNQDKHQSFSNAKVDKISTSLKNETDIELONINHEDECLKMSYENVEPVSASTI 60
Db 1 MKSKQNNHQSLSNNATVDKNTGSLNNTNTELFNFH-----EGIEPFPVSSTI 51
Qy 61 QTGIGIAGKILGTGVFPAGQVASYLSFILGELMPKGNQWEIFMEHVEEIIINQKISTYA 120
Db 52 QTGIGIVGKILGNLGVFPAGQVASYLSFILGELMPKGSQWEIFMEHVEELINQKISTYA 111
Qy 121 RNKALTDLKGDLALAVYHDSLESWGNRNNTARSVVKSOYIALELMFVQKLPSPAVSG 180
Db 112 RNKALADLKGDLALAVYHDSLESWNIENRNNTARSVVKSOYITLMLFVQSLPSPAVSG 171
Qy 181 EEVPLLPYQAANLHLLLRDASIFGKWLGSSEISTFYNQVRSAGDYSYHCVKWS 240
Db 172 EEVPLLPYQAANLHLLLRDASIFGKWLGSSEISTFYNQVRSAGDYSYHCVKWS 231
Qy 241 TGLNLRGTNAESWRYNQFRDMLMVLVDLVALFPSPYDTQMYPIKTTAQLTREYITDAI 300
Db 232 TGLNLRGMNNAESWRYNQFRDMLMVLVDLVALFPSPYDTQMYPIKTTAQLTREYITDAI 291
Qy 301 GTVHPHPSFTSTTWNNAEAEAVVRNPHLLDLEQVTIYSLLSWSNTQYNNMW 360
Db 292 GTVHPHPSFTSTTWNNAEAEAVVRNPHLLDLEQVTIYSLLSWSNTQYNNMW 351

; GENERAL INFORMATION:
; APPLICANT: Payne, Jewel
; APPLICANT: Cummings, David A.
; APPLICANT: Cannon, Raymond J.C.
; APPLICANT: Narva, Kenneth E.
; APPLICANT: Stelman, Steve
; TITLE OF INVENTION: No. 6150589el Bacillus thuringiensis Isolate Denoted
; TITLE OF INVENTION: B.t. PS1582c, Active Against Lepidopteran Pests, and Genes
```

361 GGHKLEFRITGTLNISTQSGTNTSINPVTLPFTSRDVRYESIAGLNELTQPVNGVPR 420  
DB 352 GGHKLEFRITGTLNISTQSGTNTSINPVTLPFTSRDVRYESIAGLNELTQPVNGVPR 411  
QY 421 VDFHWKFWTHPIASDNFYPGYAGIGTQLODSENELPPEATGQPNYESYSHRSLHIGLIS 480  
DB 412 VDFHWKFWTHPIASDNFYPGYAGIGTQLODSENELPPEATGQPNYESYSHRSLHIGLIS 471  
QY 481 ASHVKALVYSWTHRSAD 497  
DB 472 ASHVKALVYSWTHRSAD 488

RESULT 14  
US-07-951-715A-7  
; Sequence 7, Application US/07951715A  
; Patent No. 5625136  
; GENERAL INFORMATION:  
; APPLICANT: Koziele, Michael G.  
; APPLICANT: Desai, Nalin M.  
; APPLICANT: Lewis, Kelly S.  
; APPLICANT: Kramer, Vance C.  
; APPLICANT: Warren, Gregory W.  
; APPLICANT: Evola, Stephen V.  
; APPLICANT: Crossland, Lyle D.  
; APPLICANT: Wright, Martha S.  
; APPLICANT: Merlin, Ellis J.  
; APPLICANT: Launis, Karen L.  
; APPLICANT: Rothstein, Steven J.  
; APPLICANT: Bowman, Cindy G.  
; APPLICANT: Dawson, John L.  
; APPLICANT: Dunder, Erik M.  
; APPLICANT: Pace, Gary M.  
; APPLICANT: Suttie, Janet L.  
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE  
; NUMBER OF SEQUENCES: 94  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: CIBA-GEIGY Corporation  
; STREET: 7 Skyline Drive  
; CITY: Hawthorne  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10532  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30B  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/951,715A  
; FILING DATE: 25-SEP-1992  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/772,027  
; FILING DATE: 04-OCT-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Spruill, W. Murray  
; REGISTRATION NUMBER: 32,943  
; REFERENCE/DOCKET NUMBER: S-18805/A/CGC 1577/CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (919)541-8615  
; TELEFAX: (919)541-8689  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1207 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-07-951-715A-7

Query Match 59.8%; Score 2250.5; DB 1; Length 1207;

Best Local Similarity 64.0%; Pred. No. 1.7e-192;  
Matches 440; Conservative 77; Mismatches 151; Indels 13; Gaps 5;  
QY 40 EDCLXSEVENPEVPSASTITQTGIGIAGKILGTGVFPAGQVASLYSFIIGELWPKGN 99  
DB 10 EBSLCLAEENNDPVSASTVQTGINIAGRIILGVLGVFPAGQLASFYSFLVGLWPRGRD 69  
QY 100 QWEIEMHEVEEINQKISTYARNKALTDLKGGLDALAVYHDSLSWGNRNNTARSVVK 159  
DB 70 QWEIEMHEVEEINQKISTYARNKALTDLKGGLDALAVYHDSLSWGNRNNTARSVVK 129  
QY 160 SOVIALELMFVQKLPSFAVSGEVEPLPIYAAANLHLLLRDASIFCKEGLSSSEST 219  
DB 130 TOYIALELDPLNAMPFAIRNCEVPLLMVYAAANLHLLLRDASIFSGEGLTSQEIQR 189  
QY 220 FYNQVERAGDYSYHCVKYKWTGLNLRGTNAESWVRYNQFRDMTLMVLDAVALFPSYD 279  
DB 190 YYERQVETRDYSDYCVENYNTGLNSLRGTNAASWVRYNQFRDMTLMVLDAVALFPSYD 249  
QY 280 TOMYPIKTTAQLTREVTYDADIGTVHPHPSFTSTTWNNAAPSFAIAEAAVVENPHLLDFL 339  
DB 250 TTYTYPINTSAQLTREVTYDADIGAT--GVNMAWMWYNNAPSAFAIAEAAVVENPHLLDFL 307  
QY 340 EQVTYLSLRWSNTQYMMMGCHKLEPRITIGTGLNISTQSGTNTSINPVTLPFTSRDYY 399  
DB 308 EQLTIFSASSRWSNTRHMTYWRGHTIQSRPIGGGLNTSTHGATNTSINPVTLPFTSRDYY 367  
QY 400 RTESLAGLNF--LTQPVNGVPRVDFHWKFWTHP-----IASDNFYPGYAGIGTQLODS 452  
DB 368 RTESYAGVLLMGIIYLEPIHGVETVRNPF--TNPQNI SDRGTANYSQP-YESPGLOKDS 423  
QY 453 ENELPPEATGQPNYESYSHRSLHIGLISASHVKALVYSWTHRSADRTNTIGENRITQIPM 512  
DB 424 ETELPEPETERPENYESYSHRSLHIGLILQSRVNVVYSWTHRSADRTNTIGENRITQIPM 483  
QY 513 VKAFNLSSGAAVVRGPGFTGGDILARTNTGTGDIRVAINPPFAORYVRIRYASTDLQ 572  
DB 484 VKASELPQGTTVVRGPGFTGGDILARTNTGTGDIRVAINPPFAORYVRIRYASTDLQ 543  
QY 573 FHTSINGKAINQCNFSATMNRGEDLDYKTFRTVGTFTTFFSLDVQSTFTTIGAWNFSSGNE 632  
DB 544 FVSVRGTTVNNFRFLRTWNSGDELKYNFVRRATFTTFTTQIQIIRTSIQGLSGNGE 603  
QY 633 VIIDRIEFVPEVTYEAEDFEKAEKVYALTFTSNPRGLKTDVXDYHIDQVNLVESIS 692  
DB 604 VYIDKIEIIPVTATFEASYDLERAQEAVALFTNPNRRLKTDVTDYHIDQVNLVACLS 663  
QY 693 DEFYLDKRELEPEIVKYNELHIERNM 719  
DB 664 DEFYLDKRELEPEIVKYNELHIERNM 690

RESULT 15  
US-08-459-449A-7  
; Sequence 7, Application US/08459448A  
; Patent No. 5859336  
; GENERAL INFORMATION:  
; APPLICANT: Koziele, Michael G.  
; APPLICANT: Desai, Nalin M.  
; APPLICANT: Lewis, Kelly S.  
; APPLICANT: Kramer, Vance C.  
; APPLICANT: Warren, Gregory W.  
; APPLICANT: Evola, Stephen V.  
; APPLICANT: Crossland, Lyle D.  
; APPLICANT: Wright, Martha S.  
; APPLICANT: Merlin, Ellis J.  
; APPLICANT: Launis, Karen L.  
; APPLICANT: Rothstein, Steven J.  
; APPLICANT: Bowman, John L.  
; APPLICANT: Dawson, Cindy G.  
; APPLICANT: Dunder, Erik M.  
; APPLICANT: Pace, Gary M.  
; APPLICANT: Suttie, Janet L.



TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
 TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE  
 NUMBER OF SEQUENCES: 94  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: No. 5859336artis Corporation  
 STREET: Patent & Trademark Dept., 520 White Plains  
 STREET: Rd., POB 2005  
 CITY: Tarrytown  
 STATE: New York  
 COUNTRY: USA  
 ZIP: 10591-9005  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/459,448A  
 FILING DATE: 02-JUN-1995  
 CLASSIFICATION: 800  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/951,715  
 FILING DATE: 25-SEP-1992.  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/772,027  
 FILING DATE: 04-OCT-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Pace, Gary M.  
 REGISTRATION NUMBER: 40403  
 REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV4  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (919) 541-8582  
 TELEFAX: (919) 541-8689  
 INFORMATION FOR SEQ ID NO: 7:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1207 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-459-448A-7

Query Match	59.8%	Score	2250.5	DB 2	Length	1207			
Best Local Similarity	64.0%	Pred. No.	1.7e-192						
Matches	440	Conservative	77	Mismatches	157	Indels	13	Gaps	5

  

QY	40	EDCLKMEYENVEPVFSASTIQTGIGTAGKLTGLGVPPAGQVASLVSFILGELWPKGN	99
Db	10	EDSLCIAEGNNIDPFGASIVQTGINAGRILGVLPFGFAGQLASFSFLVGEELWPKGRD	69
QY	100	QWEIFMHEVBEIIINQKISTYARNKALTDLKGLDALAVYHDSLSWGNRNNTARSVVK	159
Db	70	QWEIFLHEVQLINQKITENARNALARLOGLGDSFRAYQOSLEDWLENRDRDARTSVLY	129
QY	160	SOVIALELMFVKQLPSFAVSGEEVPLPIYAOAANLHLLLRDASITGKEWGLSSSIST	219
Db	130	TOYIALELDFLNAMPLFAIRNQEVPLVMVAQAANLHLLLRDASLPGSEFGLTSQBIR	189
QY	220	FYNQVERAGDYSVHCVKWYSTGLNNLRGTNAESWVRYNQPRRDITLMLDLVLFPSYD	279
Db	190	YIERQVERTRDYSVCYEWYNTGLNSLRGTNAASWVRYNQPRRDLTLGVLDLVLFPYD	249
QY	280	TOYPIKTKTQLTREVYTDAGTGVHPSPSTSTWYNNAPSPSAIAAVVRNPHLLDFL	339
Db	250	TRTYPINTSAQLTREVYTDAGAT - GVNWASMNWYNNAPSPSAIAEAAIRSPHLLDFL	307
QY	340	EQWTIVSLLGRWSTQVWNNMGHKLFRITGGTLNTSTOGSTNTSINPVTLPSTSDVY	399
Db	308	EQLTIPASSRWSNTRHWYWRGHTIGSRPLGGGLNTSHGATNTSINPVTLPASRDVY	367
QY	400	RTESLAGLNIUF - LTQPVNGVPRVDFHWKFVTHP - ----TASONFYYPGAGIGTQLQDS	452
Db	368	RTESYAGVLLWGIYLEIGHGVTYVRNPF - --TNPQNISDRGTANYSP - YESPGLQKDS	423

453	Qy	ENELPPEATGQNYESYSHRLSHIGLSIASHVKALVSWTHRSADRNTTIEPNSITQIPL	512
424	Db	ETELPETTERPNYESYSHRLSHIGLIQSRWNPVYSWTHRSADRNTTGPYRIITQPM	483
513	Qy	VKAFNLSGAAVVRPGPFGTGDILRRNTGFGDIRVNINPPFAQRVVRIRVASTTDLQ	572
484	Db	VKASELPQGTTVVRPGPFGTGDILRRNTGGFGPIRVTVNGPLTQRVIGFRVASTVDFD	543
573	Qy	FHTSINGKAINOGNFSATMNRGEDLDYKTRFTVGTFTFPFSLDVQSTFTTGAWNFFSGNE	632
544	Db	FFVSRGGTTVANNFRLTRMTNSGDBLKXGNFVRRAFTTFTFTQTDIIRTSIQGLSGNGE	603
633	Qy	VVIDRIEFVPEVTVAEAYDPEKAQKVTAFTSTNPRGLKTDVKDYHIDOVSNLYSLS	692
604	Db	VVIDKIEIIPVTAIFEAYDYDERAQEAVALFTNPNRKLKTDVTDYHIDOVSNLYACL	663
693	Qy	DEFYLDKRELFETVVKYANELHIERNM	719
664	Db	DEFCLDKRELLKVKYAKRLSDRNL	690

Search completed: October 28, 2004, 18:34:16  
Job time : 25.3343 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 28, 2004, 17:51:02 ; Search time 86.6903 Seconds  
(without alignments)  
2975.262 Million cell updates/sec

Title: US-10-019-823B-56

Perfect score: 3762

Sequence: 1 MLLKNQDKHQSFSSNAKVDK.....KRELFEIVKYANELHIERNM 719

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_238sep04.\*

- 1: Geneseqp1980s.\*
- 2: Geneseqp1990s.\*
- 3: Geneseqp2000s.\*
- 4: Geneseqp2001s.\*
- 5: Geneseqp2002s.\*
- 6: Geneseqp2003as.\*
- 7: Geneseqp2003bs.\*
- 8: Geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	3762	100.0	719	4 AAB66909	Aab66909 Insectici
2	3762	100.0	719	6 AAE36273	Aae36273 B. thurin
3	3753	99.8	719	4 AAU02095	Aau02095 Bacillus
4	3749	99.7	719	4 AAB66911	Aab66911 Insectici
5	3749	99.7	719	6 AAE36275	Aae36275 B. thurin
6	3743	99.5	719	4 AAB66908	Aab66908 Insectici
7	3743	99.5	719	6 AAE36272	Aae36272 B. thurin
8	3741	99.4	719	2 AAR08041	Aar08041 81 kd end
9	3739	99.4	719	4 AAB66910	Aab66910 Insectici
10	3739	99.4	719	6 AAE36274	Aae36274 B. thurin
11	3730.5	99.2	718	6 AAE36271	Aae36271 B. thurin
12	3724.5	99.0	718	4 AAB66907	Aab66907 Insectici
13	3534	93.9	719	7 ADM74717	Adm74717 B. thurin
14	3503	93.1	719	6 AAB66912	Aab66912 Insectici
15	3503	93.1	719	6 AAE36276	Aae36276 B. thurin
16	3459.5	92.0	710	4 AAU02041	Aau02041 B. thurin
17	3380	89.8	719	3 ABB07073	Abb07073 Bacillus
18	3379	89.8	719	2 AAW49089	Aaw49089 Bacillus
19	3295	87.6	1217	4 AAU02092	Aau02092 Bacillus
20	2719	72.3	1208	4 AAU02093	Aau02093 Bacillus
21	2439	64.8	1230	8 ADK98484	Adk98484 B thuring
22	2439	64.8	1230	8 ADK98489	Adk98489 B thuring
23	2439	64.8	1230	8 ADK98481	Adk98481 B thuring
24	2439	64.8	1230	8 ADK98491	Adk98491 B thuring
25	2439	64.8	1230	8 ADK98487	Adk98487 B thuring

25	2437.5	64.8	1229	2 AAE54074	Aae54074 CryET5. 2
27	2437.5	64.8	1229	2 AAW35259	Aaw35259 Bacillus
28	2437.5	64.8	1229	2 AAW17699	Aaw17699 CryET5. 3
29	2437.5	64.8	1229	2 AAW87633	Aaw87633 CryET5 pr
30	2437.5	64.8	1229	2 AAY30923	Aay30923 B. thurin
31	2437.5	64.8	1229	8 ADK98479	Adk98479 B thuring
32	2335.5	62.1	488	2 AAW44322	Aaw44322 Bacillus
33	2335.5	62.1	488	4 AAB19947	Aab19947 Bacillus
34	2263.5	60.2	1228	2 AAR50955	Aar50955 Bacillus
35	2258.5	60.0	1209	4 AAU02094	Aau02094 Bacillus
36	2249.5	59.8	1227	2 AAY31990	Aay31990 Chimeric
37	2180.5	58.0	1227	2 AAW44321	Aaw44321 Bacillus
38	2180.5	58.0	1227	4 AAB19950	Aab19950 Bacillus
39	2171.5	57.7	1227	4 AAU02046	Aau02046 B. thurin
40	2156.5	57.3	1186	2 AAY16796	Aay16796 Amino aci
41	2141.5	56.9	1221	4 AAU00421	Aau00421 B. thurin
42	2127.5	56.6	1221	4 AAU00420	Aau00420 B. thurin
43	2101	55.8	1228	4 AAB84628	Aab84628 Amino aci
44	2101	55.8	1228	4 AAU02039	Aau02039 B. thurin
45	1923.5	51.1	643	2 AAY16797	Aay16797 Amino aci

ALIGNMENTS

RESULT 1  
AAB66909  
ID AAB66909 standard; protein; 719 AA.  
XX  
AC AAB66909;  
XX  
AC  
DT 12-APR-2001 (first entry)  
XX  
DE Insecticidal protein cryIIa3.  
XX  
KW Insecticide; transgenic plant; insect-resistance.  
XX  
OS Paecilomyces sp.  
XX  
PN WO200100841-A1.  
XX  
PD 04-JAN-2001.  
XX  
PF 23-JUN-2000; 2000WO-GB002457.  
PR 23-JUN-1999; 99GB-00015215.  
PR 23-DEC-1999; 99GB-00030536.  
XX  
PA (ZENE ) ZENECA LTD.  
PI Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;  
PI Vincent JL, Lee MD;  
XX  
DR WPI; 2001-123015/13.  
XX  
PT Novel insecticidal protein obtained from species of Paecilomyces for  
controlling insects, and for insect-resistant transgenic plant  
production.  
XX  
PS Claim 14; Page 57-59; 72pp; English.  
XX  
CC The present invention relates to novel insecticidal proteins obtained  
from Paecilomyces sp. (see AAB66909 to AAB66901 and AAB66913). The  
insecticidal proteins can be used to produce transgenic plants, which are  
insect-resistant. Also, the insecticidal proteins are useful for  
controlling insects by providing them at a locus where insects feed

Query Match 100.0%; Score 3762; DB 4; Length 719;  
Best Local Similarity 100.0%; Pred. No. 3.4e-254;  
Matches 719; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLKNQDQKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMSYENVEPVSASTI 60  
 DB 1 MKLKNQDQKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMSYENVEPVSASTI 60  
 QY 61 QTGIGIAGKILGTGVPFAGQVASYISFILGELPKGNQWEIEMEHVEEIIINQKISTYA 120  
 DB 61 QTGIGIAGKILGTGVPFAGQVASYISFILGELPKGNQWEIEMEHVEEIIINQKISTYA 120  
 QY 121 RNKALTDLKLGDALAVYHDSLESWGNRNTRARSVKQYIALELMFVKQLPSFAVSG 180  
 DB 121 RNKALTDLKLGDALAVYHDSLESWGNRNTRARSVKQYIALELMFVKQLPSFAVSG 180  
 QY 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFFYNQVERAGDYSYHCVKWS 240  
 DB 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFFYNQVERAGDYSYHCVKWS 240  
 QY 241 TGLANLRGTNAESWRYNQFRDQFDMTLMLVDLVALFPSTQYPIKTAQTREVVYDAI 300  
 DB 241 TGLANLRGTNAESWRYNQFRDQFDMTLMLVDLVALFPSTQYPIKTAQTREVVYDAI 300  
 QY 301 GTVHPHPSFTSTTWNNAPSFSAIEAAVVRNPHLLDPLEQVTTIYSLSRMSNTQYNNMW 360  
 DB 301 GTVHPHPSFTSTTWNNAPSFSAIEAAVVRNPHLLDPLEQVTTIYSLSRMSNTQYNNMW 360  
 QY 361 GGHKLEPRTIGTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGNLFITQPVNGVPR 420  
 DB 361 GGHKLEPRTIGTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGNLFITQPVNGVPR 420  
 QY 421 VDFHWKFVTHPIASDNFYYPYAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 DB 421 VDFHWKFVTHPIASDNFYYPYAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 QY 481 ASHVKALVSWTHRSADRTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 540  
 DB 481 ASHVKALVSWTHRSADRTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 540  
 QY 541 TGTFGDIRVNIAPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATNMRGEDLDYK 600  
 DB 541 TGTFGDIRVNIAPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATNMRGEDLDYK 600  
 QY 601 TERTVGFTTTPSFSLDVQSTFTTIGAWNPFSSGNEVYIDRIEFVPVEVTEAEYDFEKAQEKV 660  
 DB 601 TERTVGFTTTPSFSLDVQSTFTTIGAWNPFSSGNEVYIDRIEFVPVEVTEAEYDFEKAQEKV 660  
 QY 661 TALFTSTNPRGLKTDVKDHYDQVNLVESLSDEFYLDKEKELFEIVKYANELHIERNM 719  
 DB 661 TALFTSTNPRGLKTDVKDHYDQVNLVESLSDEFYLDKEKELFEIVKYANELHIERNM 719

## RESULT 2

AAE36273  
 ID AAE36273 standard; protein; 719 AA.  
 AC AAE36273;  
 XX  
 XX  
 DT 26-JUN-2003 (first entry)  
 XX  
 DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa3.  
 XX  
 XX Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.  
 XX  
 XX Bacillus thuringiensis.  
 XX  
 XX WO200298911-A2.  
 XX  
 PD 12-DEC-2002.  
 XX  
 PF 30-MAY-2002; 2002WO-CB0002666.  
 XX  
 PR 07-JUN-2001; 2001GB-00013900.  
 XX  
 PA (SYGN ) SYNGENTA LTD.  
 XX

PI Vincent JL, Viner R;  
 XX WPI; 2003-175137/17.  
 XX  
 PT New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.  
 XX  
 PS Claim 12; Page 47-50; 67pp; English.  
 XX  
 CC The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects.  
 CC Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is CC Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention  
 XX  
 SX Sequence 719 AA;

Query Match 100.0%; Score 3762; DB 6; Length 719;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-294;  
 Matches 719; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLKNQDQKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMSYENVEPVSASTI 60  
 DB 1 MKLKNQDQKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMSYENVEPVSASTI 60  
 QY 61 QTGIGIAGKILGTGVPFAGQVASYISFILGELPKGNQWEIEMEHVEEIIINQKISTYA 120  
 DB 61 QTGIGIAGKILGTGVPFAGQVASYISFILGELPKGNQWEIEMEHVEEIIINQKISTYA 120  
 QY 121 RNKALTDLKLGDALAVYHDSLESWGNRNTRARSVKQYIALELMFVKQLPSFAVSG 180  
 DB 121 RNKALTDLKLGDALAVYHDSLESWGNRNTRARSVKQYIALELMFVKQLPSFAVSG 180  
 QY 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFFYNQVERAGDYSYHCVKWS 240  
 DB 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFFYNQVERAGDYSYHCVKWS 240  
 QY 241 TGLANLRGTNAESWRYNQFRDQFDMTLMLVDLVALFPSTQYPIKTAQTREVVYDAI 300  
 DB 241 TGLANLRGTNAESWRYNQFRDQFDMTLMLVDLVALFPSTQYPIKTAQTREVVYDAI 300  
 QY 301 GTVHPHPSFTSTTWNNAPSFSAIEAAVVRNPHLLDPLEQVTTIYSLSRMSNTQYNNMW 360  
 DB 301 GTVHPHPSFTSTTWNNAPSFSAIEAAVVRNPHLLDPLEQVTTIYSLSRMSNTQYNNMW 360  
 QY 361 GGHKLEPRTIGTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGNLFITQPVNGVPR 420  
 DB 361 GGHKLEPRTIGTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGNLFITQPVNGVPR 420  
 QY 421 VDFHWKFVTHPIASDNFYYPYAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 DB 421 VDFHWKFVTHPIASDNFYYPYAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 QY 481 ASHVKALVSWTHRSADRTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 540  
 DB 481 ASHVKALVSWTHRSADRTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 540  
 QY 541 TGTFGDIRVNIAPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATNMRGEDLDYK 600  
 DB 541 TGTFGDIRVNIAPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATNMRGEDLDYK 600  
 QY 601 TERTVGFTTTPSFSLDVQSTFTTIGAWNPFSSGNEVYIDRIEFVPVEVTEAEYDFEKAQEKV 660  
 DB 601 TERTVGFTTTPSFSLDVQSTFTTIGAWNPFSSGNEVYIDRIEFVPVEVTEAEYDFEKAQEKV 660  
 QY 661 TALFTSTNPRGLKTDVKDHYDQVNLVESLSDEFYLDKEKELFEIVKYANELHIERNM 719  
 DB 661 TALFTSTNPRGLKTDVKDHYDQVNLVESLSDEFYLDKEKELFEIVKYANELHIERNM 719

RESULT 3
AAU02095
ID AAU02095 standard; protein; 719 AA.
XX AC
XX AC AAU02095;
XX XX
DT 07-SEP-2001 (first entry)
XX XX
DE Bacillus thuringiensis partial mutant CryIIa.
XX XX
KW Crystal protein; CryIIa; CryIba; moth; butterfly; Colorado potato beetle;
XW mutant; mutein.
XX XX
OS Bacillus thuringiensis.
XX XX
PH Key Location/Qualifiers
FT Peptide i..19
FT /label= signal_peptide
FT Protein 20..719
FT /label= Mature_CryIIa
XX XX
PN EP1099760-A1.
PD 16-MAY-2001.
XX XX
PF 09-NOV-1999; 99EP-00203723.
XX XX
PR 09-NOV-1999; 99EP-00203723.
XX XX
PA (CPRO-) CPRO-DLO CENT PLANTENVERDELINGS REPROD.
XX XX
PI De Maagd RA.; Bosch HJ;
XX XX
DR WPI; 2001-337141/36.
NR N-PSDB; AAS04855.
PT PT
PT New hybrid Bacillus thuringiensis hybrid toxins comprising structural
PT domains derived from at least 2 different crystal proteins, such as
PT CryIIa and CryIba, and having insecticidal activity, useful for combating
PT insects.
XX XX
XX Example; Page 30-32; 43pp; English.
XX XX
CC The sequence is B. thuringiensis (Bt) crystal protein CryIIa, the DNA
CC encoding which was mutated to allow cloning of domain III or domains I
CC and II, to make the hybrid protoxins of the invention. The hybrid toxins
CC of the invention, having structural domains I, II and III in this order
CC starting from the N-terminal derived from at least 2 different crystal
CC proteins, are useful for protecting plants against pest insects, e.g.
CC moths, butterflies and Colorado potato beetle or for combating insects
XX XX
SQ Sequence 719 AA;
Query Match 99.8%; Score 3753; DB 4; Length 719;
Best Local Similarity 99.7%; Pred. No. 1.8e-293;
Matches 717; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MKLKNDKHQSFSNAKVDKISTSLKNETDIELQNINHEDC LKMGEYENVVEFVSASTI 60
Db 1 MKLKNDKHQSFSNAKVDKISTSLKNETDIELQNINHEDC LKMGEYENVVEFVSASTI 60
QY 61 QTGIGIAGKILTGLVPFAGVASLYSPILGELMPKGKNQWEIFMEHVEEIQNKISTYA 120
Db 61 QTGIGIAGKILTGLVPFAGVASLYSPILGELMPKGKNQWEIFMEHVEEIQNKISTYA 120
QY 121 RNKALTDLKGLDALAVHDLSLESGWGNNNTRARSVVVKSQYTALFLMFVKLPSFAVSG 180
Db 121 RNKALTDLKGLDALAVHDLSLESGWGNNNTRARSVVVKSQYTALFLMFVKLPSFAVSG 180
QY 181 EKVPLLPYQAANHLHLLLRDASIFGKEWGLSSSEISTTFYNRQVRAGDYSYHCWKWS 240
Db 181 EKVPLLPYQAANHLHLLLRDASIFGKEWGLSSSEISTTFYNRQVRAGDYSYHCWKWS 240

CC insect-resistant. Also, the insecticidal proteins are useful for  
CC controlling insects by providing them at a locus where insects feed  
XX  
SQ Sequence 719 AA;  
  
Query Match 99.7%; Score 3749; DB 4; Length 719;  
Best Local Similarity 99.7%; Pred. No. 3.8e-293;  
Matches 717; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 MKLNQDQHQSFSNAKVDKISTDSLNKNETDIELQINHEHEDCLMKSEYENVEPVSASTI 60  
DB 1 MKLNQDQHQSFSNAKVDKISTDSLNKNETDIELQINHEHEDCLMKSEYENVEPVSASTI 60  
  
QY 61 QTGIGIAGKILGTGVPPAGQVASYLSPILGELWPKGNQWEIEMHVEEIIINQKISTYA 120  
DB 61 QTGIGIAGKILGTGVPPAGQVASYLSPILGELWPKGNQWEIEMHVEEIIINQKISTYA 120  
  
QY 121 RNKALTDLKLGDALAVVHDSLEWVGNNRNRARSVVKSOYIALELMFVKQLPSFAVSG 180  
DB 121 RNKALTDLKLGDALAVVHDSLEWVGNNRNRARSVVKSOYIALELMFVKQLPSFAVSG 180  
  
QY 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNRQVERAGDYSYHCVKWYS 240  
DB 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNRQVERAGDYSYHCVKWYS 240  
  
QY 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNRQVERAGDYSYHCVKWYS 240  
DB 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNRQVERAGDYSYHCVKWYS 240  
  
QY 241 TGLANLRCTNAESWVRNQFRDMTLMVLVALPSPYDTQMPYIKTTAQLTREVYTDAL 300  
DB 241 TGLANLRCTNAESWVRNQFRDMTLMVLVALPSPYDTQMPYIKTTAQLTREVYTDAL 300  
  
QY 301 GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWNSNTQYNNMW 360  
DB 301 GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWNSNTQYNNMW 360  
  
QY 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRYESLAGLNLFTQPVNGVPR 420  
DB 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRYESLAGLNLFTQPVNGVPR 420  
  
QY 421 VDFHWKFVTHPIASDNFYYPGAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLIS 480  
DB 421 VDFHWKFVTHPIASDNFYYPGAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLIS 480  
  
QY 481 ASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 540  
DB 481 ASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 540  
  
QY 541 TGTFGDIRVNIPTPAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATWNRGDDLYK 600  
DB 541 TGTFGDIRVNIPTPAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATWNRGDDLYK 600  
  
QY 601 TERTVGTPTPSFLDVQSTFTIGAWNFSSGNEVIDRIEFVPPVEVTEAEYDFEKAQEKV 660  
DB 601 TERTVGTPTPSFLDVQSTFTIGAWNFSSGNEVIDRIEFVPPVEVTEAEYDFEKAQEKV 660  
  
QY 661 TALFTSTNPRGLKTDVKDHYDQVNLVSESDSEFYLDKRELFEIKVYANELHIERNM 719  
DB 661 TALFTSTNPRGLKTDVKDHYDQVNLVSESDSEFYLDKRELFEIKVYANELHIERNM 719  
  
RESULT 5  
ID AAE36275  
XX AAE36275 standard; protein; 719 AA.  
AC AAE36275;  
XX  
DT 26-JUN-2003 (first entry)  
DE  
DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa5.  
XX Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.  
XX Bacillus thuringiensis.  
OS  
XX WO200298911-A2.  
PN

XX 12-DEC-2002.  
PD  
XX 30-MAY-2002; 2002WO-GB002666.  
PF  
XX 07-JUN-2001; 2001GB-00013900.  
PR  
XX (SYGN ) SYNGENTA LTD.  
PA  
XX Vincent JL, Viner R;  
PI WPI; 2003-175137/17.  
DR  
XX  
XX  
PT New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.  
PT terminus, useful as an active ingredient of a pesticide.  
XX  
XX Claim 12; Page 53-56; 67pp; English.  
XX  
XX The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects. CC Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is CC Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention  
XX  
SQ Sequence 719 AA;  
  
Query Match 99.7%; Score 3749; DB 6; Length 719;  
Best Local Similarity 99.7%; Pred. No. 3.8e-293;  
Matches 717; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 MKLNQDQHQSFSNAKVDKISTDSLNKNETDIELQINHEHEDCLMKSEYENVEPVSASTI 60  
DB 1 MKLNQDQHQSFSNAKVDKISTDSLNKNETDIELQINHEHEDCLMKSEYENVEPVSASTI 60  
  
QY 61 QTGIGIAGKILGTGVPPAGQVASYLSPILGELWPKGNQWEIEMHVEEIIINQKISTYA 120  
DB 61 QTGIGIAGKILGTGVPPAGQVASYLSPILGELWPKGNQWEIEMHVEEIIINQKISTYA 120  
  
QY 121 RNKALTDLKLGDALAVVHDSLEWVGNNRNRARSVVKSOYIALELMFVKQLPSFAVSG 180  
DB 121 RNKALTDLKLGDALAVVHDSLEWVGNNRNRARSVVKSOYIALELMFVKQLPSFAVSG 180  
  
QY 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNRQVERAGDYSYHCVKWYS 240  
DB 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNRQVERAGDYSYHCVKWYS 240  
  
QY 241 TGLANLRCTNAESWVRNQFRDMTLMVLVALPSPYDTQMPYIKTTAQLTREVYTDAL 300  
DB 241 TGLANLRCTNAESWVRNQFRDMTLMVLVALPSPYDTQMPYIKTTAQLTREVYTDAL 300  
  
QY 301 GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWNSNTQYNNMW 360  
DB 301 GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWNSNTQYNNMW 360  
  
QY 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRYESLAGLNLFTQPVNGVPR 420  
DB 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRYESLAGLNLFTQPVNGVPR 420  
  
QY 421 VDFHWKFVTHPIASDNFYYPGAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLIS 480  
DB 421 VDFHWKFVTHPIASDNFYYPGAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLIS 480  
  
QY 481 ASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 540  
DB 481 ASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 540  
  
QY 541 TGTFGDIRVNIPTPAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATWNRGDDLYK 600  
DB 541 TGTFGDIRVNIPTPAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATWNRGDDLYK 600

QY 601 TFRVGTTPPSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTVYAEYDFEKAQEKV 660  
 Db 601 TFRVGTTPPSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTVYAEYDFEKAQEKV 660  
 QY 661 TALFTSNRGLKTDVQYHIDQVSNLVESLSDEFYLDKRELFEIVKYANLHIERNM 719  
 Db 661 TALFTSNRGLKTDVQYHIDQVSNLVESLSDEFYLDKRELFEIVKYANLHIERNM 719  
 RESULT 6  
 AAB66908 standard; protein; 719 AA.  
 ID AAB66908  
 AC AAB66908;  
 XX 12-APR-2001 (first entry)  
 DT Insecticidal protein cryIIa2.  
 DE Insecticide; transgenic plant; insect-resistance.  
 KW Paecilomyces sp.  
 OS WO200100841-A1.  
 XX 04-JAN-2001.  
 XX 23-JUN-2000; 2000WO-GB002457.  
 XX 29-JUN-1999; 99GB-00015215.  
 XX 23-DEC-1999; 99GB-00030536.  
 XX (ZENE ) ZENECA LTD.  
 PI Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;  
 PI Vincent JL, Lee MD;  
 XX WPI; 2001-123015/13.  
 XX Novel insecticidal protein obtained from species of Paecilomyces for  
 PT controlling insects, and for insect-resistant transgenic plant  
 PT production.  
 XX Claim 14; Page 55-57; 72pp; English.  
 PS The present invention relates to novel insecticidal proteins obtained  
 CC from Paecilomyces sp. (see AAB6699 to AAB66901 and AAB66913). The  
 CC insecticidal proteins can be used to produce transgenic plants, which are  
 CC insect-resistant. Also, the insecticidal proteins are useful for  
 CC controlling insects by providing them at a locus where insects feed  
 XX Sequence 719 AA;  
 SQ  
 Query Match 99.5%; Score 3743; DB 4; Length 719;  
 Best Local Similarity 99.6%; Pred.No. 1.1e-292;  
 Matches 716; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 MLLKNQDKHQSFSNNAKVXKISTDSLKNETDIELQININHEDECKMSEYENVEPFVSASTI 60  
 Db 1 MLLKNQDKHQSFSNNAKVXKISTDSLKNETDIELQININHEDECKMSEYENVEPFVSASTI 60  
 QY 61 QTGIGIAGKILGTVGPAGQASVLSYFILGELWPKGKNQWEIFMEHVEIINQKISTYA 120  
 Db 61 QTGIGIAGKILGTVGPAGQASVLSYFILGELWPKGKNQWEIFMEHVEIINQKISTYA 120  
 QY 121 RNKALTDLKGDLALAYVHDSLSWGVRNNTARSVKQYIALELMFVKLPFAVSG 180  
 Db 121 RNKALTDLKGDLALAYVHDSLSWGVRNNTARSVKQYIALELMFVKLPFAVSG 180  
 QY 181 EEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSISTFPYNQVERAGDYSYHCVKWYS 240  
 Db 181 EEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSISTFPYNQVERAGDYSYHCVKWYS 240

QY 241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALFPSTYDTQMPYIKTTAQLTREVYTDAI 300  
 Db 241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALFPSTYDTQMPYIKTTAQLTREVYTDAI 300  
 QY 301 GTVHHPSTSTTWYNNAPSAEAAAVRNPHLLDLEQVTVIYSLSRNSNTQYMNW 360  
 Db 301 GTVHHPSTSTTWYNNAPSAEAAAVRNPHLLDLEQVTVIYSLSRNSNTQYMNW 360  
 QY 361 GGHKLEFRITIGTLMISTQGSTNTSINPVTLPFTTSRDVYRTESLAGNLFLTQPVNGVPR 420  
 Db 361 GGHKLEFRITIGTLMISTQGSTNTSINPVTLPFTTSRDVYRTESLAGNLFLTQPVNGVPR 420  
 QY 421 VDFHWKFVTHPIASDNFYPGYAGICTQLOSENELPPEATCOPNYESYSHRLSHIGLIS 480  
 Db 421 VDFHWKFVTHPIASDNFYPGYAGICTQLOSENELPPEATCOPNYESYSHRLSHIGLIS 480  
 QY 481 ASHVXALVYSWTHRSADRTNIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRTN 540  
 Db 481 ASHVXALVYSWTHRSADRTNIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRTN 540  
 QY 541 TGTGDIRVNIINPPFAQRYRVRIRYASTDQFHTSINGKAINQGNFSGATWNRGSDLDYK 600  
 Db 541 TGTGDIRVNIINPPFAQRYRVRIRYASTDQFHTSINGKAINQGNFSGATWNRGSDLDYK 600  
 QY 601 TERTVGTTPPSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTVYAEYDFEKAQEKV 660  
 Db 601 TERTVGTTPPSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTVYAEYDFEKAQEKV 660  
 QY 661 TALFTSNRGLKTDVQYHIDQVSNLVESLSDEFYLDKRELFEIVKYANLHIERNM 719  
 Db 661 TALFTSNRGLKTDVQYHIDQVSNLVESLSDEFYLDKRELFEIVKYANLHIERNM 719  
 RESULT 7  
 AAE36272 standard; protein; 719 AA.  
 ID AAE36272  
 XX AAE36272;  
 XX 26-JUN-2003 (first entry)  
 DT B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa2.  
 DE Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.  
 XX Bacillus thuringiensis.  
 OS WO200298911-A2.  
 XX 12-DEC-2002.  
 XX 30-MAY-2002; 2002WO-GB002666.  
 XX 07-JUN-2001; 2001GB-00013900.  
 XX (SYGN ) SYNGENTA LTD.  
 XX Vincent JL, Viner R;  
 XX WPI; 2003-175137/17.  
 XX New insecticidal protein comprising an X-glycine motif at the amino-  
 PT terminus, useful as an active ingredient of a pesticide.  
 XX Claim 12; Page 44-47; 67pp; English.  
 XX The invention relates to insecticidal protein comprising an X-glycine  
 CC motif at the amino-terminus. Polynucleotide or DNA constructs of the  
 CC invention are useful for producing plants or plant parts that are  
 CC resistant to insects. The protein or synergistic combination is useful as  
 CC an active ingredient of a pesticide or for controlling insects.  
 CC Antibodies raised to the insecticidal proteins can be used to identify

CC other proteins with insecticidal activity. The present sequence is  
 CC Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This  
 CC sequence is used in the invention  
 XX  
 SQ Sequence 719 AA;

Query Match 99.5%; Score 3743; DB 6; Length 719;  
 Best Local Similarity 99.6%; Pred. No. 1.1e-292;  
 Matches 716; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MKLNQDQHQSFSSNAKVDKISTDLSKNETDIELQININHEDECLKQSEYENVEPVSASTI 60  
 DB 1 MKLNQDQHQSFSSNAKVDKISTDLSKNETDIELQININHEDECLKQSEYENVEPVSASTI 60

QY 61 QTGIGIAGKILGTGVPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
 DB 61 QTGIGIAGKILGTGVPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120

QY 121 RNKALTDLKLGDALAVYHDSLESWGNNRNNTRARSVVKQSYIALELMFVQKLPSPFVSG 180  
 DB 121 RNKALTDLKLGDALAVYHDSLESWGNNRNNTRARSVVKQSYIALELMFVQKLPSPFVSG 180

QY 181 BEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNQVERAGDYSYHCVKWS 240  
 DB 181 BEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNQVERAGDYSYHCVKWS 240

QY 241 TGLNLRGTNAESWRYNQFRDMLVLDLVALFPSSYDTQMPYIKTTAQLTREYVTDAL 300  
 DB 241 TGLNLRGTNAESWRYNQFRDMLVLDLVALFPSSYDTQMPYIKTTAQLTREYVTDAL 300

QY 301 GTVHPHPSFTTWTNNNAPSFAIEAAVVRNPHLLDLEQVTIYSLLSRWSTNTQYMNW 360  
 DB 301 GTVHPHPSFTTWTNNNAPSFAIEAAVVRNPHLLDLEQVTIYSLLSRWSTNTQYMNW 360

QY 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFTQPVNGVPR 420  
 DB 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFTQPVNGVPR 420

QY 421 VDFHWKFVTHPIASDNFFYPYAGIGTQDSENELPPEATGQPNYESYSHRSLHIGLIS 480  
 DB 421 VDFHWKFVTHPIASDNFFYPYAGIGTQDSENELPPEATGQPNYESYSHRSLHIGLIS 480

QY 481 ASHVKALVYSWTHRSADRNTIEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRTN 540  
 DB 481 ASHVKALVYSWTHRSADRNTIEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRTN 540

QY 541 TGTFGDIRVNNPPPAQRYRIRYASTTDLOFHTSINGKAINQGNFSATNNGEDLDYK 600  
 DB 541 TGTFGDIRVNNPPPAQRYRIRYASTTDLOFHTSINGKAINQGNFSATNNGEDLDYK 600

QY 601 TERTVGTTPSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPVETVYEAEDFEKAEKV 660  
 DB 601 TERTVGTTPSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPVETVYEAEDFEKAEKV 660

QY 661 TALFTSTNPRGLKTDVKDHYDQVNLVSLSDSEFYLDKRELFEEIVKYANELHIERNM 719  
 DB 661 TALFTSTNPRGLKTDVKDHYDQVNLVSLSDSEFYLDKRELFEEIVKYANELHIERNM 719

RESULT 8

AA08041  
 ID AA08041 standard; protein; 719 AA.

XX  
 AC AA08041;

XX 24-OCT-2003 (revised)

DT 25-MAR-2003 (revised)

DT 27-FEB-1991 (first entry)

XX 81 kD endotoxin deduced from DNA carried on pJH12.

XX Crystal; insecticide; toxin; delta endotoxin.

XX

OS Bacillus thuringiensis; JHCC 4353 and 4835.  
 XX WO9013651-A.  
 XX PD 15-NOV-1990.  
 XX 09-MAY-1989; 89GB-00010624.  
 XX 09-MAY-1989; 89GB-00010624.  
 XX (ICIL ) IMPERIAL CHEM IND PLC.  
 XX Blenk RG, Ely S, Tailor RH, Tippett JM;  
 XX WPI; 1990-361486/48.  
 XX N-PSDB; AAQ06636.  
 XX Bacillus thuringiensis strains - used for producing an endotoxin for  
 XX protecting plants against insects, partic. Lepidoptera and Coleoptera.  
 XX Claim 5; Fig 5-10; 66pp; English.  
 XX The sequence carried on pJH12 which was isolated from B. thurin- giensis  
 CC strains JHCC4835 and JHCC 4353 (NCIB 40091 and 40090 resp.). The DNA can  
 CC be used to produce transformants E.coli strain MC12022/pJH12 (NCIB 40278,  
 CC or bacteriophage EMBA4 vector (NCIB 40279) or E.coli strain BL21/pJH11  
 CC (NCIB 40275). The delta-endo- toxin produced by the transformants can be  
 CC used in formulations for combatting Lepidoptera and Coleoptera pests.  
 CC (Updated on 25-MAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to  
 CC standardise OS field)

SQ Sequence 719 AA;

Query Match 99.4%; Score 3741; DB 2; Length 719;

Best Local Similarity 99.4%; Pred. No. 1.7e-292;

Matches 715; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MKLNQDQHQSFSSNAKVDKISTDLSKNETDIELQININHEDECLKQSEYENVEPVSASTI 60  
 DB 1 MKLNQDQHQSFSSNAKVDKISTDLSKNETDIELQININHEDECLKQSEYENVEPVSASTI 60

QY 61 QTGIGIAGKILGTGVPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
 DB 61 QTGIGIAGKILGTGVPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120

QY 121 RNKALTDLKLGDALAVYHDSLESWGNNRNNTRARSVVKQSYIALELMFVQKLPSPFVSG 180  
 DB 121 RNKALTDLKLGDALAVYHDSLESWGNNRNNTRARSVVKQSYIALELMFVQKLPSPFVSG 180

QY 181 BEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNQVERAGDYSYHCVKWS 240  
 DB 181 BEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNQVERAGDYSYHCVKWS 240

QY 241 TGLNLRGTNAESWRYNQFRDMLVLDLVALFPSSYDTQMPYIKTTAQLTREYVTDAL 300  
 DB 241 TGLNLRGTNAESWRYNQFRDMLVLDLVALFPSSYDTQMPYIKTTAQLTREYVTDAL 300

QY 301 GTVHPHPSFTTWTNNNAPSFAIEAAVVRNPHLLDLEQVTIYSLLSRWSTNTQYMNW 360  
 DB 301 GTVHPHPSFTTWTNNNAPSFAIEAAVVRNPHLLDLEQVTIYSLLSRWSTNTQYMNW 360

QY 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFTQPVNGVPR 420  
 DB 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFTQPVNGVPR 420

QY 421 VDFHWKFVTHPIASDNFFYPYAGIGTQDSENELPPEATGQPNYESYSHRSLHIGLIS 480  
 DB 421 VDFHWKFVTHPIASDNFFYPYAGIGTQDSENELPPEATGQPNYESYSHRSLHIGLIS 480

QY 481 ASHVKALVYSWTHRSADRNTIEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRTN 540  
 DB 481 ASHVKALVYSWTHRSADRNTIEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRTN 540



QY 541 TGTGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLDYK 600  
Db 541 TGTGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLDYK 600  
QY 601 TFRVGTTPPSFLDVOSTTIGAWNFSSGNEVYIDRIEFVPEVTEAYSDFEKAQEKV 660  
Db 601 TFXVGTTPPSFLDVOSTTIGAWNFSSGNEVYIDRIEFVPEVTEAYSDFEKAQEKV 660  
QY 661 TALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDEFYLDKRELFEIVKYNELHIERNM 719  
Db 661 TALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDEFYLDKRELFEIVKYNELHIERNM 719

RESULT 9  
ID AAB66910 standard; protein; 719 AA.

XX AAB66910;  
DT 12-APR-2001 (first entry)  
XX Insecticidal protein cryIIa4.  
DE Insecticide; transgenic plant; insect-resistance.  
XX Paecilomyces sp.  
XX WO200100841-A1.  
XX 04-JAN-2001.  
XX 23-JUN-2000; 2000WO-GB002457.  
XX 29-JUN-1999; 99GB-00015215.  
XX 23-DEC-1999; 99GB-00030536.  
XX (ZENE ) ZENECA LTD.  
XX Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;  
PI Vincent JL, Lee MB;  
XX WPI; 2001-123015/13.  
XX Novel insecticidal protein obtained from species of Paecilomyces for  
PT controlling insects, and for insect-resistant transgenic plant  
PT production.  
XX Claim 14; Page 60-62; 72pp; English.  
XX The present invention relates to novel insecticidal proteins obtained  
CC from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The  
CC insecticidal proteins can be used to produce transgenic plants, which are  
CC insect-resistant. Also, the insecticidal proteins are useful for  
CC controlling insects by providing them at a locus where insects feed  
XX Sequence 719 AA;

Query Match 99.4%; Score 3739; DB 4; Length 719;  
Best Local Similarity 99.4%; Pred. No. 2.4e-292;  
Matches 715; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
QY 1 MKLNQDQKHSFSSNAKVXISTDSLNKQETDIELQINIHEDCLKMSEYENVEPVFSASTI 60  
Db 1 MKLNQDQKHSFSSNAKVXISTDSLNKQETDIELQINIHEDCLKMSEYENVEPVFSASTI 60  
QY 61 QTGGIAGKLTGLGVFPAGQVSLYFTLIGELWPKGKQWEIFMSEHVEIINQKISTYA 120  
Db 61 QTGGIAGKLTGLGVFPAGQVSLYFTLIGELWPKGKQWEIFMSEHVEIINQKISTYA 120  
QY 121 RNKALTDLKGLDALVYHDSLSWGVRNNTARSVKSQYIALEIMFVKLPSPAVSG 180  
Db 121 RNKALTDLKGLDALVYHDSLSWGVRNNTARSVKSQYIALEIMFVKLPSPAVSG 180

QY 181 BEVPILPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFFYNQVERAGDYSYHCVKWS 240  
Db 181 BEVPILPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFFYNQVERAGDYSYHCVKWS 240  
QY 241 TGLNLRGTAESWRYNQFRDMLMVLDLVALPSPYDTQMPYIKTTAQLFREYVTDAL 300  
Db 241 TGLNLRGTAESWRYNQFRDMLMVLDLVALPSPYDTQMPYIKTTAQLFREYVTDAL 300  
QY 301 GTVHPHPSFTSTWYNNNAPSFAEAAVVRNPHLLDFLEQVTIYSLLSRWSTQVMNMW 360  
Db 301 GTVHPHPSFTSTWYNNNAPSFAEAAVVRNPHLLDFLEQVTIYSLLSRWSTQVMNMW 360  
QY 361 GGHKLEFRITGTLNISTQGSTNTSINPVTLPFTSRDVRVYTESLAGLNLFLTQPVNGVPR 420  
Db 361 GGHKLEFRITGTLNISTQGSTNTSINPVTLPFTSRDVRVYTESLAGLNLFLTQPVNGVPR 420  
QY 421 VDFHWKFTVTHPIASDNFYVPGVAGIGTOLQDSENELPPEATGQPNYVSHLSHIGLIS 480  
Db 421 VDFHWKFTVTHPIASDNFYVPGVAGIGTOLQDSENELPPEATGQPNYVSHLSHIGLIS 480  
QY 481 ASHVKALVYSWTHRSADRINTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
Db 481 ASHVKALVYSWTHRSADRINTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
QY 541 TGTGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLDYK 600  
Db 541 TGTGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLDYK 600  
QY 601 TERTVGTTPPSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAYSDFEKAQEKV 660  
Db 601 TERTVGTTPPSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAYSDFEKAQEKV 660  
QY 661 TALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDEFYLDKRELFEIVKYNELHIERNM 719  
Db 661 TALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDEFYLDKRELFEIVKYNELHIERNM 719

RESULT 10  
ID AAE36274 standard; protein; 719 AA.

XX AAE36274;  
XX 26-JUN-2003 (first entry)  
DT B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa4.  
DE Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.  
XX Bacillus thuringiensis.  
XX WO200298911-A2.  
XX 12-DEC-2002.  
XX 30-MAY-2002; 2002WO-GB002666.  
XX 07-JUN-2001; 2001GB-00013900.  
XX (SYGN ) SYNGENTA LTD.  
XX Vincent JL, Viner R;  
XX WPI; 2003-175137/17.

PT New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.  
XX Claim 12; Page 50-53; 67pp; English.  
XX The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are

CC resistant to insects. The protein or synergistic combination is useful as  
 CC an active ingredient of a pesticide or for controlling insects.  
 CC Antibodies raised to the insecticidal proteins can be used to identify  
 CC other proteins with insecticidal activity. The present sequence is  
 CC Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This  
 CC sequence is used in the invention  
 XX  
 XX Sequence 719 AA;

Query Match 99.4%; Score 3739; DB 6; Length 719;  
 Best Local Similarity 99.4%; Pred. No. 2.4e-292;  
 Matches 715; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MKLNQDKHQSFSSNAKVDKISTDSLNKNETDIELQNHEDCLKMSYENVEPVSASTI 60  
 DB 1 MKLNQDKHQSFSSNAKVDKISTDSLNKNETDIELQNHEDCLKMSYENVEPVSASTI 60

QY 61 QTGIGIAGKILGTGVPFAGQVASYLSIFGLMFKGNQWEIEMHVEEILNQKISTYA 120  
 DB 61 QTGIGIAGKILGTGVPFAGQVASYLSIFGLMFKGNQWEIEMHVEEILNQKISTYA 120

QY 121 RNKALTDLKGDLAVYHDSLESWGNRNTRARSVVKSQYIALELMFVKLPFAVSG 180  
 DB 121 RNKALTDLKGDLAVYHDSLESWGNRNTRARSVVKSQYIALELMFVKLPFAVSG 180

QY 181 BEVPLLPYIAQAANLHLLLRDASIFGKESWGLSSSEISTFNNRQVERAGDYSYHCVKWS 240  
 DB 181 BEVPLLPYIAQAANLHLLLRDASIFGKESWGLSSSEISTFNNRQVERAGDYSYHCVKWS 240

QY 241 TGLNNLRGTNAESWRYNQFRDMLVLDLVALPSPYDTOMYPIKTTAQLTRVYTDAL 300  
 DB 241 TGLNNLRGTNAESWRYNQFRDMLVLDLVALPSPYDTOMYPIKTTAQLTRVYTDAL 300

QY 301 GTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDLEQVTTIYSLSRWSNTQYNNMW 360  
 DB 301 GTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDLEQVTTIYSLSRWSNTQYNNMW 360

QY 361 GGHKLEFRTIGTGLNISQGSTNTSINPVTLPFTSRDVRTESLAGLNLFLOPVGVP 420  
 DB 361 GGHKLEFRTIGTGLNISQGSTNTSINPVTLPFTSRDVRTESLAGLNLFLOPVGVP 420

QY 421 VDFHMKFVTHPIASDNFYYPGYAGIGTQDSENELPPEATQPNYESYSHLSHIGLIS 480  
 DB 421 VDFHMKFVTHPIASDNFYYPGYAGIGTQDSENELPPEATQPNYESYSHLSHIGLIS 480

QY 481 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 540  
 DB 481 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 540

QY 541 TGTFGDIRVNNPPPAQRVYRIRVASTTDLQFHTSINGKAINQGNFSATNRCEDLDYK 600  
 DB 541 TGTFGDIRVNNPPPAQRVYRIRVASTTDLQFHTSINGKAINQGNFSATNRCEDLDYK 600

QY 601 TPTVGTFTPTSPFLDVQSTFTIGAWNFSNGNEVIDRIEFVPEVTEAEVDPEKAEKV 660  
 DB 601 TPTVGTFTPTSPFLDVQSTFTIGAWNFSNGNEVIDRIEFVPEVTEAEVDPEKAEKV 660

QY 661 TALFTSTNPRGLTKDVKDHYDQVNLVESLSDEFYLDKELFEIVKAYANELHIERNM 719  
 DB 661 TALFTSTNPRGLTKDVKDHYDQVNLVESLSDEFYLDKELFEIVKAYANELHIERNM 719

RESULT 11  
 ID AAE36271  
 XX AAE36271 standard; protein; 718 AA.  
 AC AAE36271;  
 XX  
 XX 26-JUN-2003 (first entry)  
 XX  
 DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa.  
 XX  
 XX Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.  
 KW

XX Bacillus thuringiensis.  
 OS WO200298911-A2.  
 PN 12-DEC-2002.  
 XX 30-MAY-2002; 2002WO-GB002666.  
 XX 07-JUN-2001; 2001GB-00013900.  
 PR (SYGN ) SYNGENTA LTD.  
 PA Vincent JL, Viner R;  
 XX MPI; 2003-175137/17.  
 XX New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.  
 PT Claim 12; Page 42-44; 67pp; English.  
 XX The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects.  
 CC Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is  
 CC Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This  
 CC sequence is used in the invention  
 XX  
 XX Sequence 718 AA;

Query Match 99.2%; Score 3730.5; DB 6; Length 718;  
 Best Local Similarity 99.4%; Pred. No. 1.2e-291;  
 Matches 715; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 1 MKLNQDKHQSFSSNAKVDKISTDSLNKNETDIELQNHEDCLKMSYENVEPVSASTI 60  
 DB 1 MKLNQDKHQSFSSNAKVDKISTDSLNKNETDIELQNHEDCLKMSYENVEPVSASTI 60

QY 61 QTGIGIAGKILGTGVPFAGQVASYLSIFGLMFKGNQWEIEMHVEEILNQKISTYA 120  
 DB 61 QTGIGIAGKILGTGVPFAGQVASYLSIFGLMFKGNQWEIEMHVEEILNQKISTYA 120

QY 121 RNKALTDLKGDLAVYHDSLESWGNRNTRARSVVKSQYIALELMFVKLPFAVSG 180  
 DB 121 RNKALTDLKGDLAVYHDSLESWGNRNTRARSVVKSQYIALELMFVKLPFAVSG 180

QY 181 BEVPLLPYIAQAANLHLLLRDASIFGKESWGLSSSEISTFNNRQVERAGDYSYHCVKWS 240  
 DB 181 BEVPLLPYIAQAANLHLLLRDASIFGKESWGLSSSEISTFNNRQVERAGDYSYHCVKWS 240

QY 241 TGLNNLRGTNAESWRYNQFRDMLVLDLVALPSPYDTOMYPIKTTAQLTRVYTDAL 300  
 DB 241 TGLNNLRGTNAESWRYNQFRDMLVLDLVALPSPYDTOMYPIKTTAQLTRVYTDAL 300

QY 301 GTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDLEQVTTIYSLSRWSNTQYNNMW 360  
 DB 301 GTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDLEQVTTIYSLSRWSNTQYNNMW 360

QY 361 GGHKLEFRTIGTGLNISQGSTNTSINPVTLPFTSRDVRTESLAGLNLFLOPVGVP 420  
 DB 361 GGHKLEFRTIGTGLNISQGSTNTSINPVTLPFTSRDVRTESLAGLNLFLOPVGVP 420

QY 421 VDFHMKFVTHPIASDNFYYPGYAGIGTQDSENELPPEATQPNYESYSHLSHIGLIS 480  
 DB 421 VDFHMKFVTHPIASDNFYYPGYAGIGTQDSENELPPEATQPNYESYSHLSHIGLIS 480

QY 481 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 540  
 DB 481 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 540

QY 541 TGTGDIRVNINPPFAQRYRIRYASTTDLOFHTSINGKAINQGNFSATWNRGSDLDYK 600  
 Db 540 TGTGDIRVNINPPFAQRYRIRYASTTDLOFHTSINGKAINQGNFSATWNRGSDLDYK 599  
 QY 601 TFRVGTFTPSFLDVOSTFTTIGAWNFSSGNEVYDRIEFVPEVTVYEAEDPEKAQEKV 660  
 Db 600 TFRVGTFTPSFLDVOSTFTTIGAWNFSSGNEVYDRIEFVPEVTVYEAEDPEKAQEKV 659  
 QY 661 TALFTSTNPRGLKTDVKDHYDQVSNLVESLSDFYLDKRELFEIVKYAKQLHIERNM 719  
 Db 660 TALFTSTNPRGLKTDVKDHYDQVSNLVESLSDFYLDKRELFEIVKYAKQLHIERNM 718

RESULT 12  
 AAB66907 standard; protein; 718 AA.  
 XX AAB66907;  
 AC  
 DT 12-APR-2001 (first entry)  
 DE Insecticidal protein cryIIa1.  
 XX  
 XX Insecticide; transgenic plant; insect-resistance.  
 KW  
 OS Paecilomyces sp.  
 XX  
 XX WO200100841-A1.  
 PN  
 PD 04-JAN-2001.  
 XX  
 XX 23-JUN-2000; 2000WO-GB002457.  
 XX  
 XX 29-JUN-1999; 99GB-00015215.  
 PR 23-DEC-1999; 99GB-00030536.  
 XX  
 XX (ZENE) ZENECA LTD.  
 PA  
 XX Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;  
 PI Vincent JL, Lee MD;  
 XX WPI; 2001-123015/13.  
 XX  
 PT Novel insecticidal protein obtained from species of Paecilomyces for  
 PT controlling insects, and for insect-resistant transgenic plant  
 PT production.  
 XX  
 XX Claim 14; Page 53-55; 72pp; English.  
 XX  
 CC The present invention relates to novel insecticidal proteins obtained  
 CC from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The  
 CC insecticidal proteins can be used to produce transgenic plants, which are  
 CC insect-resistant. Also, the insecticidal proteins are useful for  
 CC controlling insects by providing them at a locus where insects feed  
 XX  
 SQ Sequence 718 AA;

Query Match 99.0%; Score 3724.5; DB 4; Length 718;  
 Best Local Similarity 99.3%; Pred. No. 3.6e-291;  
 Matches 714; Conservative 1; Mismatches 3; Indels 1; Gaps 1;  
 QY 1 MKLNQDQKXOFSSNAKVDKISTDSLKNETDIELQNHEDCLKMEYENVEPFVSASTI 60  
 Db 1 MKLNQDQKXOFSSNAKVDKISTDSLKNETDIELQNHEDCLKMEYENVEPFVSASTI 60  
 QY 61 QTGIGIAGKILGTGVFPFAQVSLYSFILGELWPKGQWEIFMEHVEEINQKISTYA 120  
 Db 61 QTGIGIAGKILGTGVFPFAQVSLYSFILGELWPKGQWEIFMEHVEEINQKISTYA 120  
 QY 121 RNKALTDLKGLDALVYHDSLESWGVRNNTPARSVKSYIALBLMFVKQLPSFVSG 180  
 Db 121 RNKALTDLKGLDALVYHDSLESWGVRNNTPARSVKSYIALBLMFVKQLPSFVSG 180

QY 181 BEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWYS 240  
 Db 181 BEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWYS 240  
 QY 241 TGNLNLRGNTNABSWRYNQFRDWTLMVLDIVALPESVDYDQMYPIKTTAQLTREVYTDAL 300  
 Db 241 TGNLNLRGNTNABSWRYNQFRDWTLMVLDIVALPESVDYDQMYPIKTTAQLTREVYTDAL 300  
 QY 301 GTVHPHPSFTSTWYNNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWNTQYMNW 360  
 Db 301 GTVHPHPSFTSTWYNNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWNTQYMNW 360  
 QY 361 GGHKLEFRTIGTLMNISTQGSTNTSINPVLPTFTSRDVTRESLAGLNLFLTPQVNGVPR 420  
 Db 361 GGHKLEFRTIGTLMNISTQGSTNTSINPVLPTFTSRDVTRESLAGLNLFLTPQV 419  
 QY 421 VDFHWKFVTHPIASDNFYYPGAGIGTOLQDSENELPPEATGQPNYESYSHRSLHIGLIS 480  
 Db 420 VDFHWKFVTHPIASDNFYYPGAGIGTOLQDSENELPPEATGQPNYESYSHRSLHIGLIS 479  
 QY 481 ASHVKALVYSWTHRSADRTNTEPNSTIQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540  
 Db 480 ASHVKALVYSWTHRSADRTNTEPNSTIQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 539  
 QY 541 TGTGDIRVNINPPFAQRYRIRYASTTDLOFHTSINGKAINQGNFSATWNRGSDLDYK 600  
 Db 540 TGTGDIRVNINPPFAQRYRIRYASTTDLOFHTSINGKAINQGNFSATWNRGSDLDYK 599  
 QY 601 TFRVGTFTPSFLDVOSTFTTIGAWNFSSGNEVYDRIEFVPEVTVYEAEDPEKAQEKV 660  
 Db 600 TFRVGTFTPSFLDVOSTFTTIGAWNFSSGNEVYDRIEFVPEVTVYEAEDPEKAQEKV 659  
 QY 661 TALFTSTNPRGLKTDVKDHYDQVSNLVESLSDFYLDKRELFEIVKYAKQLHIERNM 719  
 Db 660 TALFTSTNPRGLKTDVKDHYDQVSNLVESLSDFYLDKRELFEIVKYAKQLHIERNM 718

RESULT 13  
 ADM74717  
 ID ADM74717 standard; protein; 719 AA.  
 XX  
 AC ADM74717;  
 XX  
 DT 03-JUN-2004 (first entry)  
 XX  
 DE B. thuringiensis cryIIel SEQ ID NO:2.  
 XX  
 KW cryI; toxicity; lepidoptera; cryIab; cryIba; coleoptera; diptera;  
 KW cryIIel.  
 XX  
 OS Bacillus thuringiensis.  
 XX  
 PN CN1401772-A.  
 XX  
 PD 12-MAR-2003.  
 XX  
 PF 20-AUG-2001; 2001CN-00124163.  
 XX  
 XX 20-AUG-2001; 2001CN-00124163.  
 PR  
 XX (PLAN-) PLANT PROTECTION INST CHINESE ACAD AGRIC.  
 PA  
 XX Song F, Zhang J, Huang D;  
 PI WPI; 2003-442339/42.  
 DR N-PSDB; ADM74716.  
 XX  
 XX Bacillus thuringiensis cryI gene, expression vector, nucleotide sequence  
 PT with high-toxicity to lepidoptera pests, encoded protein, primer  
 PT sequences and the shuttle vector pSXY422b, useful as a pesticide.  
 XX  
 PS Example 3; SEQ ID NO:2; 29pp; Chinese.

```
XX CC The invention relates to a novel Bacillus thuringiensis cryI gene, gene
CC combination, expression vector, nucleotide sequence of the B
CC thuringiensis cryI gene with high-toxicity to lepidoptera pests and the
CC amino acid sequence of the protein encoded by it, cooperative use of the
CC cryI gene with the expression product of cryIaB or cryIaC, primer
CC sequences for expressing the genes, and the constructed shuttle vector
CC pSx422b. The gene in combination with the cryIaB or cryIaC genes
CC displays high toxicity to the lepidoptera, coleoptera and diptera pests.
XX The present sequence represents the cryIIel protein.
XX Sequence 719 AA;

Query Match 93.9%; Score 3534; DB 7; Length 719;
Best Local Similarity 93.2%; Pred. No. 8.3e-276; Mismatches 22; Indels 0; Gaps 0;
Matches 670; Conservative 27;

QY 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNIHEDCLKMSYEYENVEPVSASTI 60
DB 1 MKLKNPDKHQSLSSNAKVDKISTDSLKNETDIELKNIHEDFLRMSEHESIDPVSASTI 60

QY 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNOWEIMFHVHEIINQKISTYA 120
DB 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNOWEIMFHVHEIINQKISTYA 120

QY 121 RNKALTDLKGDLAVYHDSLESVGNRNNTARSVVKSQYIALELMFVQKLPSPFAVSG 180
DB 121 RNIALADLKGDLAVYHDSLESVGNRNNTARSVVKSQYIALELMFVQKLPSPFAVSG 180

QY 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSHVCWKYS 240
DB 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSHVCWKYS 240

QY 241 TGLNNLRGNTAESWRYNQFRKDMTLMVLDLVALPSPSYDTQMPYIKTAQITREVVYDAI 300
DB 241 TGLNNLRGNTAESWRYNQFRKDMTLMVLDLVALPSPSYDTQMPYIKTAQITREVVYDAI 300

QY 301 GTVHPHPSFTSTWYNNAPSFSAEAAVVRNPHLLDFLEQVTIYSLLSRWNTQYNNMW 360
DB 301 GTVHPNASFSTWYNNAPSFSAEAAVVRNPHLLDFLEQVTIYSLLSRWNTQYNNMW 360

QY 361 GGHKLEFRITGGTINISTQGSTNTSINPVTLPFTSRDVTYRTESLAGLNLFTQPVNGVPR 420
DB 361 GGHKLEFRITGGTINISTQGSTNTSINPVTLPFTSRDVTYRTESLAGLNLFTQPVNGVPR 420

QY 421 VDFHWKFVTHPIASDNFYYPGAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLIS 480
DB 421 VDFHWKFATLPASDNFYYPGAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLIS 480

QY 481 ASHVKALVSWTHRADRTNIERNSTQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 540
DB 481 ASHVKALVSWTHRADRTNIERNSTQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 540

QY 541 TGTFGDIRVNIINPPAQVRVRIYASTTDLQFHTSINGKAINQGNFSATWNRGEDLDYK 600
DB 541 TGTFGDIRVNIINPPAQVRVRIYASTTDLQFHTSINGKAINQGNFSATWNRGEDLDYK 600

QY 601 TPTRTVGFTPTPSFLDVQSTFTIGANFSGNEVYIDRIEFVPEVVEYAEVDFEKAQEKV 660
DB 601 TPTRTVGFTPTPSFLDVQSTFTIGANFSGNEVYIDRIEFVPEVVEYAEVDFEKAQEKV 660

QY 661 TALFTSTNPRGLTKDVKDHIDQVNLVLESIDFEYLDKRELFEIVKYANELHIERNM 719
DB 661 TALFTSTNPRGLTKDVKDHIDQVNLVLESIDFEYLDKRELFEIVKYAQIHIERNM 719

RESULT 14
ID AAB66912
XX AAB66912 standard; protein; 719 AA.
AC AAB66912;
XX 12-APR-2001 (first entry)
```

```
XX Insecticidal protein cryIb1.
DE Insecticide; transgenic plant; insect-resistance.
KW Paecilomyces sp.
OS WO200100841-A1.
PN 04-JAN-2001.
PD 23-JUN-2000; 2000WO-GB002457.
PF 29-JUN-1999; 99GB-00015215.
PR 23-DEC-1999; 99GB-00030536.
PX (ZENE ) ZENECA LTD.
PY Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;
PI Vincent JL, Lee MD;
XX WPI; 2001-123015/13.
DR Novel insecticidal protein obtained from species of Paecilomyces for
PT controlling insects, and for insect-resistant transgenic plant
production.
XX Claim 14; Page 64-66; 72pp; English.
XX The present invention relates to novel insecticidal proteins obtained
CC from Paecilomyces sp. (see AAB66912 to AAB66913). The
CC insecticidal proteins can be used to produce transgenic plants, which are
CC insect-resistant. Also, the insecticidal proteins are useful for
CC controlling insects by providing them at a locus where insects feed
XX Sequence 719 AA;

Query Match 93.1%; Score 3503; DB 4; Length 719;
Best Local Similarity 92.5%; Pred. No. 2.6e-273; Mismatches 22; Indels 0; Gaps 0;
Matches 665; Conservative 32;

QY 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNIHEDCLKMSYEYENVEPVSASTI 60
DB 1 MKLKNPDKHQSLSSNAKVDKISTDSLKNETDIELKNIHEDFLRMSEHESIDPVSASTI 60

QY 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNOWEIMFHVHEIINQKISTYA 120
DB 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNOWEIMFHVHEIINQKISTYA 120

QY 121 RNKALTDLKGDLAVYHDSLESVGNRNNTARSVVKSQYIALELMFVQKLPSPFAVSG 180
DB 121 RNKALSDLAGDLAVYHDSLESVGNRNNTARSVVKSQYIALELMFVQKLPSPFAVSG 180

QY 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSHVCWKYS 240
DB 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSHVCWKYS 240

QY 241 TGLNNLRGNTAESWRYNQFRKDMTLMVLDLVALPSPSYDTQMPYIKTAQITREVVYDAI 300
DB 241 TGLNNLRGNTAESWRYNQFRKDMTLMVLDLVALPSPSYDTQMPYIKTAQITREVVYDAI 300

QY 301 GTVHPHPSFTSTWYNNAPSFSAEAAVVRNPHLLDFLEQVTIYSLLSRWNTQYNNMW 360
DB 301 GTVHPNQAFSTWYNNAPSFSAEAAVVRNPHLLDFLEQVTIYSLLSRWNTQYNNMW 360

QY 361 GGHKLEFRITGGTINISTQGSTNTSINPVTLPFTSRDVTYRTESLAGLNLFTQPVNGVPR 420
DB 361 GGHKLEFRITGGTINISTQGSTNTSINPVTLPFTSRDVTYRTESLAGLNLFTQPVNGVPR 420

QY 421 VDFHWKFVTHPIASDNFYYPGAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLIS 480
DB 421 VDFHWKFPTLPASDNFYYPGAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLIS 480
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QY 481 ASHVXALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRTN 540  
DB 481 ASHVXALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRTN 540  
QY 541 TGTGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLDYK 600  
DB 541 TGTGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLDYK 600  
QY 601 TFRVGTFTTFFSFLDVOSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAAYDDEKAQEKV 660  
DB 601 TFRVGTFTTFFSFLDVOSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAAYDDEKAQEKV 660  
QY 661 TALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719  
DB 661 TALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719

RESULT 15

AAE36276 standard; protein; 719 AA.

AAE36276;

26-JUN-2003 (first entry)

B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIb1.  
Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.

Bacillus thuringiensis.

W0200298911-A2.

12-DEC-2002.

30-MAY-2002; 2002WO-GB002566.

07-JUN-2001; 2001GB-00013900.

(SYGN ) SYNGENTA LTD.

Vincent JL, Viner R;

WPI; 2003-175137/17.

New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.

Claim 12; Page 56-58; 67pp; English.

The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects. Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention

Sequence 719 AA;

Query Match 93.1%; Score 3503; DB 6; Length 719;  
Best Local Similarity 92.5%; Pred. No. 2.6e-273;  
Matches 665; Conservative 32; Mismatches 22; Indels 0; Gaps 0;

QY 1 MKLNQDKHQSFSNAKVXDISTDSLNKNETDIELQNHEDCLKMSEYENVEPFFVASTI 60  
DB 1 MKLNQDKHQSFSNAKVXDISTDSLNKNETDIELQNHEDCLKMSEYENVEPFFVASTI 60  
QY 61 QTGIGIAGKILGLVGPFAQIASLSFILGELWPKGKQWEIFMEHVEEIIINOKISTYA 120  
DB 61 QTGIGIAGKILGLVGPFAQIASLSFILGELWPKGKQWEIFMEHVEEIIINOKILTYA 120

QY 121 RNKALTDLKGLDALAVYHDSLESVGNENNRTRRSVYKSOVIALELMFVQKLPSFAVSG 180  
DB 121 RNKALSDUEGLDALAVYHDSLESVGNENNRTRRSVYKSOVIALELMFVQKLPSFAVSG 180  
QY 181 BEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFFYNRQVERAGDYSYHCVKWS 240  
DB 181 BEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFFYNRQVERAGDYSYHCVKWS 240  
QY 241 TGNNLRGTNAESWRYNQFRDMLMVLVALPSPYDTOMYPIKTAQLTREVYTDAL 300  
DB 241 TGNNLRGTNAESWRYNQFRDMLMVLVALPSPYDTOMYPIKTAQLTREVYTDAL 300  
QY 301 GTVHPHPSFTSTWYNNNAPSAAEAAVWRNPHLLDLEOVYIYSLLSRWSNTQYMMW 360  
DB 301 GTVHPHPSFTSTWYNNNAPSAAEAAVWRNPHLLDLEOVYIYSLLSRWSNTQYMMW 360  
QY 361 GGHLEFRITGGTLNISTGGSTNTSINPVTLPFTGRDVYRTESLAGLNLFTQPVNGVPR 420  
DB 361 GGHLEFRITGGTLNISTGGSTNTSINPVTLPFTGRDVYRTESLAGLNLFTQPVNGVPR 420  
QY 421 VDFHWKFVTHPIASDNFYYPGAGIGTQDSENELPPEATGQPNYESYSHLSHIGLIS 480  
DB 421 VDFHWKFVTHPIASDNFYYPGAGIGTQDSENELPPEATGQPNYESYSHLSHIGLIS 480  
QY 481 ASHVXALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRTN 540  
DB 481 ASHVXALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRTN 540  
QY 541 TGTGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLDYK 600  
DB 541 TGTGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLDYK 600  
QY 601 TFRVGTFTTFFSFLDVOSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAAYDDEKAQEKV 660  
DB 601 TFRVGTFTTFFSFLDVOSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAAYDDEKAQEKV 660  
QY 661 TALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719  
DB 661 TALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719

Search completed: October 28, 2004, 18:19:59  
Job time : 91.6903 secs



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## OM protein - protein search, using sw model

Run on: October 28, 2004, 18:10:58 ; Search time 65.6795 Seconds  
(without alignments)  
3549.224 Million cell updates/sec

Title: US-10-019-823B-56

Perfect score: 3762

Sequence: 1 MLLKNQDKHQSFSSNAKVDK.....KRELFIVKYANELHIERNM 719

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1370721 seqs, 32415800 residues

Total number of hits satisfying chosen parameters: 1370721

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

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- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pap.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pap.\*
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- 19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pap.\*
- 20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	3743	99.5	719	17	US-10-782-020-10 Sequence 10, Appl
2	3743	99.5	719	17	US-10-782-141-8 Sequence 8, Appl
3	3743	99.5	719	17	US-10-782-096-10 Sequence 10, Appl
4	3743	99.5	719	17	US-10-782-570-7 Sequence 7, Appl
5	3459.5	92.0	710	14	US-10-428-961-42 Sequence 42, Appl
6	2263.5	60.2	1228	16	US-10-809-953-10 Sequence 10, Appl
7	2250.5	59.8	1207	10	US-09-988-462-7 Sequence 7, Appl
8	2271.5	57.7	1227	14	US-10-428-961-63 Sequence 63, Appl
9	2156.5	57.3	1186	9	US-09-826-660-23 Sequence 23, Appl
10	2101	55.8	1228	14	US-10-428-961-38 Sequence 38, Appl
11	2101	55.8	1228	15	US-10-614-524-2 Sequence 2, Appl
12	1923.5	51.1	643	9	US-09-826-660-25 Sequence 25, Appl
13	1707.5	45.4	1167	14	US-10-089-678-1 Sequence 1, Appl

14	1678.5	44.6	653	14	US-10-428-961-6	Sequence 6, Appl
15	1655.5	44.0	1157	17	US-10-782-141-36	Sequence 16, Appl
16	1655.5	44.0	1157	17	US-10-782-096-17	Sequence 17, Appl
17	1655.5	44.0	1157	17	US-10-782-570-13	Sequence 13, Appl
18	1496	39.8	1206	13	US-10-032-717-2	Sequence 2, Appl
19	1496	39.8	1206	14	US-10-414-637-2	Sequence 2, Appl
20	1496	39.8	1206	15	US-10-606-320-2	Sequence 2, Appl
21	1496	39.8	1206	17	US-10-746-914-2	Sequence 2, Appl
22	1480	39.3	1210	13	US-10-032-717-4	Sequence 4, Appl
23	1480	39.3	1210	14	US-10-414-637-4	Sequence 4, Appl
24	1480	39.3	1210	15	US-10-606-320-4	Sequence 4, Appl
25	1480	39.3	1210	17	US-10-746-914-4	Sequence 4, Appl
26	1476.5	39.2	1156	14	US-10-099-285-72	Sequence 72, Appl
27	1476.5	39.2	1156	14	US-10-428-961-28	Sequence 28, Appl
28	1452	38.6	1155	9	US-09-756-643-2	Sequence 2, Appl
29	1452	38.6	1155	10	US-09-988-462-9	Sequence 9, Appl
30	1452	38.6	1155	14	US-10-136-998A-2	Sequence 2, Appl
31	1452	38.6	1177	14	US-10-035-060-6	Sequence 6, Appl
32	1452	38.6	1181	10	US-09-988-462-11	Sequence 11, Appl
33	1452	38.6	1181	10	US-09-988-462-13	Sequence 13, Appl
34	1452	38.6	1181	10	US-09-988-462-15	Sequence 15, Appl
35	1452	38.6	1181	10	US-09-988-462-17	Sequence 17, Appl
36	1452	38.6	1181	10	US-09-988-462-28	Sequence 28, Appl
37	1452	38.6	1181	14	US-10-136-998A-4	Sequence 4, Appl
38	1452	38.6	1181	14	US-10-136-998A-8	Sequence 8, Appl
39	1452	38.6	1181	14	US-10-136-998A-10	Sequence 10, Appl
40	1452	38.6	1181	14	US-10-136-998A-12	Sequence 12, Appl
41	1447	38.5	1177	14	US-10-035-060-2	Sequence 2, Appl
42	1445	38.4	1177	14	US-10-035-060-8	Sequence 8, Appl
43	1444	38.4	1177	14	US-10-102-469-24	Sequence 24, Appl
44	1428.5	38.0	1176	17	US-10-782-141-6	Sequence 6, Appl
45	1428.5	38.0	1176	17	US-10-782-096-7	Sequence 7, Appl

## ALIGNMENTS

## RESULT 1

US-10-782-020-10  
; Sequence 10, Application US/10782020  
; Publication No. US20040197916A1  
; GENERAL INFORMATION:  
; APPLICANT: Carozzi, Nadine  
; APPLICANT: Hargiss, Tracy  
; APPLICANT: Kozziel, Michael G.  
; APPLICANT: Duck, Nicholas B.  
; APPLICANT: Carr, Brian  
; TITLE OF INVENTION: AXMI-004, A Delta-Endotoxin Gene and  
; TITLE OF INVENTION: Methods for Its Use  
; FILE REFERENCE: 045600/274139  
; CURRENT APPLICATION NUMBER: US/10/782,020  
; CURRENT FILING DATE: 2004-02-19  
; PRIOR APPLICATION NUMBER: 60/448,810  
; PRIOR FILING DATE: 2003-02-20  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 719  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
; US-10-782-020-10

Query Match 99.5%; Score 3743; DB 17; Length 719;

Best Local Similarity 99.6%; Pred. No. 3.7e-307;

Matches 716; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MLLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKNSEYENVPFVSASTI 60

Db 1 MLLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKNSEYENVPFVSASTI 60

QY 61 QTGTGIACKILGTGLVPPAGQVASYLSFILGELPKGNQWEIEMHEVERILNOKISTYA 120

Db 61 QTGTGIACKILGTGLVPPAGQVASYLSFILGELPKGNQWEIEMHEVERILNOKISTYA 120

121 RNKALTDLKGIGDALAVYHDSLEWVGNNRNRARSVVKSOYIALELMFVQKLPFAVSG 180  
 121 RNKALTDLKGIGDALAVYHDSLEWVGNNRNRARSVVKSOYIALELMFVQKLPFAVSG 180  
 181 BEVPLLPPIYAQAANLHLLLRDASIFGKWLSSSEISTFYNNRQVERAGDYSYHCVKWS 240  
 181 BEVPLLPPIYAQAANLHLLLRDASIFGKWLSSSEISTFYNNRQVERAGDYSYHCVKWS 240  
 241 TGLNLRGTNAESWVRNQFRDMLVLDLVALPSPYDTQMPYIKTTAQLTREVTDAI 300  
 241 TGLNLRGTNAESWVRNQFRDMLVLDLVALPSPYDTQMPYIKTTAQLTREVTDAI 300  
 301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYNNMW 360  
 301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYNNMW 360  
 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRYSYSHRSLSHIGLIS 420  
 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRYSYSHRSLSHIGLIS 420  
 421 VDFHWKFTVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRSLSHIGLIS 480  
 421 VDFHWKFTVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRSLSHIGLIS 480  
 481 ASHVKALVYSWTHRSADRNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 540  
 481 ASHVKALVYSWTHRSADRNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 540  
 541 TGTGDIRVNIAPPQARYRVRIRYASTTDLOQFHTSINGKAINQGNFSATWNRGEDLDYK 600  
 541 TGTGDIRVNIAPPQARYRVRIRYASTTDLOQFHTSINGKAINQGNFSATWNRGEDLDYK 600  
 601 TPTVGTFTTFFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVYEAEDFKAQEKV 660  
 601 TPTVGTFTTFFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVYEAEDFKAQEKV 660  
 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVSDEFLDEKRELFEIVKAYANELHIERNM 719  
 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVSDEFLDEKRELFEIVKAYANELHIERNM 719

RESULT 2  
 US-10-782-141-8  
 ; Sequence 8, Application US/10782141  
 ; Publication No. US20040197917A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Carozzi, Nadine  
 ; APPLICANT: Hargiss, Tracy  
 ; APPLICANT: Koziel, Michael G.  
 ; APPLICANT: Duck, Nicholas B.  
 ; APPLICANT: Cart, Brian  
 ; TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and  
 ; TITLE OF INVENTION: Methods for Its Use  
 ; FILE REFERENCE: 045600/274143  
 ; CURRENT APPLICATION NUMBER: US/10/782,141  
 ; CURRENT FILING DATE: 2004-02-20  
 ; PRIOR FILING DATE: 2003-02-20  
 ; NUMBER OF SEQ ID NOS: 23  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 8  
 ; LENGTH: 719  
 ; TYPE: PRT  
 ; ORGANISM: Bacillus thuringiensis  
 US-10-782-141-8

Query Match 99.5%; Score 3743; DB 17; Length 719;  
 Best Local Similarity 99.6%; Pred. No. 3.7e-307;  
 Matches 716; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

1 MKLKNQDQHQSPSSNAKVDKISTDSLKNETDIELQINHNHEDCLKMSYENVEPFFVASTI 60  
 |||||

1 MKLKNQDQHQSPSSNAKVDKISTDSLKNETDIELQINHNHEDCLKMSYENVEPFFVASTI 60  
 61 QTGIGIAGKILGTGVPFAGQVASYLSIFLGELMPKGNQWEIFMEHVVEEIIINOKISTYA 120  
 61 QTGIGIAGKILGTGVPFAGQVASYLSIFLGELMPKGNQWEIFMEHVVEEIIINOKISTYA 120  
 121 RNKALTDLKGIGDALAVYHDSLEWVGNNRNRARSVVKSOYIALELMFVQKLPFAVSG 180  
 121 RNKALTDLKGIGDALAVYHDSLEWVGNNRNRARSVVKSOYIALELMFVQKLPFAVSG 180  
 181 BEVPLLPPIYAQAANLHLLLRDASIFGKWLSSSEISTFYNNRQVERAGDYSYHCVKWS 240  
 181 BEVPLLPPIYAQAANLHLLLRDASIFGKWLSSSEISTFYNNRQVERAGDYSYHCVKWS 240  
 241 TGLNLRGTNAESWVRNQFRDMLVLDLVALPSPYDTQMPYIKTTAQLTREVTDAI 300  
 241 TGLNLRGTNAESWVRNQFRDMLVLDLVALPSPYDTQMPYIKTTAQLTREVTDAI 300  
 301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYNNMW 360  
 301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYNNMW 360  
 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRYSYSHRSLSHIGLIS 420  
 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRYSYSHRSLSHIGLIS 420  
 421 VDFHWKFTVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRSLSHIGLIS 480  
 421 VDFHWKFTVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRSLSHIGLIS 480  
 481 ASHVKALVYSWTHRSADRNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 540  
 481 ASHVKALVYSWTHRSADRNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 540  
 541 TGTGDIRVNIAPPQARYRVRIRYASTTDLOQFHTSINGKAINQGNFSATWNRGEDLDYK 600  
 541 TGTGDIRVNIAPPQARYRVRIRYASTTDLOQFHTSINGKAINQGNFSATWNRGEDLDYK 600  
 601 TPTVGTFTTFFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVYEAEDFKAQEKV 660  
 601 TPTVGTFTTFFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVYEAEDFKAQEKV 660  
 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVSDEFLDEKRELFEIVKAYANELHIERNM 719  
 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVSDEFLDEKRELFEIVKAYANELHIERNM 719

RESULT 3  
 US-10-782-096-10  
 ; Sequence 10, Application US/10782096  
 ; Publication No. US20040210964A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Carozzi, Nadine  
 ; APPLICANT: Hargiss, Tracy  
 ; APPLICANT: Koziel, Michael G.  
 ; APPLICANT: Duck, Nicholas B.  
 ; APPLICANT: Cart, Brian  
 ; TITLE OF INVENTION: AXMI-009, A Delta-Endotoxin Gene and  
 ; TITLE OF INVENTION: Methods for Its Use  
 ; FILE REFERENCE: 045600/274148  
 ; CURRENT APPLICATION NUMBER: US/10/782,096  
 ; CURRENT FILING DATE: 2004-02-19  
 ; PRIOR APPLICATION NUMBER: 60/448,633  
 ; PRIOR FILING DATE: 2003-02-20  
 ; NUMBER OF SEQ ID NOS: 23  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 10  
 ; LENGTH: 719  
 ; TYPE: PRT  
 ; ORGANISM: Bacillus thuringiensis  
 US-10-782-096-10

Query Match 99.5%; Score 3743; DB 17; Length 719;



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; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
; US-10-782-570-7
Query Match      99.5%; Score 3743; DB 17; Length 719;
Best Local Similarity 99.6%; Pred. No. 3.7e-307;
Matches 716; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 M K L N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y E N V E P F V S A S T I 60
Db 1 M K L N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y E N V E P F V S A S T I 60
QY 61 Q T G I G I A G K I L G T L G V P F A G Q V A S L Y S F I L G E L M P K G K N Q W E I F M E H V E E I I N Q I S T Y A 120
Db 61 Q T G I G I A G K I L G T L G V P F A G Q V A S L Y S F I L G E L M P K G K N Q W E I F M E H V E E I I N Q I S T Y A 120
QY 121 R N K A L T D L K G L G D A L A V H D S L E S W G N R N N T R A S V V K S Q Y I A L E M F V K L P S F A V S G 180
Db 121 R N K A L T D L K G L G D A L A V H D S L E S W G N R N N T R A S V V K S Q Y I A L E M F V K L P S F A V S G 180
QY 181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S E I S T F Y N R O V E R A G D Y S H C V K W Y S 240
Db 181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S E I S T F Y N R O V E R A G D Y S H C V K W Y S 240
QY 241 T G L N L R G T N A E S W R Y N Q F R D M T L M V L D L V A L F P S Y D T Q M Y P I K T T A Q L T R E V Y T D A I 300
Db 241 T G L N L R G T N A E S W R Y N Q F R D M T L M V L D L V A L F P S Y D T Q M Y P I K T T A Q L T R E V Y T D A I 300
QY 301 G T V H P H P S F S T T W Y N N N A P S F S A E A A V R N P H L L D F L E Q V T I Y S L L S R W S N T O Y M N W 360
Db 301 G T V H P H P S F S T T W Y N N N A P S F S A E A A V R N P H L L D F L E Q V T I Y S L L S R W S N T O Y M N W 360
QY 361 G G H K L E F R T I G G T L N I S T Q G S T N T S I N P V L P F T S R D V Y R T E S L A G L N L F L T O P V N G V P R 420
Db 361 G G H K L E F R T I G G T L N I S T Q G S T N T S I N P V L P F T S R D V Y R T E S L A G L N L F L T O P V N G V P R 420
QY 421 V D F H W K V T H P I A S D N F Y P G Y A G I G T O L Q D S E N E L P P E A T G Q P N Y E S Y S H R L S H I G L I S 480
Db 421 V D F H W K V T H P I A S D N F Y P G Y A G I G T O L Q D S E N E L P P E A T G Q P N Y E S Y S H R L S H I G L I S 480
QY 481 A S H V K A L V Y S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G D I L R T N 540
Db 481 A S H V K A L V Y S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G D I L R T N 540
QY 541 T G T F G D I R V N I N P P A Q R Y R V R I Y A S T T D L Q P H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 600
Db 541 T G T F G D I R V N I N P P A Q R Y R V R I Y A S T T D L Q P H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 600
QY 601 T F R T V G F T T P F S F L D V Q S T T I G A W N F S S G N E V Y I D R I E F V P V E V Y E A E Y D F E K A Q E K V 660
Db 601 T F R T V G F T T P F S F L D V Q S T T I G A W N F S S G N E V Y I D R I E F V P V E V Y E A E Y D F E K A Q E K V 660
QY 661 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D F Y L D E K R E L F E I V K Y A N E L H I E R N M 719
Db 661 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D F Y L D E K R E L F E I V K Y A N E L H I E R N M 719

RESULT 4
US-10-782-570-7
; Sequence 7, Application US/10782570
; Publication No. US20040210965A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMT-007, A Delta-Endotoxin Gene and
; TITLE OF INVENTION: Methods for Its Use
; FILE REFERENCE: 045600/274144
; CURRENT APPLICATION NUMBER: US/10782, 570
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: 60/448, 812
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 719

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; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
; US-10-782-570-7
Query Match      99.5%; Score 3743; DB 17; Length 719;
Best Local Similarity 99.6%; Pred. No. 3.7e-307;
Matches 716; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 M K L N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y E N V E P F V S A S T I 60
Db 1 M K L N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y E N V E P F V S A S T I 60
QY 61 Q T G I G I A G K I L G T L G V P F A G Q V A S L Y S F I L G E L M P K G K N Q W E I F M E H V E E I I N Q I S T Y A 120
Db 61 Q T G I G I A G K I L G T L G V P F A G Q V A S L Y S F I L G E L M P K G K N Q W E I F M E H V E E I I N Q I S T Y A 120
QY 121 R N K A L T D L K G L G D A L A V H D S L E S W G N R N N T R A S V V K S Q Y I A L E M F V K L P S F A V S G 180
Db 121 R N K A L T D L K G L G D A L A V H D S L E S W G N R N N T R A S V V K S Q Y I A L E M F V K L P S F A V S G 180
QY 181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S E I S T F Y N R O V E R A G D Y S H C V K W Y S 240
Db 181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S E I S T F Y N R O V E R A G D Y S H C V K W Y S 240
QY 241 T G L N L R G T N A E S W R Y N Q F R D M T L M V L D L V A L F P S Y D T Q M Y P I K T T A Q L T R E V Y T D A I 300
Db 241 T G L N L R G T N A E S W R Y N Q F R D M T L M V L D L V A L F P S Y D T Q M Y P I K T T A Q L T R E V Y T D A I 300
QY 301 G T V H P H P S F S T T W Y N N N A P S F S A E A A V R N P H L L D F L E Q V T I Y S L L S R W S N T O Y M N W 360
Db 301 G T V H P H P S F S T T W Y N N N A P S F S A E A A V R N P H L L D F L E Q V T I Y S L L S R W S N T O Y M N W 360
QY 361 G G H K L E F R T I G G T L N I S T Q G S T N T S I N P V L P F T S R D V Y R T E S L A G L N L F L T O P V N G V P R 420
Db 361 G G H K L E F R T I G G T L N I S T Q G S T N T S I N P V L P F T S R D V Y R T E S L A G L N L F L T O P V N G V P R 420
QY 421 V D F H W K V T H P I A S D N F Y P G Y A G I G T O L Q D S E N E L P P E A T G Q P N Y E S Y S H R L S H I G L I S 480
Db 421 V D F H W K V T H P I A S D N F Y P G Y A G I G T O L Q D S E N E L P P E A T G Q P N Y E S Y S H R L S H I G L I S 480
QY 481 A S H V K A L V Y S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G D I L R T N 540
Db 481 A S H V K A L V Y S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G D I L R T N 540
QY 541 T G T F G D I R V N I N P P A Q R Y R V R I Y A S T T D L Q P H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 600
Db 541 T G T F G D I R V N I N P P A Q R Y R V R I Y A S T T D L Q P H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 600
QY 601 T F R T V G F T T P F S F L D V Q S T T I G A W N F S S G N E V Y I D R I E F V P V E V Y E A E Y D F E K A Q E K V 660
Db 601 T F R T V G F T T P F S F L D V Q S T T I G A W N F S S G N E V Y I D R I E F V P V E V Y E A E Y D F E K A Q E K V 660
QY 661 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D F Y L D E K R E L F E I V K Y A N E L H I E R N M 719
Db 661 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D F Y L D E K R E L F E I V K Y A N E L H I E R N M 719

RESULT 5
US-10-428-961-42
; Sequence 42, Application US/10428961
; Publication No. US20030237111A1
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Chu, Chih-Rei
; APPLICANT: Donovan, William P.
; APPLICANT: Gilmer, Amy J.
; APPLICANT: Rupar, Mark J.
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin
; FILE REFERENCE: MECO201--1
; CURRENT APPLICATION NUMBER: US/10/428, 961
; CURRENT FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: 09/661, 322

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; PRIOR FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: 60/153,995
; PRIOR FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 42
; LENGTH: 710
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2007..(200)
; OTHER INFORMATION: The 'xaa' at location 200 stands for any naturally occurring amino acid
US-10-428-961-42

Query Match          92.0%; Score 3459.5; DB 14; Length 710;
Best Local Similarity 92.1%; Pred. No. 3.4e-283;
Matches 562; Conservative 16; Mismatches 32; Indels 9; Gaps 1;

QY 1 MKLKNQDQXQSSNAKVDKISTDSLKNETDIELQNHEDCLCKSEYENVEPVSASTI 60
DB 1 MKSKQNNHQSLNNATVDKFTGSLNNTTELQNFH-----EGIEPVSASTI 51

61 QTGIGIAGKILGTLGVPAGQVASYLSYFILGELPKGNQWEIFMEHVEEIIHQKISTYA 120
DB 52 QTGIGIAGKILGTLGVPAGQVASYLSYFILGELPKGNQWEIFMEHVEEIIHQKISTYA 111

121 RNKALTDLKGADALAVYHDSLESVGNRNTRARSVYKQVIALELMFVQKLPSPAVSG 180
DB 112 RNKALADLKGADALAVYHDSLESVGNRNTRARSVYKQVIALELMFVQKLPSPAVSG 171

181 EEPVLLPIYAQAANLHLLLDASIFGKWEGLSSSEISTFYNRQVERAGDYSHCVKWSY 240
DB 172 EEPVLLPIYAQAANLHLLLDASIFGKWEGLSSSEISTFYNRQVERAGDYSHCVKWSY 231

241 TGLNLRGTNAESWRYNQFRDMLMVLDLVALPSPDYDTQMPYIKTTAQLTREYVTD 300
DB 232 TGLNLRGTNAESWRYNQFRDMLMVLDLVALPSPDYDTQMPYIKTTAQLTREYVTD 291

301 GTVHPHPSFTSTTWNNAAPSAEAAAVRNPHLLDLEQVITYSLSRWSNTQYNNMW 360
DB 292 GTVHPHPSFTSTTWNNAAPSAEAAAVRNPHLLDLEQVITYSLSRWSNTQYNNMW 351

361 GGHKLEFRTIGTLNISTQGSTNTSINPVTLPFTSRDVRYSAGLNLFLTPQVNGVPR 420
DB 352 GGHKLEFRTIGTLNISTQGSTNTSINPVTLPFTSRDVRYSAGLNLFLTPQVNGVPR 411

421 VDFHWKFTVTHPIASDNFYYPGAGIGTQDSENELPPEATGQPNYSYSHRLSHIGLIS 480
DB 412 VDFHWKFTVTHPIASDNFYYPGAGIGTQDSENELPPEATGQPNYSYSHRLSHIGLIS 471

481 ASHVKALVYSWTHRSADRNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
DB 472 ASHVKALVYSWTHRSADRNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 531

541 TGTGDIRVNIAPPQAQRVRIYASTTDLOFHTSINGKAINQGNFSATNWRGEDLDYK 600
DB 532 TGTGDIRVNIAPPQAQRVRIYASTTDLOFHTSINGKAINQGNFSATNWRGEDLDYK 591

601 TPTVGTTPPSFLDQSTFTIGANFSSGNEVYIDRIEFVPEVVEYBAEYDFEKAQEKV 660
DB 592 TPTVGTTPPSFLDQSTFTIGANFSSGNEVYIDRIEFVPEVVEYBAEYDFEKAQEKV 651

661 TALFTSTNPRGLKTDVQYHIDQVSNLVESLDEFYLDKRELFEIVKYANELHIERNM 719
DB 652 TALFTSTNPRGLKTDVQYHIDQVSNLVESLDEFYLDKRELFEIVKYANELHIERNM 710

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RESULT 6  
 US-10-809-953-10  
 ; Sequence 10, Application US/10809953  
 ; Publication No. US20040181825A1  
 ; GENERAL INFORMATION:

```

; APPLICANT: Van Mellaert, Herman
; APPLICANT: Botterman, Johan
; APPLICANT: Van Rie, Jeroen
; APPLICANT: Joos, Henk
; TITLE OF INVENTION: RECOMBINANT PLANT EXPRESSING NON-COMPETITIVELY BINDING BT INSECTICIDAL PROTEINS
; TITLE OF INVENTION: CRYSTAL PROTEINS
; FILE REFERENCE: 021565-078
; CURRENT APPLICATION NUMBER: US/10/809,953
; CURRENT FILING DATE: 2004-03-26
; PRIOR APPLICATION NUMBER: US/09/661,016
; PRIOR FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: PCT/EP90/00905
; PRIOR FILING DATE: 1990-05-30
; PRIOR APPLICATION NUMBER: GB 89401499.2
; PRIOR FILING DATE: 1989-05-31
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 10
; LENGTH: 1228
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
; US-10-809-953-10

Query Match          60.2%; Score 2263.5; DB 16; Length 1228;
Best Local Similarity 62.4%; Pred. No. 1e-181;
Matches 447; Conservative 79; Mismatches 165; Indels 25; Gaps 6;

QY 23 TDSLKNETDIELQNH-----EDCLKMSEYENVEPVSASTIQTGIGIAGKI 70
DB 2 TSNRKNENSIINAVNSHSAQMDLLPDARIEDSLCAEGNNIDFFVSASTVQTGINIAGRI 61

71 LGTLGVPPAGQVASYLSYFILGELPKGNQWEIFMEHVEEIIHQKISTYARNKALTDLKG 130
DB 62 LGTLGVPPAGQVASYLSYFILGELPKGNQWEIFMEHVEEIIHQKISTYARNKALTDLKG 121

131 LGDALAVYHDSLESVGNRNTRARSVYKQVIALELMFVQKLPSPAVSGEVPVLLPIYA 190
DB 122 LGDSFRAYQOQSLDLENRDDARTSVLHTQVIALELDPLNAMPFAIRNQEVPVLLPIYA 181

191 QAANLHLLLRDASIFGKWEGLSSSEISTFYNRQVERAGDYSHCVKWSYTGNNLRGTN 250
DB 182 QAANLHLLLRDASIFGSEFGTSGEIQRYEYERQVTRDYSDYCVIEWNTGLNLRGTN 241

251 ASWRYNQFRDMLMVLDLVALPSPDYDTQMPYIKTTAQLTREYVTDAGTVHHPHPSFT 310
DB 242 AASWRYNQFRDMLMVLDLVALPSPDYDTQMPYIKTTAQLTREYVTDAGTVHHPHPSFT 299

311 SITTYNNNAPSATAEAAVVRNPHLLDLEQVITYSLSRWSNTQYNNMWGGHKLFEFTI 370
DB 300 SMNWNNAAPSATAEAAVVRNPHLLDLEQVITYSLSRWSNTQYNNMWGGHKLFEFTI 359

371 GGTNLNSTQGSTNTSINPVTLPFTSRDVRYSAGLNLFLTPQVNGVPRDVFHWKFTV 428
DB 360 GGTNLNSTQGSTNTSINPVTLPFTSRDVRYSAGLNLFLTPQVNGVPRDVFHWKFTV 416

429 THP-----TASDNFYYPGAGIGTQDSENELPPEATGQPNYSYSHRLSHIGLISASH 483
DB 417 TPNQNSIDRGTYNSQOP-YESPGLQKQSETELPETTERPNEYSYSHRLSHIGLISASH 475

484 VKALVYSWTHRSADRNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 543
DB 476 VNVVYVSWTHRSADRNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 535

544 FGDIRVNIAPPQAQRVRIYASTTDLOFHTSINGKAINQGNFSATNWRGEDLDYK 603
DB 536 FGDIRVNIAPPQAQRVRIYASTTDLOFHTSINGKAINQGNFSATNWRGEDLDYK 595

604 TVGFTTPPSFLDQSTFTIGANFSSGNEVYIDRIEFVPEVVEYBAEYDFEKAQEKV 663
DB 596 RRAFTTPTFTQIDIRTSIQGLSGNGEVYIDRIEFVPEVVEYBAEYDFEKAQEKV 655

664 FTSTNPRGLKTDVQYHIDQVSNLVESLDEFYLDKRELFEIVKYANELHIERNM 719

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Db 656 FTTNPRRLKTDVTDYHIDQVSNLVACLSDBFCLDEKRELLKVKYAKRLSDERNL 711

RESULT 7

US-09-988-462-7

; Sequence 7, Application US/09988462

; Publication No. US20030046726A1

; GENERAL INFORMATION:

; APPLICANT: Koziel, Michael G.

; Desai, Nalini M.

; Lewis, Kelly S.

; Kramer, Vance C.

; Warten, Gregory W.

; Evola, Stephen V.

; Crossland, Lyle D.

; Wright, Martha S.

; Merlin, Ellis J.

; Launis, Karen L.

; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED

; INSECTICIDAL ACTIVITY IN MAIZE

; NUMBER OF SEQUENCES: 94

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Syngenta Biotechnology, Inc.

; STREET: 3054 Cornwallis Road

; CITY: Research Triangle Park

; STATE: NC

; COUNTRY: USA

; ZIP: 27709

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/988,462

; FILING DATE: 20-No. US20030046726A1-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 09/547,422

; FILING DATE: 11-APR-2000

; APPLICATION NUMBER: US 08/459,504

; FILING DATE: 02-JUN-1995

; APPLICATION NUMBER: US 07/951,715

; FILING DATE: 25-SEP-1992

; APPLICATION NUMBER: US 07/772,027

; FILING DATE: 04-OCT-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Meigs, J. Timothy

; REGISTRATION NUMBER: 38,241

; REFERENCE/DOCKET NUMBER: S-188051

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (919)541-8587

; TELEFAX: (919)541-8589

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1207 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 7:

US-09-988-462-7

Query Match 59.8%; Score 2250.5; DB 10; Length 1207;

Best Local Similarity 64.0%; Pred. No. 1.3e-180;

Matches 440; Conservative 77; Mismatches 157; Indels 13; Gaps 5;

40 EDCLKMEYENVPFVASTIQIGIAGKILGTGLVFPFAGQVASYFSLGELNPKGN 99

10 EDSLCTAEGNNIDPFVSAVQGTGINIAGRIILVGLVFPFAGQVASYFSLGELNPKGRD 69

100 QWEIFMHEVEIINOKISTYARNKALTDLKLGDALAVYHDSLESVMGNNRNTARSVVK 159

70 QWEIFLHVQLINQITENARNTALRLQGLGDSFRAVQOQSLDLENRDRARTSVLY 129

160 SOVIALELMFVKLPSPFVSGVEVPLPIYAAANLHLLLRDASIFGKEWGLSSSEIST 219

130 TQYIALELDFINAMPLFAIRNCEVEVLLVYAAANLHLLLRDASLFGSEFLTSQEIOR 189

220 FYNQVERAGDYSYHCWKVYSTGLANLRTGNAESWVRYNQFRDMTLMVLVLPFSSVD 279

190 YVERQVERTRDYSYCVENYNTGLNSLRTGNAASWVRYNQFRDLTLGLVLDLVALFPSSVD 249

280 TQWPIKTTAQLTREVYTDALCTVHPHPSFTTTHVNNNAPSFALEAAVVENPHLLDEL 339

250 TRYPINTSAQLTREVYTDALCAT--GVNMMNNNNNAPSFALEAAAIKSPHLLDEL 307

340 EQVTIYSLLSRWSNTQYMMNMGHKLFEFTIGTGLNISTQGSTNTSINPVTLPFTSRDYY 399

308 EQLTIFSASSRWSNTRHMTYWGHTIQSRPIGGGLNSTHGATNTSINPVTILRFASRDYY 367

400 RTESLAGLNLFP--LTQPVNGVRVDFHWKFVTHP-----IASDNFYFGYAGIGTQLQDS 452

368 RTESYAGVLLWGIYLEPIHGVPTVRFNF---TNPNQISDRGTANYSQP-YESPGQLKDS 423

453 ENELPPEATGQPNYSYSHRLSHIGLISASHVKALVYSWTHRSADRTNTIPNSITQIPL 512

424 ETLELPETTERENYSYSHRLSHIGLILQSRVNVVYVSWTHRSADRTNTIGNRITQIPM 483

513 VKAFNLSSGAAVVRGPGFTGGDILRRNTGTGDIIRVNINPPFAQRYRVIRYASTTDLQ 572

484 VKASELPQGTTVVRGPGFTGGDILRRNTGTGDIIRVNINPPFAQRYRVIRYASTTDFD 543

573 FHTSINGKAINQGNFSATMNGEDLDYKTFRTVGTTPPSFLDVQSTFTIGAWNFSNGNE 632

544 FVSRGGTTVNNFRFLRTMNSGDELYGNFVRATTTFTTQIQDIIRTSIQGLSGNGE 603

633 VYIDRIEFPVPEVTEAYEYDFEKAQEKVLTALFTSNPRGLKTDVKDYHIDQVSNLVESLS 692

604 VYIDKIEIPVTATPEAYEDLERAQEAVALFTNPNRLKTDVTDYHIDQVSNLVACLIS 663

693 DEFYLDKRELPETVVKYANELHIERNM 719

664 DEFCLDEKRELLKVKYAKRLSDERNL 690

RESULT 8

US-10-428-961-63

; Sequence 63, Application US/10428961

; Publication No. US20030237111A1

; GENERAL INFORMATION:

; APPLICANT: Baum, James A.

; APPLICANT: Chu, Chih-Rei

; APPLICANT: Donovan, William P.

; APPLICANT: Gilmer, Amy J.

; APPLICANT: Rugar, Mark J.

; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin

; FILE OF INVENTION: Polynucleotides, Compositions, and Methods of Use (Amended)

; FILE REFERENCE: MEG0201--1

; CURRENT APPLICATION NUMBER: US/10/428,961

; CURRENT FILING DATE: 2003-05-02

; PRIOR APPLICATION NUMBER: 09/661,322

; PRIOR FILING DATE: 2000-09-13

; PRIOR APPLICATION NUMBER: 60/153,995

; PRIOR FILING DATE: 1999-09-15

; NUMBER OF SEQ ID NOS: 63

; SOFTWARE: Patentin version 3.2

; SEQ ID NO 63

; LENGTH: 1227

; TYPE: PRT

; ORGANISM: Bacillus thuringiensis

US-10-428-961-63

Query Match 57.7%; Score 2171.5; DB 14; Length 1227;

Best Local Similarity 59.0%; Pred. No. 6.2e-174;

Matches 421; Conservative 104; Mismatches 176; Indels 13; Gaps 3;



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; PRIOR FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: 60/153,995
; PRIOR FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
; LENGTH: 1228
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-428-961-38

Query Match      55.8%; Score 2101; DB 14; Length 1228;
Best Local Similarity 59.2%; Pred. No. 5.7e-168;
Matches 422; Conservative 97; Mismatches 184; Indels 10; Gaps 7;

QY 13 SSNAKVDKISTDSLKN-ETDIELQ-NINHEDECLMSEYENVEPVSASTIQTGIGIAGKI 70
DB 7 NENEINALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGINIAGRI 66
QY 71 LGTLGVPPAGQVSLSYFILGELWPKGNQWEIFMEHVEEIIINOKISTYARNKALTDLKG 130
DB 67 LGVLGVPPAGQIASFYSLVGLWPRGRDQWEIFLEHVEQLINQOITENARNTALARIQ 126
QY 131 LGDALAVYHDSLSWGNRNNTRARSVVKSQYIALELMFVQKLPSPAVSGEVPPLPIYA 190
DB 127 LGDSFRAYQOSLEDWLENRDARTSRVLYTQYIALELDFLAMPFLFAIRNQEVPPLMVA 186
QY 191 QAAHLHLLLDASIFCKEWGLASSEISTFYNQVERAGDYSYHCVKWYSTGLNNLRGTN 250
DB 187 QAAHLHLLLDASLFGSEFGLTSQEIORYYERQVQTRDYSYCVWYNTGLNSLRGTN 246
QY 251 AESWRYNQPRRDMTMLVLDLVALFPSSYDTQMPYIKTTAQLTREYVYTDAGTGVHPHPSFT 310
DB 247 AASWRYNQPRRDLTLGVLDLVALFPSSYDTRTYPINTSAQLTREYVYTDAGAT--GVNMA 304
QY 311 STTWYNNAPSFSAIEAAVNRPHLLDLEQVITYLSLSWSNTQYNNMGGHKLFRFI 370
DB 305 SMWYNNAPSFSAIEATAVIRSPHLLDLEQVITYLSLSWSNTQYNNMGGHKLFRFI 364
QY 371 GGTINISTQSTNTSINPVLPTSRDVRVYTESLAGNLF--LTQPVNGVPRVDFHMKFV 428
DB 365 GGGLTSTHGSTNTSINPVLSPFSRDVYVWTESYAGVLLWGIYLEPIHGVTVPFRNRP 424
QY 429 --THPIASDNFYPGYAGIGTQLODSENELPPEATQPNYESYSHRLSHIGLISASHVKA 486
DB 425 QNTFERGTANYSQP--YESPGLQKDSLETLPPTTERPNYESYSHRLSHIGLISQSRVHV 483
QY 487 LVYSWTHRSADRTNTIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRNTTGTFGD 546
DB 484 PVSWTHRSADRTNTISSDITQIPLVKSFNLSGTSVVSQPGFTGGDIIRTNVNGSVLS 543
QY 547 IRVNIPTPAQRVVRIRYASTTDLQPHSTINGKAINQGNFSAATMNRGEBLDYKTPRTVG 606
DB 544 MGLNFNTSLQRYVRVRYAASQTMVLRTVVGSTTFDQGFPTMSANESLTQSFRFAE 603
QY 607 FTTPPSFLDVQSTFTIGAWNFSSGNEVYIDRIEFPVVEVTEAEYDFEKAQKVLTALFTS 666
DB 604 FPVGISAGSQ--TAGISISNAGRQTFHDKIEIPITATFEAYDLERAQEAVALNFTN 662
QY 667 TNPRGLKTDVKDHYHIDQVSNLVESLSDFFYLDEKRELFEIVKYANELHIERNM 719
DB 663 TNPRLKTVDTDYHIDQVSNLVACLSDFFCLDEKRELLEKVKYAKRLSDERNL 715

RESULT 11
US-10-614-524-2
; Sequence 2, Application US/10614524
; Publication No. US20040016020A1
; GENERAL INFORMATION:
; APPLICANT: Arraut, Greta
; APPLICANT: Boets, Annemie
; APPLICANT: Damme, Nicole
; APPLICANT: Mathieu, Eva

```

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; APPLICANT: Vanneste, Stijn
; APPLICANT: Van Rie, Jeroen
; TITLE OF INVENTION: Insecticidal proteins from Bacillus thuringiensis.
; FILE REFERENCE: NEWBTSUS2
; CURRENT APPLICATION NUMBER: US/10/614,524
; CURRENT FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: US/09/739,243
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/173387
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1228
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-614-524-2

Query Match      55.8%; Score 2101; DB 15; Length 1228;
Best Local Similarity 59.2%; Pred. No. 5.7e-168;
Matches 422; Conservative 97; Mismatches 184; Indels 10; Gaps 7;

QY 13 SSNAKVDKISTDSLKN-ETDIELQ-NINHEDECLMSEYENVEPVSASTIQTGIGIAGKI 70
DB 7 NENEINALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGINIAGRI 66
QY 71 LGTLGVPPAGQVSLSYFILGELWPKGNQWEIFMEHVEEIIINOKISTYARNKALTDLKG 130
DB 67 LGVLGVPPAGQIASFYSLVGLWPRGRDQWEIFLEHVEQLINQOITENARNTALARIQ 126
QY 131 LGDALAVYHDSLSWGNRNNTRARSVVKSQYIALELMFVQKLPSPAVSGEVPPLPIYA 190
DB 127 LGDSFRAYQOSLEDWLENRDARTSRVLYTQYIALELDFLAMPFLFAIRNQEVPPLMVA 186
QY 191 QAAHLHLLLDASIFCKEWGLASSEISTFYNQVERAGDYSYHCVKWYSTGLNNLRGTN 250
DB 187 QAAHLHLLLDASLFGSEFGLTSQEIORYYERQVQTRDYSYCVWYNTGLNSLRGTN 246
QY 251 AESWRYNQPRRDMTMLVLDLVALFPSSYDTQMPYIKTTAQLTREYVYTDAGTGVHPHPSFT 310
DB 247 AASWRYNQPRRDLTLGVLDLVALFPSSYDTRTYPINTSAQLTREYVYTDAGAT--GVNMA 304
QY 311 STTWYNNAPSFSAIEAAVNRPHLLDLEQVITYLSLSWSNTQYNNMGGHKLFRFI 370
DB 305 SMWYNNAPSFSAIEATAVIRSPHLLDLEQVITYLSLSWSNTQYNNMGGHKLFRFI 364
QY 371 GGTINISTQSTNTSINPVLPTSRDVRVYTESLAGNLF--LTQPVNGVPRVDFHMKFV 428
DB 365 GGGLTSTHGSTNTSINPVLSPFSRDVYVWTESYAGVLLWGIYLEPIHGVTVPFRNRP 424
QY 429 --THPIASDNFYPGYAGIGTQLODSENELPPEATQPNYESYSHRLSHIGLISASHVKA 486
DB 425 QNTFERGTANYSQP--YESPGLQKDSLETLPPTTERPNYESYSHRLSHIGLISQSRVHV 483
QY 487 LVYSWTHRSADRTNTIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRNTTGTFGD 546
DB 484 PVSWTHRSADRTNTISSDITQIPLVKSFNLSGTSVVSQPGFTGGDIIRTNVNGSVLS 543
QY 547 IRVNIPTPAQRVVRIRYASTTDLQPHSTINGKAINQGNFSAATMNRGEBLDYKTPRTVG 606
DB 544 MGLNFNTSLQRYVRVRYAASQTMVLRTVVGSTTFDQGFPTMSANESLTQSFRFAE 603
QY 607 FTTPPSFLDVQSTFTIGAWNFSSGNEVYIDRIEFPVVEVTEAEYDFEKAQKVLTALFTS 666
DB 604 FPVGISAGSQ--TAGISISNAGRQTFHDKIEIPITATFEAYDLERAQEAVALNFTN 662
QY 667 TNPRGLKTDVKDHYHIDQVSNLVESLSDFFYLDEKRELFEIVKYANELHIERNM 719
DB 663 TNPRLKTVDTDYHIDQVSNLVACLSDFFCLDEKRELLEKVKYAKRLSDERNL 715

RESULT 12
US-09-826-660-25

```

```

; Sequence 25, Application US/09826660
; Patent No. US20010026940A1
; GENERAL INFORMATION:
; APPLICANT: Cardineau, Guy A.
; APPLICANT: Stelman, Steven J.
; APPLICANT: Naiva, Kenneth E.
; TITLE OF INVENTION: Plant-Optimized
; FILE REFERENCE: MA-714XC2D1
; CURRENT APPLICATION NUMBER: US/09/8/25
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/178,255
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: 60/065,211
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/076,441
; PRIOR FILING DATE: 1998-03-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 25
; LENGTH: 643
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Toxin encoded by
; US-09-826-660-25

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Query Match	51.1%	Score 1923.5	DB 9	Length 643
Best Local Similarity	57.5%	Pred. No. 2.1e-153		
Matches 370	Conservative 100	Mismatches 160	Indels 13	Gaps 3
QY	13	SSNAKVDKISTDSLKN-----ETDLELQINHECLKMSYENVPEFVSASTTQTGIG	65	
DB	7	NENEIINALSPVNSHSAQNLSTDARI-----EDSLCLAEGNNDIPFVSASTVQTGIN	61	
QY	66	IAGKILGTGLVPPFAGQVNASLYSFILGELWPKGNQWEIFMEHVEEIIINOKISTYARNKAL	125	
DB	62	IAGRILGLVPPFAGQIASFYSFVLGELWPRGRDPWEIFLEHVEQLIROOVVETNRDAL	121	
QY	126	TDLKGIGDALAVYHDSLESWYGNENNRAPSVVKSOVIALELMFWCKLPSFAVSGEEVPL	185	
DB	122	ARLQGLGNSFRAYQOOSLEDWLENRDDARTSRVLYTQYIALELDFLNAMFLFAIRNQEVPL	181	
QY	186	LPIYAQAAANLHLLLRDASIPFGKEWGLSSSEISTFYNNQVERAGDYSYHCVKMYSTGLNN	245	
DB	182	LMVYAQAAANLHLLLRDASLFGSFGTLQSOEIQRYYERQVEKTRYSYDCASWYNTGLNN	241	
QY	246	LRGTNAESWRYNQFRDMLTAVLDLVALSPSYDTQWYPIKTTAQLTREVVYDAIGTVHP	305	
DB	242	LRGTNAESWLRYNQFRDLTUGVLDLVALPSPSDTRVYPMNTSAQUTREIYIDPLGRINA	301	
QY	306	HPSFTSTTYNNANPFSFAIEAAVVRNPHLLDLFEOVTIYSLLSRWNSTQYNNMGHGKL	365	
DB	302	PSGFASTWNFNANPFSFAIEAAVIREPHLLDFPEQLTIFSVLSRWNSTQYNNYVWGHL	361	
QY	366	EPRTTGGTLINTSTQGSINTSNIPVTLFTGSDVYVRTESLAGNLPLTQVNGVQVPRVDHWM	425	
DB	362	ESRTIRGSLSTSTGNTNTSNIPVTLQFTSRDYRTESFAGINILTTPVNGVQVWARFNW	421	
QY	426	KEVTHPIASDNFYYPVYAGICTQODSENELPPEATGQPNYESYSHRISHIGLISASHVK	485	
DB	422	RNPLNSLRGSLLYTIGYTGVTQLFDSETELPETTERPNYESYSHRLSNIRLISGNTLR	481	
QY	486	ALUYSWTHRSADRNTNTEPNSITQIPLVKAPNLSSGAAVRGPFGTGGDILRRTWTGFG	545	
DB	482	APVYSWTHRSADRNTNTESSDSITQIPLVKSFNLSNGSTSVVSGPFGTGGDIIRTNVNGSVL	541	
QY	546	DIRVAINPPFAQRVVRVIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDIIDYKFTTV	605	
DB	542	SNGLFNNTSLQRVVRVRYVASQTMVLRVTVGSGSTTFDQGPSTMSANESLTSQSFRFA	601	
QY	606	GFTTFPFLDVQSTFTIGAMNFFSGNEVYIDRIEFVVPVEVYIE	648	
DB	602	EPFVGISAGSGO-TAGTISINNAQRQTFHFDKIEFIPATLE	643	

RESULT 13  
 US-10-089-678-1  
 ; Sequence 1, Application US/10089678  
 ; Publication No. US20030017967A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: AASNO, Shinichiro  
 ; TITLE OF INVENTION: PROTEIN HAVING INSECTICIDAL ACTIVITY, DNA ENCODING THE PROTEIN, AN  
 ; TITLE OF INVENTION: NOXIOUS ORGANISM-CONTROLLING AGENT AND METHOD  
 ; FILE REFERENCE: Q68821  
 ; CURRENT APPLICATION NUMBER: US/10/089,678  
 ; CURRENT FILING DATE: 2002-05-02  
 ; PRIOR APPLICATION NUMBER: JP 2000-236140  
 ; PRIOR FILING DATE: 2000-08-03  
 ; PRIOR APPLICATION NUMBER: PCT/JP01/06660  
 ; PRIOR FILING DATE: 2001-08-02  
 ; NUMBER OF SEQ ID NOS: 3  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 1  
 ; LENGTH: 1167  
 ; TYPE: PRT  
 ; ORGANISM: Bacillus thuringiensis  
 US-10-089-678-1

Query Match	45.4%	Score 1707.5	DB 14	Length 1167
Best Local Similarity	47.6%	Pred. No. 9.8e-135		
Matches 359	Conservative 125	Mismatches 221	Indels 49	Gaps 12
Qy	1	MLKLNQDKHQ--SFSNAKVDKISTSLAKNETDIELONIHEDCLKMSYE-----NV	51	
Db	1	MSNNQNEYELDASSSTSVSDNSVRYPLANDOTTILQNNYKYDLKMSGEHPELFCNP	60	
Qy	52	EPFVSASTIQTGIGIAGKILGTGVFAGQVASLYFILGELWPKGK-NQWEIFMEHVEE	110	
Db	61	ETFISSSTVQTGIGIVQVLGALGVFAGQIASFYFIVGQLWPSSTSVSWEMIMKQVED	120	
Qy	111	IINQKISTYARNKALITDLKGLDALAVYHDSLESWVCNRNNTTARSVVVKSQYTALELMFV	170	
Db	121	LIDDKITSVRKATAGLOGLGGLDVOYQKSLKNWLENRNDTARSVVVYQYTALELDVF	180	
Qy	171	QKLPSFAVSGEEVPLPIYAAQANLHLLLRDASIFGKEMGLSSSEISTEYNRQVERAGD	230	
Db	181	AKIPSPAISQEEVPLLSVYAAQANLHLLLRDASIFGAENGFTPGGEISTEYDRQVTRTAQ	240	
Qy	231	YSHVCWKVSTGLNNIGTNAESWVRYNQPRDWTLMVLIDLVALFSYDQFMVPIKTTAQ	290	
Db	241	YSYCYVKWYNTGDJLKGITNAASLWKYQPRREMTLLVLDLVALFPNYDRTPIETTTAQ	300	
Qy	291	LTRREVYTDAGTIVHPSPSTSTWYNNNAPSFAIAAAVVRNPHLLDFLBQVYIYSLLS-	349	
Db	301	LTRREVYTDPIVFNRETSGGFCRWSLNSDISFSEVESAVIRSPHLDFILSEIFYTTTRAG	360	
Qy	350	-RWSNTQYVMWGGHLEPRTIGCTLNI STQGTNTSINPVTLPFTSRD VYRTESL-AGL	407	
Db	361	LP LNNTSELEYWYGHISIKYKNTNASSALERNYGTITSNKIKYYDLANKDKIFQVRSLGADL	420	
Qy	408	NLFELTPVNGVRPVDPHWKFVTHPIASDNPYPYGYAGIG-----TQLQDSE	453	
Db	421	ANYIAQ-VYGVVPASF-----TILDKN---TGSGSVGGFTYSKEHTTMOVCTQNVNTI	469	
Qy	454	NELPPEATGQPNYESYSHRLSHGLGIS-----ASHVKALVYSWTHRGADRTNTEPN	505	
Db	470	DEIPPE--NEPLSRGYSHRLSHITSYSFSGNASSPARYGNLPVFAWTHRSADVNTVYSD	527	
Qy	506	SITQIPLVKAFNLSGGAAVVRGPGFGGDIILRTNTGTGFDIRWNIINPPPAQRYRVAIRY	565	
Db	528	KITQI PVKRAHTLVSGTTVIKGEGFTGGNLIKRTSSGPLAYTSVSVKSPUSQRYRAIRY	587	
Qy	566	ASTDLDQFHTSINGKAINOGNFASATNRGDDLDYKTRTVTGFTTPPSFLDVQSTFTIGAW	625	
Db	588	ASTNLRLFTVTSCTRIYSINVKNTKMGDDLFNTFDLTIATGTFTSNYSLSLTVGAD	647	







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OM protein - protein search, using sw model

Run on: October 28, 2004, 17:52:12 ; Search time 98.4365 Seconds  
(without alignments)  
4202.652 Million cell updates/sec

Title: US-10-019-823B-56

Perfect score: 3762

Sequence: 1 MLLKNQDKHQSPSSNAKVDK.....KRELFIIVKYNELHIERNM 719

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt\_02:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	3752	99.7	719	2	CAC85964
2	3743	99.5	719	1	C1A1_BACTK
3	3743	99.5	719	2	O6X181
4	3743	99.5	719	2	AAP86782
5	3738	99.4	719	2	O93NJ5
6	3737	99.3	719	2	O85796
7	3608	95.9	719	2	O8KV61
8	3534	93.9	719	2	O9F0P8
9	3503	93.1	719	1	C1B1_BACTE
10	3380	89.8	719	1	C1D1_BACTU
11	3379	89.8	719	1	C1C1_BACTU
12	2437.5	64.8	1229	1	C1B1_BACTU
13	2437.5	64.8	1233	1	C1B1_BACTM
14	2263.5	60.2	1228	2	O93J75
15	2262.5	60.1	1228	1	C1B1_BACTK
16	2254.5	59.9	1228	2	O93NM5
17	2180.5	58.0	849	2	O6PYW8
18	2180.5	58.0	849	2	AAS93797
19	2180.5	58.0	1227	1	C1B1_BACTU
20	2103.5	55.9	1231	2	O8KNY2
21	2098.5	55.8	1231	1	C1B1_BACTZ
22	1979.5	52.6	1215	2	C1K1_BACTM
23	1895	50.4	381	2	O45740
24	1655.5	44.0	1157	1	C8AA_BACUK
25	1643	43.7	1144	2	O8KZL7
26	1483	39.4	1157	1	C9CA_BACTO
27	1471.5	39.1	1169	1	C8BA_BACUK
28	1469	39.0	1167	1	C1JA_BACTU
29	1467.5	39.0	1166	1	C1G1_BACTU
30	1467	39.0	1169	1	C1FB_BACTM
31	1461	38.8	1174	2	O45749

32	1452	38.6	1155	1	C1AB_BACTK	P06578 bacillus th
33	1452	38.6	1155	2	Q7BE98	Q7BE98 bacillus th
34	1452	38.6	1155	2	Q9F296	Q9F296 bacillus th
35	1452	38.6	1155	2	AA76494	AA76494 bacillus
36	1452	38.6	1155	2	AAO13302	AAO13302 bacillus
37	1450	38.5	1118	2	O9AM83	O9AM83 bacillus th
38	1447	38.5	1156	2	O6GUA7	O6GUA7 bacillus th
39	1442	38.3	1177	2	O8EIX3	O8EIX3 bacillus th
40	1440	38.3	1155	2	Q9J121	Q9J121 bacillus th
41	1439.5	38.3	793	2	Q6PYW7	Q6PYW7 bacillus th
42	1439.5	38.3	793	2	AA93798	AA93798 bacillus
43	1439.5	38.3	1180	2	Q9S5V8	Q9S5V8 bacillus th
44	1438.5	38.2	1176	2	O7WZT9	O7WZT9 bacillus th
45	1434.5	38.1	1181	1	C1AE_BACTL	Q03748 bacillus th

RESULT 1  
CAC85964 PRELIMINARY; PRT; 719 AA.

AC CAC85964;  
DT 02-MAR-2004 (TREMREL. 27, Created)  
DT 02-MAR-2004 (TREMREL. 27, Last sequence update)  
DT 02-MAR-2004 (TREMREL. 27, Last annotation update)  
DE Delta-endotoxin.  
GN CRYIIA.  
OS Bacillus thuringiensis (subsp. kurstaki).  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;  
OC Bacillus cereus group; Bacillus thuringiensis.  
OX NCBI\_TaxID=29339;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BNS3;  
RA Tounsi S.; Zouari N.; Jaoua S.;  
RT "Cloning and study of the expression of a novel cryIIa-type gene from  
RT Bacillus thuringiensis subsp. kurstaki.";  
RL J. Appl. Microbiol. 95:23-28(2003).  
DR EMBL; AJ315121; CAC85964.1; -;  
SQ SEQUENCE 719 AA; 81203 MW; 8676E5A6C25DAFE8 CRC64;

Query Match	99.7%;	Score	3752;	DB	2;	Length	719;
Best Local Similarity	99.9%;	Pred. No.	1.7e-252;				
Matches	718;	Conservative	0;	Mismatches	1;	Indels	0;
Gaps	0;						
QY	1	MLKNQDKHQSPSSNAKVDKISTDLSKNETDIELQININHEDECLMSEYENVEPFFVSASTI	60				
DB	1	MLKNQDKHQSPSSNAKVDKISTDLSKNETDIELQININHEDECLMSEYENVEPFFVSASTI	60				
QY	61	QTGIGIAGKILGTGVPFAGQVASYLSYFILGELWPKGNQWEIFMEHVEEIIINQKISTYA	120				
DB	61	QTGIGIAGKILGTGVPFAGQVASYLSYFILGELWPKGNQWEIFMEHVEEIIINQKISTYA	120				
QY	121	RNKALTDLKGGLDALAVYHDSLESWGNRNTRARSVVKSOYIALELMFVKLPSPFVSG	180				
DB	121	RNKALTDLKGGLDALAVYHDSLESWGNRNTRARSVVKSOYIALELMFVKLPSPFVSG	180				
QY	181	EEVPLLPPIYAQAANLHLLLRDASIFGKWLSSSEISTFTYNRQVERAGDYSYHCWKYS	240				
DB	181	EEVPLLPPIYAQAANLHLLLRDASIFGKWLSSSEISTFTYNRQVERAGDYSYHCWKYS	240				
QY	241	TGLNNLRGTNAESWRYNQPRDMLVLDLVALFPSTDYDTOMYPIKTTAQLTREYVTDAL	300				
DB	241	TGLNNLRGTNAESWRYNQPRDMLVLDLVALFPSTDYDTOMYPIKTTAQLTREYVTDAL	300				
QY	301	GTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRSNQTQYMMW	360				
DB	301	GTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRSNQTQYMMW	360				
QY	361	GGHKLEPFTIGTGLNISTQGSTINSINPTLFPFTRSDRYRTESLAGNLFITQPVNGVPR	420				
DB	361	GGHKLEPFTIGTGLNISTQGSTINSINPTLFPFTRSDRYRTESLAGNLFITQPVNGVPR	420				

QY 421 VDFHWKFTVTHPIASDNFYYPYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 Db 421 VDFHWKFTVTHPIASDNFYYPYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 QY 481 ASHKVALVYSTHRSADRTNIENSITQIPLVKAFNLSSGAAVVRPGFTGGDILRTN 540  
 Db 481 ASHKVALVYSTHRSADRTNIENSITQIPLVKAFNLSSGAAVVRPGFTGGDILRTN 540  
 QY 541 TGTGDIRVNPFPQAQRYRIRIYASTDLOQFHTSINGKAINQGNFSATMARGEDLDYK 600  
 Db 541 TGTGDIRVNPFPQAQRYRIRIYASTDLOQFHTSINGKAINQGNFSATMARGEDLDYK 600  
 QY 601 TFRVTGFTPTPSFELDVQSTFTIGAWNFSSGNEVYDRIEFVVPVETVEAEVDPEKAEKV 660  
 Db 601 TFRVTGFTPTPSFELDVQSTFTIGAWNFSSGNEVYDRIEFVVPVETVEAEVDPEKAEKV 660  
 QY 661 TALFTSTNPRGLKTDVQYHIDQVSNLVESLDSBFDYLDKRELFPEIVKYANELHIERNM 719  
 Db 661 TALFTSTNPRGLKTDVQYHIDQVSNLVESLDSBFDYLDKRELFPEIVKYANELHIERNM 719

RESULT 2  
 CLIA, BACTK  
 ID CLIA BACTK STANDARD; PRT; 719 AA.  
 AC Q45752; P71092; Q45750; Q45751; Q45756;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Pesticidal crystal protein cryIIa (insecticidal delta-endotoxin  
 DE CryII(a)) (Crystalline entomocidal protoxin) (81 kDa crystal protein).  
 GN Name=cryIIa; Synonyms=cryII(a), cryV, cryVI, GCryV;  
 OS Bacillus thuringiensis (subsp. kurstaki).  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 CX NCBI\_TaxID=29339;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=DSIR732;  
 RX MEDLINE=93298009; PubMed=8517758;  
 RA Gleave A.P., Williams R., Hedges R.J.;  
 RT "Screening by polymerase chain reaction of Bacillus thuringiensis  
 RT serotypes for the presence of cryV-like insecticidal protein genes and  
 RT characterization of a cryV gene cloned from B. thuringiensis subsp.  
 RT kurstaki.";  
 RL Appl. Environ. Microbiol. 59:1683-1687 (1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=JHCC4835;  
 RX MEDLINE=92269582; PubMed=1588820;  
 RA Tailor K., Tippett J., Gibbs G., Pells S., Pike D., Jordan L., Ely S.;  
 RT "Identification and characterization of a novel Bacillus thuringiensis  
 RT delta-endotoxin entomocidal to coleopteran and lepidopteran larvae.";  
 RL Mol. Microbiol. 6:1211-1217 (1992).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=HD-1;  
 RX MEDLINE=95314293; PubMed=7793960;  
 RA Shin B.-S., Park S.-H., Choi S.-K., Koo B.T., Lee S.T., Kim J.I.;  
 RT "Distribution of cryV-type insecticidal protein genes in Bacillus  
 RT thuringiensis and cloning of cryV-type genes from Bacillus  
 RT thuringiensis subsp. kurstaki and Bacillus thuringiensis subsp.  
 RT entomocidus.";  
 RL Appl. Environ. Microbiol. 61:2402-2407 (1995).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=AB88;  
 RX MEDLINE=96178985; PubMed=8606196;  
 RA Kostichka K., Warren G.W., Mullins M., Mullins A.D., Palekar N.V.,  
 RA Craig J.A., Koziel M.G., Estruch J.J.;  
 RT "Cloning of a cryV-type insecticidal protein gene from Bacillus  
 RT thuringiensis: the cryV-encoded protein is expressed early in  
 RT stationary phase.";  
 RL J. Bacteriol. 178:2141-2144 (1996).

BN SEQUENCE FROM N.A.  
 RP STRAIN=61;  
 RC Selvapandiyar A., Bhatnagar R.K.;  
 RT "Isolation, cloning and expression of cryV gene.";  
 RL Submitted (Oct-1996) to the EMBL/GenBank/DBJ databases.  
 CC !- FUNCTION: Promotes colloidomotic lysis by binding to the midgut  
 CC epithelial cells of certain coleopteran and lepidopteran species.  
 CC Active on Plutella xylostella and Bombyx mori.  
 CC !- DEVELOPMENTAL STAGE: The crystal protein is produced during  
 CC sporulation and is accumulated both as an inclusion and as part of  
 CC the spore coat.  
 CC !- MISCELLANEOUS: Toxic segment of the protein is located in the N-  
 CC terminus.  
 CC !- SIMILARITY: Belongs to the delta endotoxin family.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
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 CC use by non-profit institutions as long as its content is in no way  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC  
 CC EMBL; M98544; AAA22354.1; -  
 CC EMBL; X62821; CAA44633.1; -  
 CC EMBL; L36338; AAC36999.1; -  
 CC EMBL; L49391; AAB00958.1; -  
 CC EMBL; Y08920; CAA70124.1; -  
 CC FIR; I39815; I39815.  
 CC FIR; S25383; S25383.  
 CC HSSP; P02965; LC1Y.  
 CC InterPro; IPR001178; Endotoxin.  
 CC InterPro; IPR005638; endotoxin C.  
 CC InterPro; IPR005639; endotoxin N.  
 CC InterPro; IPR008979; Gal bind like.  
 CC Pfam; PF03944; Endotoxin\_C; 1.  
 CC Pfam; PF00555; Endotoxin\_M; 1.  
 CC Pfam; PF03945; Endotoxin\_N; 1.  
 CC Sporulation; Toxin.  
 CC VARIANT 159 159 K -> R (in strain 61).  
 CC VARIANT 233 233 D -> Y (in strain JHCC4835 and strain HD-  
 CC 1).  
 CC VARIANT 443 443 A -> V (in strain AB88).  
 CC VARIANT 711 712 KQ -> NE (in strain HD-1 and strain 61).  
 CC SEQUENCE 719 AA; 81216 MW; 3627ESA6C25DAFFS CRC64;  
 Query Match 99.5%; Score 3743; DB 1; Length 719;  
 Best Local Similarity 99.6%; Pred. No. 7.2e-252;  
 Matches 716; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETIELQININHECLKMSYENVEPFSASTI 60  
 Db 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETIELQININHECLKMSYENVEPFSASTI 60  
 QY 61 QTGIGIAGKILGTGVPPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQISTYA 120  
 Db 61 QTGIGIAGKILGTGVPPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQISTYA 120  
 QY 121 RNKALTDLKGLDALAVYHDSLSWVGNNNTRASVVKSVQVIALELMFVOKLPSFAVSG 180  
 Db 121 RNKALTDLKGLDALAVYHDSLSWVGNNNTRASVVKSVQVIALELMFVOKLPSFAVSG 180  
 QY 181 EKVPELLPIYAQAANLHLLLRDASIFGKWEGLSSSEISTFFYNRQVERAGDYSYHCVKWYS 240  
 Db 181 EKVPELLPIYAQAANLHLLLRDASIFGKWEGLSSSEISTFFYNRQVERAGDYSYHCVKWYS 240  
 QY 241 TGLNNLRGTNAESWRYNQFRDMTLMVLDLVALPSSYDTQMPYIKTTAQUTREYITDAI 300  
 Db 241 TGLNNLRGTNAESWRYNQFRDMTLMVLDLVALPSSYDTQMPYIKTTAQUTREYITDAI 300  
 QY 301 GTVHEPSPSTSTWYNNNAPSATEAAVVRNPHLDLEQVTIYISLLSRNSNTQYMNW 360

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Db 301 GTVHPHSFTSTWYNNAPSAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYVMW 360
Qy 361 GGHKLEFRTIGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPR 420
Db 361 GGHKLEFRTIGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPR 420
Qy 421 VDFHWKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATQPNYESYSHRLSHIGLIS 480
Db 421 VDFHWKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATQPNYESYSHRLSHIGLIS 480
Qy 481 ASHVKALVYSWTHSADRTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 540
Db 481 ASHVKALVYSWTHSADRTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 540
Qy 541 TGTGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKALNQNFSATMNRGEDLDYK 600
Db 541 TGTGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKALNQNFSATMNRGEDLDYK 600
Qy 601 TFRVVGFTTTPSFLDVOSTFTTIGANFSSGNEVYIDRIEFVPEVYEAAYDEFEKAQEKV 660
Db 601 TFRVVGFTTTPSFLDVOSTFTTIGANFSSGNEVYIDRIEFVPEVYEAAYDEFEKAQEKV 660
Qy 661 TALFTSTNPRGLKTDVKDHYDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719
Db 661 TALFTSTNPRGLKTDVKDHYDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719

RESULT 3
Q6X181
ID AC Q6X181 PRELIMINARY; PRT; 719 AA.
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE CryII.
GN Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RA Espindola R., Lemos M.V.F., Lemos E.G.M., Sena J.A.D.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY262167; AAP86782.1; -.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin.C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal_bind_Like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
SQ SEQUENCE 719 AA; 81216 MW; 3627B5A6C25DAFF5 CRC64;

Query Match 99.5%; Score 3743; DB 2; Length 719;
Best Local Similarity 99.6%; Pred. No. 7.2e-252;
Matches 716; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINIHEDCLKMGSEYENVEPVSASTI 60
Db 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINIHEDCLKMGSEYENVEPVSASTI 60
Qy 61 QTGIGIAGKILGTGVPPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINOKISTYA 120
Db 61 QTGIGIAGKILGTGVPPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINOKISTYA 120
Qy 121 RNKALTDKLGDLAVYHDSLSWGNRNNTTRARSVVKSQYIALELMFVKLPSPFAVSG 180
Db 121 RNKALTDKLGDLAVYHDSLSWGNRNNTTRARSVVKSQYIALELMFVKLPSPFAVSG 180
Qy 181 EEPVLLPIYAQAANLHLLLRDASIIFGKEWGLSSSEISTFTFYNQVERAGDYSYHCVKWS 240
Db 181 EEPVLLPIYAQAANLHLLLRDASIIFGKEWGLSSSEISTFTFYNQVERAGDYSYHCVKWS 240

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Qy 241 TGLNLRGTNAESWVRYNQFRDMLTLMVLDAVALPSPSYDTOMYPIKTTAQLTREVYTDI 300
Db 241 TGLNLRGTNAESWVRYNQFRDMLTLMVLDAVALPSPSYDTOMYPIKTTAQLTREVYTDI 300
Qy 301 GTVHPHSFTSTWYNNAPSAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYVMW 360
Db 301 GTVHPHSFTSTWYNNAPSAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYVMW 360
Qy 361 GGHKLEFRTIGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPR 420
Db 361 GGHKLEFRTIGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPR 420
Qy 421 VDFHWKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATQPNYESYSHRLSHIGLIS 480
Db 421 VDFHWKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATQPNYESYSHRLSHIGLIS 480
Qy 481 ASHVKALVYSWTHSADRTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 540
Db 481 ASHVKALVYSWTHSADRTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 540
Qy 541 TGTGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKALNQNFSATMNRGEDLDYK 600
Db 541 TGTGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKALNQNFSATMNRGEDLDYK 600
Qy 601 TFRVVGFTTTPSFLDVOSTFTTIGANFSSGNEVYIDRIEFVPEVYEAAYDEFEKAQEKV 660
Db 601 TFRVVGFTTTPSFLDVOSTFTTIGANFSSGNEVYIDRIEFVPEVYEAAYDEFEKAQEKV 660
Qy 661 TALFTSTNPRGLKTDVKDHYDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719
Db 661 TALFTSTNPRGLKTDVKDHYDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719

RESULT 4
AAP86782
ID AAP86782 PRELIMINARY; PRT; 719 AA.
AC AAP86782;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE CryII.
GN Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RA Espindola R., Lemos M.V.F., Lemos E.G.M., Sena J.A.D.;
RL "Complete sequence of cryII gene of isolate T01 328 from Bacillus thuringiensis from Cubatao (Sp - Brazil) soil.";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY262167; AAP86782.1; -.
SQ SEQUENCE 719 AA; 81216 MW; 3627B5A6C25DAFF5 CRC64;

Query Match 99.5%; Score 3743; DB 2; Length 719;
Best Local Similarity 99.6%; Pred. No. 7.2e-252;
Matches 716; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINIHEDCLKMGSEYENVEPVSASTI 60
Db 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINIHEDCLKMGSEYENVEPVSASTI 60
Qy 61 QTGIGIAGKILGTGVPPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINOKISTYA 120
Db 61 QTGIGIAGKILGTGVPPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINOKISTYA 120
Qy 121 RNKALTDKLGDLAVYHDSLSWGNRNNTTRARSVVKSQYIALELMFVKLPSPFAVSG 180
Db 121 RNKALTDKLGDLAVYHDSLSWGNRNNTTRARSVVKSQYIALELMFVKLPSPFAVSG 180
Qy 181 EEPVLLPIYAQAANLHLLLRDASIIFGKEWGLSSSEISTFTFYNQVERAGDYSYHCVKWS 240

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181 EVVPLPIYAQAANLHLLLDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCWKYS 240
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241 TGLNNLRGTNAESWRYNQFRDMTLMVLDLVALFPSTYDQMPYIKTTAQLTREVTDAI 300
301 GTVHPHPSFTSTTWYNNAPSPSAIEAAVVRNPHLLDLEQVITYSLLSWSNTQYNNMW 360
301 GTVHPHPSFTSTTWYNNAPSPSAIEAAVVRNPHLLDLEQVITYSLLSWSNTQYNNMW 360
361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRRTESLAGNLFLOTPVNGVPR 420
361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRRTESLAGNLFLOTPVNGVPR 420
421 VDFHWKFTVTHPIASDNFYPGVAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480
421 VDFHWKFTVTHPIASDNFYPGVAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480
481 ASHVKALVYSWTHRSADRNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 540
481 ASHVKALVYSWTHRSADRNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 540
541 TGTFGDIRVNINPPFAQRYRIRYASTTDLOFHTSINGKAINQGNFSATWNRGDDLYK 600
541 TGTFGDIRVNINPPFAQRYRIRYASTTDLOFHTSINGKAINQGNFSATWNRGDDLYK 600
601 TPTVTGFTTPTSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVTYEAEDFEKAQEKV 660
601 TPTVTGFTTPTSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVTYEAEDFEKAQEKV 660
661 TALFTSTNPRGLKTDVKDHYDQVSNLVESLSDFFYLDEKRELFEIVKYAKQLHIERNM 719
661 TALFTSTNPRGLKTDVKDHYDQVSNLVESLSDFFYLDEKRELFEIVKYAKQLHIERNM 719

RESULT 5
Q93NJ5 PRELIMINARY; PRT; 719 AA.
AC Q93NJ5;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Crylla.
GN Name=crylla;
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RA Song F., Zhang J., Gu A., Huang D., Li G.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF373207; AAK66742.1; -
DR HSSP; P02965; 1CIY.
DR GO; GO:0005102; P:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:patogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR Pfam; PF03944; Endotoxin C; 1.
DR Pfam; PF00555; Endotoxin M; 1.
DR Pfam; PF03945; Endotoxin N; 1.
SQ SEQUENCE 719 AA, 81225 MW, C629DF2C44827241 CRC64;

Query Match 99.4%; Score 3738; DB 2; Length 719;
Best Local Similarity 99.4%; Pred. No. 1.6e-251;
Matches 715; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MLLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHINHEDCLKSEYENVEPVSASTI 60
DB 1 MLLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHINHEDCLKSEYENVEPVSASTI 60

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61 QTGIGIAGKILGTLGVPFAGQVASIYSFILGELWPKGNQWEIFMEHVEETINQKISTYA 120
61 QTGIGIAGKILGTLGVPFAGQVASIYSFILGELWPKGNQWEIFMEHVEETINQKISTYA 120
121 RNKALTDLKGLGDALAVYHDSLESWVGNRNTRARSVVKSQVIALELMFVKLSFAVSG 180
121 RNKALTDLKGLGDALAVYHDSLESWVGNRNTRARSVVKSQVIALELMFVKLSFAVSG 180
181 BEVPLPIYAQAANLHLLLDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCWKYS 240
181 BEVPLPIYAQAANLHLLLDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCWKYS 240
241 TGLNNLRGTNAESWRYNQFRDMTLMVLDLVALFPSTYDQMPYIKTTAQLTREVTDAI 300
241 TGLNNLRGTNAESWRYNQFRDMTLMVLDLVALFPSTYDQMPYIKTTAQLTREVTDAI 300
301 GTVHPHPSFTSTTWYNNAPSPSAIEAAVVRNPHLLDLEQVITYSLLSWSNTQYNNMW 360
301 GTVHPHPSFTSTTWYNNAPSPSAIEAAVVRNPHLLDLEQVITYSLLSWSNTQYNNMW 360
361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRRTESLAGNLFLOTPVNGVPR 420
361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRRTESLAGNLFLOTPVNGVPR 420
421 VDFHWKFTVTHPIASDNFYPGVAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480
421 VDFHWKFTVTHPIASDNFYPGVAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480
481 ASHVKALVYSWTHRSADRNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 540
481 ASHVKALVYSWTHRSADRNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 540
541 TGTFGDIRVNINPPFAQRYRIRYASTTDLOFHTSINGKAINQGNFSATWNRGDDLYK 600
541 TGTFGDIRVNINPPFAQRYRIRYASTTDLOFHTSINGKAINQGNFSATWNRGDDLYK 600
601 TPTVTGFTTPTSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVTYEAEDFEKAQEKV 660
601 TPTVTGFTTPTSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVTYEAEDFEKAQEKV 660
661 TALFTSTNPRGLKTDVKDHYDQVSNLVESLSDFFYLDEKRELFEIVKYAKQLHIERNM 719
661 TALFTSTNPRGLKTDVKDHYDQVSNLVESLSDFFYLDEKRELFEIVKYAKQLHIERNM 719

RESULT 6
O85796 PRELIMINARY; PRT; 719 AA.
AC O85796;
DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Insecticidal protein.
GN Name=cryV101;
OS Bacillus thuringiensis (subsp. kurstaki).
OC Plasmid large plasmid.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=29339;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=SL01;
RA Zhong Q., Deng R., Long Q., Yuan M., Pang Y., Wang X.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF076953; AAC26910.1; -
DR HSSP; P02965; 1CIY.
DR GO; GO:0005102; P:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:patogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal_bind_like.
DR Pfam; PF03944; Endotoxin C; 1.
DR Pfam; PF00555; Endotoxin M; 1.
DR Pfam; PF03945; Endotoxin N; 1.
SQ SEQUENCE 719 AA, 81225 MW, C629DF2C44827241 CRC64;

Query Match 99.4%; Score 3738; DB 2; Length 719;
Best Local Similarity 99.4%; Pred. No. 1.6e-251;
Matches 715; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MLLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHINHEDCLKSEYENVEPVSASTI 60
DB 1 MLLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHINHEDCLKSEYENVEPVSASTI 60

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DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
KW Plasmid.
SQ SEQUENCE 719 AA; 81230 MW; 42746D478359BBA7 CRC64;

Query Match          99.3%; Score 3737; DB 2; Length 719;
Best Local Similarity 99.4%; Pred. No. 1.9e-251;
Matches 715; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 M K L N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y N E V P F V S A S T I 60
Db 1 M K L N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y N E V P F V S A S T I 60
Qy 61 Q T G I G I A G K I L G T L G V P F A G V A S L Y S F I L G E L W P K G N Q W E I F M E H V E E I I N Q K I S T Y A 120
Db 61 Q T G I G I A G K I L G T L G V P F A G V A S L Y S F I L G E L W P K G N Q W E I F M E H V E E I I N Q K I S T Y A 120
Qy 121 R N K A L T D L K G L D A L A V Y H D S L E S W G N R N T R A S V V K S Q Y I A L E M F V Q K L P S F A V S G 180
Db 121 R N K A L T D L K G L D A L A V Y H D S L E S W G N R N T R A S V V K S Q Y I A L E M F V Q K L P S F A V S G 180
Qy 181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S E I S T F Y N Q V E R A G D Y S H C V K W Y S 240
Db 181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S E I S T F Y N Q V E R A G D Y S H C V K W Y S 240
Qy 241 T G L N L R G T N A E S W R Y N Q F R D M T L M V L D L V A L F P S Y D T O M Y P I K T T A Q L T R E V Y T D A I 300
Db 241 T G L N L R G T N A E S W R Y N Q F R D M T L M V L D L V A L F P S Y D T O M Y P I K T T A Q L T R E V Y T D A I 300
Qy 301 G T V H P H S F S T T W Y N N A P S F S A I E A A V V R N P H L D F L E Q V T I Y S L L S R S N T Q Y M N W 360
Db 301 G T V H P H S F S T T W Y N N A P S F S A I E A A V V R N P H L D F L E Q V T I Y S L L S R S N T Q Y M N W 360
Qy 361 G G H K L E P R T I G T L N I S T Q S T N T S I N P V L P T S R D V Y R T E S L A G L N L F L T Q P V N G V P R 420
Db 361 G G H K L E P R T I G T L N I S T Q S T N T S I N P V L P T S R D V Y R T E S L A G L N L F L T Q P V N G V P R 420
Qy 421 V D F H W K F V T H P I A S D N F Y P G Y A G I G T Q L O D S E N E L P P E A T G Q P N Y E S Y S H R L S H I G L I S 480
Db 421 V D F H W K F V T H P I A S D N F Y P G Y A G I G T Q L O D S E N E L P P E A T G Q P N Y E S Y S H R L S H I G L I S 480
Qy 481 A S H V K A L V Y S W T H S A D R T N I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G G D I L R R T N 540
Db 481 A S H V K A L V Y S W T H S A D R T N I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G G D I L R R T N 540
Qy 541 T G T F G D I R V N I P P F A Q R Y R V R I Y A S T T D L Q F H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 600
Db 541 T G T F G D I R V N I P P F A Q R Y R V R I Y A S T T D L Q F H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 600
Qy 601 T F R T V G F T T P F S F L D V Q S T F T I G A W N F S S G N E V I D R I E F V P V E V T Y E A E Y D F E K A Q E K V 660
Db 601 T F R T V G F T T P F S F L D V Q S T F T I G A W N F S S G N E V I D R I E F V P V E V T Y E A E Y D F E K A Q E K V 660
Qy 661 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K Y A N E L H I E R N M 719
Db 661 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K Y A N E L H I E R N M 719

RESULT 7
Q8KY61 PRELIMINARY; PRT; 719 AA.
AC Q8KY61
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Cry.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RA Porcar M., Martinez C., Caballero P.;
```

DT 01-MAR-2001 (TREMEL-rel. 16, Created)  
 DT 01-MAR-2001 (TREMEL-rel. 16, Last sequence update)  
 DT 01-MAR-2004 (TREMEL-rel. 26, Last annotation update)  
 DE Cryll.  
 GN Name=cryll;  
 OS Bacillus thuringiensis.  
 OG Plasmid pFC19.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1428;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ETC007;  
 RX MEDLINE=22837682; PubMed=12957903;  
 RA Song F., Zhang J., Gu A., Wu Y., Han L., He K., Chen Z., Yao J.,  
 RA Hu Y., Li G., Huang D.;  
 RT "Identification of cryII-type genes from Bacillus thuringiensis  
 RT strains and characterization of a novel cryII-type gene";  
 RL Appl. Environ. Microbiol. 69:5207-5211 (2003).  
 DR EMBL AF211190; FAG43526.1; --  
 DR HSSP; P02965; ICYI.  
 DR GO; GO:0005102; F:receptor binding; IEA.  
 DR GO; GO:0006952; P:defense response; IEA.  
 DR GO; GO:0009405; P:pathogenesis; IEA.  
 DR InterPro; IPR001178; Endotoxin.  
 DR InterPro; IPR005638; endotoxin\_C.  
 DR InterPro; IPR008979; Gal\_bind\_Like.  
 DR Pfam; PF03944; Endotoxin\_C; 1.  
 DR Pfam; PF00555; Endotoxin\_M; 1.  
 DR Pfam; PF03945; Endotoxin\_N; 1.  
 KW Plasmid.  
 SQ SEQUENCE 719 AA; 81024 MW; 7E17481922C435E6 CRC64;

Query Match 93.9%; Score 3534; DB 2; Length 719;  
 Best Local Similarity 93.2%; Pred. No. 2.6e-237;  
 Matches 670; Conservative 27; Mismatches 22; Indels 0; Gaps 0;

QY 1 MKLKNQKHQSSNAKYDKISTSLKNETDIELQNHEDCLKMSYENVPEVVSASTI 60  
 DB 1 MKLKNPDKHQLSSNAKYDKATSLKNETDIELKNHEDFLMSHESIDPVSASTI 60  
 QY 61 QTGIGIAKILGTIGVPAGQVASYSPILGELMPKGNQWEIEMHVEELINQISTYA 120  
 DB 61 QTGIGIAKILGTIGVPAGQIASYSPILGELMPKGNQWEIEMHVEELIDQISTYA 120  
 QY 121 RNKALTDLKGLDALAVHDSLESVGNRNTRARSVVKSOYIALELMFVKLPSPAVSG 180  
 DB 121 RNIAADLKLGLDALAVHDSLESWKNNRNARATSVVKSOYIALELLFVKLPSPAVSG 180  
 QY 181 EVPLLPPIYAQAANLHLLLRDASIFGKWLSSSEISTFYNRQVERAGDYSYHCWKYS 240  
 DB 181 EVPLLPPIYAQAANLHLLLRDASVFGKWLSSSQISTFYNRQVERTSDYSDHCWKYS 240  
 QY 241 TGLNNIRGTNAESWRYNQFRDMLTMDLVALPPSYDTOMYPIKTAQLTRVYTDAL 300  
 DB 241 TGLNNIRGTNAESWRYNQFRDMLTMDLVALPPSYDTUVPYIKTSQTRVYTDAL 300  
 QY 301 GTVHPHPSFTSTTWNNAFSAFSAEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYNNMW 360  
 DB 301 GTVHPNASFATWNNNAFSAFSAEAVVRNPHLLDFLEQVTIYSLLSRWSTQYNNMW 360  
 QY 361 GGHKLEPFTIGTLNISTQGSTNTSINPVTLPFTSRDVRRESLAGNLFITQVNGVPR 420  
 DB 361 GGHRLPFTIGTLNISTQGSTNTSINPVTLPFTSRDVRRESLAGNLFITQVNGVPR 420  
 QY 421 VDPHKKFVTHPIASDNFYYPGAGIGTQLODSENELPEATGQPNYSYSHRLSHIGLIS 480  
 DB 421 VDPHKKFATLPASDNFYYPGAGIGTQLODSENELPETTGQPNYSYSHRLSHIGLIS 480  
 QY 481 ASHVKALVYSWTHRADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 540  
 DB 481 ASHVKALVYSWTHRADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 540

QY 541 TCTFGDIRVNIINPPFAQRYRVRIRVASTTDLOFHTSINGKAINQGNFSATWNRGDDLYK 600  
 DB 541 TCTFGDIRVNIINPPFAQRYRVRIRVASTTDLOFHTSINGKAINQGNFSATWNRGDDLYK 600  
 QY 601 TERTVGTTPRSLDVQSTFTIGANNFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEKV 660  
 DB 601 TERTVGTTPRSLDVQSTFTIGANNFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEKV 660  
 QY 661 TALFTSTNPRGLTKDVKYHIDQVSNLVESLSDEYFLDEKRELFEIVYAKQIHIERNM 719  
 DB 661 TALFTSTNPRGLTKDVKYHIDQVSNLVESLSDEYFLDEKRELFEIVYAKQIHIERNM 719

## RESULT 9

CLIB\_BACTE STANDARD; PRT; 719 AA.  
 ID CLIB\_BACTE  
 AC Q45709;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Pesticidal crystal protein cryIIb (insecticidal delta-endotoxin  
 DE Name=cryIIb) (Crystalline entomocidal protoxin) (81 kDa crystal protein).  
 GN Name=cryIIb; Synonyms=cryII(b), cryV, cryV465;  
 OS Bacillus thuringiensis (subsp. entomocidus).  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1436;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BP465;  
 RX MEDLINE=95314293; PubMed=7793960;  
 RA Shin B.-S., Park S.-H., Choi S.-K., Koo B.T., Lee S.T., Kim J.I.;  
 RT "Distribution of cryV-type insecticidal protein genes in Bacillus  
 RT thuringiensis and cloning of cryV-type genes from Bacillus  
 RT thuringiensis subsp. kurstaki and Bacillus thuringiensis subsp.  
 RT entomocidus";  
 RL Appl. Environ. Microbiol. 61:2402-2407 (1995).  
 CC -!- FUNCTION: Promotes colloidotomic lysis by binding to the midgut  
 CC epithelial cells of certain coleopteran and lepidopteran species.  
 CC Active on Plutella xylostella but not on Bombyx mori.  
 CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during  
 CC sporulation and is accumulated both as an inclusion and as part of  
 CC the spore coat.  
 CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-  
 CC terminus.  
 CC -!- SIMILARITY: Belongs to the delta endotoxin family.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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EMBL; U07642; AAA82114.1; --  
 DR F02965; ICYI.  
 DR HSSP; P02965; ICYI.  
 DR InterPro; IPR001178; Endotoxin.  
 DR InterPro; IPR005638; endotoxin\_C.  
 DR InterPro; IPR005639; endotoxin\_N.  
 DR InterPro; IPR008979; Gal\_bind\_Like.  
 DR Pfam; PF03944; Endotoxin\_C; 1.  
 DR Pfam; PF00555; Endotoxin\_M; 1.  
 DR Pfam; PF03945; Endotoxin\_N; 1.  
 KW Sporulation; Toxin.  
 SQ SEQUENCE 719 AA; 81295 MW; E8210ABEAE97688E CRC64;

Query Match 93.1%; Score 3503; DB 1; Length 719;  
 Best Local Similarity 92.5%; Pred. No. 3.7e-235;  
 Matches 665; Conservative 32; Mismatches 22; Indels 0; Gaps 0;

QY 1 MKLKNQKHQSSNAKYDKISTSLKNETDIELQNHEDCLKMSYENVPEVVSASTI 60

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Db 1 MKNPNPKHOSLSSNAKVDKIATDSLKNVETDIELKNMNNEDYLRKSEHESIDPFVSASTI 60
QY 61 QTGIGIAGKILGTLGVFPAGQVASYLFIKELWPKGNQWEIEMHEVHEEIIINQKISTYA 120
Db 61 QTGIGIAGKILGTLGVFPAGQVASYLFIKELWPKGNQWEIEMHEVHEEIIINQKILTYA 120
QY 121 RNKALTDLKLGDALAVYHDSLESWVGNNRNRTRARSVVKQYIALELMFVKQLPSFAVSG 180
Db 121 RNKALSDRLGLDALAVVHESLESWVENNRNRTRARSVVKQYIALELMFVKQLPSFAVSG 180
QY 181 EEPVLLPIYAQAANLHLLLDASIFGKWLSSSEISTFYNQVVERAGDYSYHCVKWS 240
Db 181 EEPVLLPIYAQAANLHLLLDASIFGKWLSSSEISTFYNQVVERTRDYSYHCHKWYN 240
QY 241 TGLNLRGTNAESWVRVYQNRDMLVLDLVALFPPSYDTQMYPKIKTAQLTREVTYDAI 300
Db 241 TGLNLRGTNAESWVRVYQNRDMLVLDLVALFPPSYDTQVLPKIKTSQLTREVTYDAI 300
QY 301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVITYSLLSRWSNTQYNNMW 360
Db 301 GTVHPNQAFATSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVITYSLLSRWSNTQYNNMW 360
QY 361 GGHKLEPRTTGGTLNISTQGSTNTSINPVTLPFTSRDVRVRESLAGLNLFLTQPVNGVPR 420
Db 361 GGHLESRRPIGGALNTSTQGSTNTSINPVTLPFTSRDVRVRESLAGLNLFLTQPVNGVPR 420
QY 421 VDFHWKFTVTHPIASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480
Db 421 VDFHWKFTPLPIASDNFYLYGAGVGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480
QY 481 ASHVKALVYSWTHESADRTNTIENSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 540
Db 481 ASHVKALVYSWTHESADRTNTIENSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 540
QY 541 TGFEGDIRVNIINPPFAQRYVRIRYASTDLQFHTSINGKAINQGNFSAATMRGEEDLYK 600
Db 541 TGFEGDIRVNIINPPFAQRYVRIRYASTDLQFHTSINGKAINQGNFSAATMRGEEDLYK 600
QY 601 TFRVGTFTTSPFLDVOSTTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660
Db 601 TFRVGTFTTSPFLDVOSTTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660
QY 661 TALFTSNRGLKTDVKDHYDIDQVSNLVESIDSEFYLDKRELFVYKVADELHIERNM 719
Db 661 TALFTSNRGLKTDVKDHYDIDQVSNLVESIDSEFYLDKRELFVYKVAQHIERNM 719

RESULT 10
Ciid BACTU
ID Ciid BACTU STANDARD; PRT; 719 AA.
AC Q9XDL;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 03-JUL-2004 (Rel. 44, Last annotation update)
DE Pesticidal crystal protein cryIId (insecticidal delta-endotoxin
DE CryII(d) (crystalline entomocidal protoxin) (81 kDa crystal protein).
GN Name=cryIId; Synonyms=cryII(d), NrcryV;
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BR30;
RX MEDLINE=20374042; PubMed=10919402;
RA Choi S.-K., Shin B.-S., Kong E.-M., Rho H.M., Park S.-H.;
RT "Cloning of a new Bacillus thuringiensis cryII-type crystal protein
RT Gene.";
RL Curr. Microbiol. 41:65-69(2000).
CC -!- FUNCTION: Promotes colloid osmotic lysis by binding to the midgut
CC epithelial cells of many lepidopteran larvae. Active on Plutella
CC xylostella and on Bombyx mori.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of

```

```

CC the spore coat.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -!- SIMILARITY: Belongs to the delta endotoxin family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch)
CC -----
CC EMBL: AF047579; AAD44366.1; -.
CC HSSP: P02965; 1CIY.
CC InterPro: IPR001178; Endotoxin.
CC InterPro: IPR005638; endotoxin_C.
CC InterPro: IPR005639; endotoxin_N.
CC InterPro: IPR008979; Gal_bind_like.
CC Pfam: PF03944; Endotoxin_C; 1.
CC Pfam: PF0555; Endotoxin_M; 1.
CC Pfam: PF03945; Endotoxin_N; 1.
CC Sporulation: Toxin.
CC KW SEQUENCE 719 AA; 81403 MW; F335F5689D3B0C45 CRC64;
CC SQ
Query Match 89.8%; Score 3380; DB 1; Length 719;
Best Local Similarity 89.4%; Pred. No. 1.4e-226;
Matches 643; Conservative 36; Mismatches 40; Indels 0; Gaps 0;
QY 1 MKNQDQKHSPPSSNAKVDKISTDSLKNETDIELQINNHEDCLKNSEYENVEPPVSASTI 60
Db 1 MKNQNMRYRSPSSNATVDKSTFDPLEHNTNNELONSHEDCLKNSEYEVFPVSVSTI 60
QY 61 QTGIGIAGKILGTLGVFPAGQVASYLFIKELWPKGNQWEIEMHEVHEEIIINQKISTYA 120
Db 61 QTGIGIAGKILGTLGVFPAGQVASYLFIKELWPKGNQWEIEMHEVHEEIIINQKISTYA 120
QY 121 RNKALTDLKLGDALAVYHDSLESWVGNNRNRTRARSVVKQYIALELMFVKQLPSFAVSG 180
Db 121 RNKALADLKLGDALAVYHESLESWVENNRNRTRARSVVKQYIALELMFVKQLPSFAVSG 180
QY 181 EEPVLLPIYAQAANLHLLLDASIFGKWLSSSEISTFYNQVVERAGDYSYHCVKWS 240
Db 181 EEPVLLPIYAQAANLHLLLDASIFGKWLSSSEISTFYNQVVERAGDYSYHCVKWS 240
QY 241 TGLNLRGTNAESWVRVYQNRDMLVLDLVALFPPSYDTQMYPKIKTAQLTREVTYDAI 300
Db 241 TGLNLRGTNAESWVRVYQNRDMLVLDLVALFPPSYDTQMYPKIKTAQLTREVTYDAI 300
QY 301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVITYSLLSRWSNTQYNNMW 360
Db 301 GTVHPNASFATSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVITYSLLSRWSNTQYNNMW 360
QY 361 GGHKLEPRTTGGTLNISTQGSTNTSINPVTLPFTSRDVRVRESLAGLNLFLTQPVNGVPR 420
Db 361 GGHKLEPRTTGGTLNISTQGSTNTSINPVTLPFTSRDVRVRESLAGLNLFLTQPVNGVPR 420
QY 421 VDFHWKFTVTHPIASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480
Db 421 VDFHWKFTVTHPIASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480
QY 481 ASHVKALVYSWTHESADRTNTIENSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 540
Db 481 ASHVKALVYSWTHESADRTNTIENSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 540
QY 541 TGFEGDIRVNIINPPFAQRYVRIRYASTDLQFHTSINGKAINQGNFSAATMRGEEDLYK 600
Db 541 TGFEGDIRVNIINPPFAQRYVRIRYASTDLQFHTSINGKAINQGNFSAATMRGEEDLYK 600
QY 601 TFRVGTFTTSPFLDVOSTTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660
Db 601 TFRVGTFTTSPFLDVOSTTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660

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661 TALTFTSTNPRGLKTDVKDYHIDQVSNLVESLSDSEFYLDKRELFPEIVKYANELHIERNM 719
661 TALTFTSTNPRGLKTDVKDYHIDQVSNLVESLSDSEFYLDKRELFPEIVKYAKQLNIERNM 719

RESULT 11
CLIC_BACTU STANDARD; PRT; 719 AA.
AC 087404;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pestidicial crystal protein cryIIc (insecticidal delta-endotoxin
DE CryII(c) (Crystalline entomocidal protoxin) (81 kDa crystal protein).
GN Name=cryIIc; Synonyms=cryII(c);
OS Bacillus thuringiensis.
OG Plasmid.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=C18 / Egypt;
RA Osman Y.A., Madkour M.A., Bulla L.A. Jr.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut
CC epithelial cells of insects.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -!- SIMILARITY: Belongs to the delta endotoxin family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF056933; AACG2933.1; -.
DR HSSP; P02965; IC1Y.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin C.
DR InterPro; IPR005639; endotoxin N.
DR InterPro; IPR008979; Gal_bind_like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
DR Plasmid; Sporulation; Toxin.
KW KW
SQ SEQUENCE 719 AA; 81210 MW; 8370B3F06B905DFF CRC64;

Query Match 89.8%; Score 3379; DB 1; Length 719;
Best Local Similarity 89.7%; Fred. No. 1.6e-226;
Matches 645; Conservative 34; Mismatches 40; Indels 0; Gaps 0;

QY 1 MKLKNQDQHQFSSNAKVDKISTDSLKNETDIELQNIHEDCLKMSYENVPEFVSASTI 60
DB 1 MKLKNPDKHQTLSSNAKVDKIATDSLKNETDIELKNMNEIDYLRMSHESIDPFVSASTI 60
QY 61 QTGIGIAGKILGTLGVPPAGQVASYLSFILGELPKGNQWEIEMHEVEELINOKISTYA 120
DB 61 QTGIGIAGKILGTLGVPPGQTASYSFILGELPKGKSQWEIEMHEVEALINRKISTYA 120
QY 121 RNKALTDLKGGLDALAVHDSLESWGNRNTRARSVVKSOYIALELMFVQKLSFAVSG 180
DB 121 RNKALTDLKGGLDALAVHDSLESWGNRNTRARSVVKQYIALELMFVQKLSFAVSG 180
QY 181 EVPLLPYIAQANLHLLLRDASIFGKXWGLSSSEISTFTFNQVRAGDYSYHCVKWYS 240
DB 181 EVPLLPYIAQANLHLLLRDASIFERNKGLSASEISTFTFNQVRERDYSYHCVKWNN 240

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241 TGANNLGRGNAESWRYNQFPRDMTLMVLVLDVALPPSYDTQWYPIKTKTAOLTREVYTDAL 300
241 TGANNLRATNGQSWRYNQFPRKDLBELMVLVLRVPFPPSYDTLVYPIKTKSQUTREVYTDAL 300
301 GTVHPHPFTSTTWNNNAPGSAIEAAVVRNPHLLDLEQVQTIYSLLSRWSNTQYMNMM 360
301 GTVDNQALRSTTWNNNAPGSAIEAAVVRNPHLLDLEKVTIYSLLSRWSNTQYMNMM 360
361 GGHKLEFRTIGTLNISTGGSTNTSINPVTLPTFSRDVYRTESLAGLNLFTQPVNGVPR 420
361 GGHRLSPRIGGALNTSGSTNTSINPVTLQFTSRDFYRTESWAGLNLFTQPVNGVPR 420
421 VDFHWKFTVHTPIASDNFYVPGVAGTQLOQSENELPPEATGQPNYESYSHRLSHIGLIS 480
421 VDFHWKFTVHTPIASDNFYVPGVAGTQLOQSENELPPEATGQPNYESYSHRLSHIGLIS 480
481 ASHVXALVYSWTHRSADRTNTEPNSTIQIPLVKAFNLSGGAUVVRGPGFTGGDILRRTN 540
481 GSHVXALVYSWTHRSADRTNTEPNSTIQIPLVKAFNLSGGAUVVRGPGFTGGHILRRTK 540
541 TGTGDIRVNIINPPAQRVYRIRVASTTDLQFHTSINGKAINQGNFSATWNRGEDLDYK 600
541 SGTGHIRVNIINPPAQRVYRIRVASTTDLQFHTSINGKAINQGNFSATWNRGEDLDYK 600
601 TERTVGTFTTFFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVYVYEAEDFEKAQEKV 660
601 TERTVGTFTTFFSFLDVQSTFTIGAWNFSSGNEVYIGRIEFVPEVYVYEAEDFEKAQEKV 660
661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDSEFYLDKRELFPEIVKYANELHIERNM 719
661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDSEFYLDKRELFPEIVKYAKQLNIERNM 719

RESULT 12
CLIB_BACTU STANDARD; PRT; 1229 AA.
AC 045739;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pestidicial crystal protein cryIbB (insecticidal delta-endotoxin
DE CryIb(b)) (Crystalline entomocidal protoxin) (140 kDa crystal protein).
DE Name=cryIbB; Synonyms=cryIb(b), cryE15;
GN Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
CX NCBI_TaxID=1428;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=NRRL B-21110 / EGS847;
RA Donovan W.P., Tan Y., Jany C.S., Gonzalez J.M. Jr.;
RT "Bacillus thuringiensis cryet4 and cryet5 toxin genes and proteins
RT toxic to lepidopteran insects.";
RL Patent number US5322687, 21-JUN-1994.
CC -!- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut
CC epithelial cells of many lepidopteran larvae.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -!- SIMILARITY: Belongs to the delta endotoxin family.
CC
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CC
CC EMBL; L32020; AAA22344.1; -.
DR HSSP; P02965; IC1Y.
DR InterPro; IPR001178; Endotoxin.

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300  SMWYNNAPSPSATEAAAIRSPHLLDFLEQLTIFSSASSRWNRHMTVMRGHTTIQSRPI 359
371  GGTLANISTGSGNTSINPVTLPFTGRDVYRTSLAGLNLF--LTPVNGVPRVDFHWKFV 428
360  GCGLNTSTHGATNTSINPVTLPFASGRDVYRTSYAGVLLWGLTYLPFIHGVPVTRFNF--- 416
429  THP-----IASDNFYVGGVAGTGTQLODSENLPEATGQPNVYESYSHRLSHIGITSASH 483
417  THPQNISRGATANYSQP-YESFQLQKDSETHLPETTERPNVYESYSHRLSHIGILQSR 475
484  VKALVYSWTHRSADRNTTIEPNSITQIPLVKAFNLSGGAAVRGPGFTGCDILRRNTGT 543
476  VNVPVYSWTHRSADRNTTIGPNRITQIPMKASASELPQGTTVVREGPGFTGCDILRRNTGG 535
544  FGDIRVNIINPPAQRYVRPIRVASTYTDLQFHTSINGKALNQGNFSATMNRGDDLDYKTF 603
536  FGPRIVTNNGPLTQRYRIGRFRVASTVDDFFVSRGGTTVNNFRFLRTMNSGDELKXGNFV 595
604  TVGFTTFPFLDVQSGTFTTICAWNFSSGNEVYIDRIEFVPEVITYEAYDPKAEKVTAL 663
596  RRAFTTPTFTQIDRIIRTSIQGLSGNGEVIDKIBIIPVTATFEAYDLERAQEAVALN 655
664  FTSTNPRGLKTDVKYHIDQVNLVESLSDEYLDKRELFEIVKYANELHIERNM 719
656  FTNTNPRRLKTDVTHIDQVNLVACLSEDFCLDEKRELEKVKYAKRLSDERNL 711

RESULT 15
CIBA_BACTK
ID CIBA_BACTK STANDARD; PRT; 1228 AA.
AC P05517; Q45731;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pepticidinal crystal protein crylBa (Insecticidal delta-endotoxin
DE crylB(a)) (Crystalline entomocidal protoxin) (140 kDa crystal protein).
GN Name-crylBa; Synonyms-crylB(a), cryA4.
OS Bacillus thuringiensis (subsp. kurstaki), and
OS Bacillus thuringiensis (subsp. entomocidus).
OS Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
ON NCBI_TaxID=29339, 1436;
OX [1]
RN SEQUENCE FROM N.A.
RP SPECIES=B.t.kurstaki; STRAIN=HD-2;
RC MEDLINE=88203216; PubMed=3362680;
RA Brizzard B.L., Whetley H.R.;
RT "Nucleotide sequence of an additional crystal protein gene cloned from
RT Bacillus thuringiensis subsp. thuringiensis.",
RT Nucleic Acids Res. 16:2723-2723(1988).
RN [2]
RN SEQUENCE FROM N.A.
RP SPECIES=B.t.entomocidus; STRAIN=HD-110;
RC Soetaert P.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
CC -I- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut
CC epithelial cells of insects.
CC -I- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -I- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -I- SIMILARITY: Belongs to the delta endotoxin family.
CC
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CC
CC EMBL; X06711; CAA29898.1; --
CC EMBL; X95704; CAA65003.1; --

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DR PIR; S00873; S00873.
DR HSSP; P07130; IDLC.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal_bind_Like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
DR Sporulation; Toxin.
KW VARIANT
SQ SEQUENCE 150 150 Y -> H (in strain HD-110).
SEQUENCE 1228 AA; 139647 MW; C8E3A19F5D98575 CRC64;

Query Match 60.1%; Score 2262.5; DB 1; Length 1228;
Best Local Similarity 62.4%; Pred.No. 2.1e-148;
Matches 447; Conservative 79; Mismatches 165; Indels 25; Gaps 6;

QY 23 TDSLKNETDIELOINH-----EDCLKMSEYENVEPVVSASTIOTGIGTAGKI 70
DB 2 TSNRKNEIINAVNSHSAQMDLLPDARIEDSLCIAEGNNIDPFVSASTVOTGINIAGRI 61

QY 71 LGTLGVFPAGQVASYFIILGELMPKGNQWEIFMEHVEEIIINQKISTYARNKALTDLKG 130
DB 62 LGVLGVFPAGQASFYSLVGLMPCRGDQWEIFLEHVEQLINQOITENARNTALARLQ 121

QY 131 LGDALAVYHDSLESWGNRNTRARSVVKSQYIALELMFVQKLPSPAVSGEEVPLPIYA 190
DB 122 LGDSFRAYQOSLEDWLENDDARTSVLYTQYIALELDFLNAMPLFAIRNQEVPELLMVA 181

QY 191 QAANLHLLLRDASIFKMGWGLSSSEISFTYNQVERAGDSYHCVKWSYSTGLNNLRGTN 250
DB 182 QAANLHLLLRDASLFQSEFGLTSQEIQRYYERQVETRDYSDYCVENYNTGLNSLGTN 241

QY 251 AESWRYNQRRDWTMLMVLQVLPSPDYQMPPIKTAQLTREVYTDGIVTVPHPSET 310
DB 242 AASWRYNQRRDLTLGLVDLVALPSPDYTRTPINTSAQLTREVYTDGAT--GVNVA 299

QY 311 STTWYNNAPSFGEAEAAVVRNPHLLDFLCVITYLSLRSWNTQYNNMMGGHKLFRIT 370
DB 300 SMWYNNAPSFGEAEAAVVRNPHLLDFLCVITYLSLRSWNTQYNNMMGGHKLFRIT 359

QY 371 GGTINISTQSTNTSINPVTLPFTSRDVRYSLAGLNLF--LTQPVNGVPRYDFHKKFV 428
DB 360 GGGINTSTHGATNTSINPVTLPFTSRDVRYSLAGLNLF--LTQPVNGVPRYDFHKKFV 416

QY 429 THP-----IASDNFYPGVAGIGTQLODSENELPPEATGQPNYESYSHRSLHIGLISAH 483
DB 417 TNFQNSDRGTANYQP--YESPGLQKDSLETLPETTERPNYESYSHRSLHIGLISAH 475

QY 484 VKALVSWTHRSADRTNTEIPNSITQIPLVKAFLNLSGAAVVRGPGFTGDIILRRNTGT 543
DB 476 VNVPVSWTHRSADRTNTEIPNSITQIPLVKAFLNLSGAAVVRGPGFTGDIILRRNTGT 535

QY 544 EGDIVNINPPFAGRIYRIRYASTTDLQHTSINGKAINQGNFSATMNRGDELDTYKTPR 603
DB 536 FGPRTVTWNGELTQRYAIGFYASTVDFFVSRGGTTVNNFRFLTRMSGDGLKYGNFV 595

QY 604 TVGFTTPEFLDVCSTETICAMNFSNGEYVIDRIEVPVEVYEAEDYFEKAEKVITAL 663
DB 596 RRAFTTPTTQDIIRTSIQGLSNGEYVIDRIEVPVEVYEAEDYFEKAEKVITAL 655

QY 664 FTSTNPRGLTKVDKHIDQVSNLVSLSDEFYLDKRELFEIVKYANELHIERNM 719
DB 656 FTNTNPRRLKTDVTHIDQVSNLVSLSDEFYLDKRELFEIVKYANELHIERNM 711

```

Search completed: October 28, 2004, 18:29:54  
Job time : 101.579 secs



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OM protein - protein search, using sw model

Run on: October 28, 2004, 17:52:12 ; Search time 98.4365 Seconds  
(without alignments)  
4202.652 Million cell updates/sec

Title: US-10-019-823B-57

Perfect score: 3760

Sequence: 1 MRLKNQKHQSPSSNAKVDK.....KRELFEIVKYAKQLHIERNM 719

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot\_02.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3756	99.9	719	1	C11A_BACTK
2	3756	99.9	719	2	Q6X181
3	3756	99.9	719	2	RA086782
4	3751	99.8	719	2	Q93N05
5	3750	99.7	719	2	O85796
6	3748	99.7	719	2	CAC85964
7	3621	96.3	719	2	O8KY61
8	3547	94.3	719	2	Q9F0P8
9	3516	93.5	719	1	C11B_BACTE
10	3393	90.2	719	1	C11D_BACTU
11	3373	89.7	719	1	C11C_BACTU
12	2445.5	65.0	1229	1	C11B_BACTU
13	2445.5	65.0	1233	1	C11C_BACTM
14	2277.5	60.5	1228	1	Q93T75
15	2276.5	60.5	1228	1	C1BA_BACTK
16	2268.5	60.3	1228	2	Q93NNM5
17	2195.5	58.4	849	2	O6PYW8
18	2195.5	58.4	849	2	RA093797
19	2195.5	58.4	1227	1	C1BE_BACTU
20	2111.5	56.2	1231	1	O8KNY2
21	2106.5	56.0	1231	1	C1BD_BACTZ
22	1984.5	52.8	1215	1	C1KA_BACTM
23	1904	50.6	381	1	Q45739
24	1669.5	44.4	1157	1	C8AA_BACUK
25	1660	44.1	1144	2	O8KZL7
26	1494	39.7	1157	1	C9CA_BACTO
27	1485.5	39.5	1169	1	C8BA_BACUK
28	1482.5	39.4	1166	1	C1GA_BACTU
29	1482	39.4	1167	1	C1JA_BACTU
30	1475	39.2	1169	1	C1FB_BACTM
31	1469	39.1	1174	2	Q45749

#### RESULT 1

ID	C11A_BACTK	STANDARD;	PRT;	719 AA.
AC	Q45752; P71092; Q45750; Q45751; Q45756;			
DT	30-MAY-2000 (Rel. 39, Created)			
DT	30-MAY-2000 (Rel. 39, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	Pesticidal crystal protein cryIIa (insecticidal)			
DE	CryII(a) (Crystalline entomocidal protoxin) (81 kDa crystal protein).			
GN	Names-cryIIa; Synonyms-cryII(a), cryV, cryVI, CGCryV;			
OS	Bacillus thuringiensis (subsp. kurstaki).			
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.			
OX	NCBI_TaxID=29339;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=DSIR732;			
RX	MEDLINE=93298009; PubMed=8517758;			
RA	Gleave A.P., Williams R., Hedges R.J.;			
RT	"Screening by polymerase chain reaction of Bacillus thuringiensis			
RT	serotypes for the presence of cryV-like insecticidal protein genes and			
RT	characterization of a cryV gene cloned from B. thuringiensis subsp.			
RT	kurstaki".			
RL	Appl. Environ. Microbiol. 59:1683-1687(1993).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=JHCC4835;			
RX	MEDLINE=92269582; PubMed=1588820;			
RA	Taylor R., Tippet J., Gibb G., Pells S., Pike D., Jordan L., Ely S.;			
RT	"Identification and characterization of a novel Bacillus thuringiensis			
RT	delta-endotoxin entomocidal to coleopteran and lepidopteran larvae."			
RL	Mol. Microbiol. 6:1211-1217(1992).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=HD-1;			
RX	MEDLINE=95314293; PubMed=7793960;			
RA	Shin B.-S., Park S.-H., Choi S.-K., Koo B.-T., Lee S.-T., Kim J.-I.;			
RT	"Distribution of cryV-type insecticidal protein genes in Bacillus			
RT	thuringiensis and cloning of cryV-type genes from Bacillus			
RT	thuringiensis subsp. kurstaki and Bacillus thuringiensis subsp.			
RT	entomocidus."			
RL	Appl. Environ. Microbiol. 61:2402-2407(1995).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=AB88;			
RX	MEDLINE=96178985; PubMed=8606196;			
RA	Kostichka K., Warren G.W., Mullins M., Mullins A.D., Palekar N.V.,			
RA	Craig J.A., Kozl M.G., Estruch J.J.;			
RT	"Cloning of a cryV-type insecticidal protein gene from Bacillus			
RT	thuringiensis: the cryV-encoded protein is expressed early in			
RT	stationary phase."			
RL	J. Bacteriol. 178:2141-2144(1996).			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=61;			

32	1465	39.0	1155	1	C1AB_BACTK	P06578 bacillus th
33	1465	39.0	1155	2	Q7BE98	Q7BE98 bacillus th
34	1465	39.0	1155	2	Q9F296	Q9F296 bacillus th
35	1465	39.0	1155	2	AA076494	AA076494 bacillus
36	1465	39.0	1155	2	AA013302	AA013302 bacillus
37	1463	38.9	1118	2	Q9AM83	Q9AM83 bacillus th
38	1460	38.8	1156	2	Q6GUA7	Q6GUA7 bacillus th
39	1458.5	38.8	1180	2	Q9S5V8	Q9S5V8 bacillus th
40	1457.5	38.8	1176	2	Q7WZT9	Q7WZT9 bacillus th
41	1455	38.7	1177	2	Q6EIX3	Q6EIX3 bacillus th
42	1453	38.6	1155	2	Q93T21	Q93T21 bacillus th
43	1452.5	38.6	793	2	O6PYW7	Q6PYW7 bacillus th
44	1452.5	38.6	793	2	AA093798	AA093798 bacillus
45	1451.5	38.6	1176	2	Q45736	Q45736 bacillus th

#### ALIGNMENTS

RA Selvapandian A., Bhatnagar R.K.;  
 RT "isolation, cloning and expression of cryV gene";  
 RL Submitted-(06-1996)-to-the-EMBL/GenBank/DDBJ databases.  
 CC -!- FUNCTION: Promotes colloid osmotic lysis by binding to the midgut  
 CC epithelial cells of certain coleopteran and lepidopteran species.  
 CC Active on *Plutella xylostella* and *Bombyx mori*.  
 CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during  
 CC sporulation and is accumulated both as an inclusion and as part of  
 CC the spore coat.  
 CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-  
 CC terminus.  
 CC -!- SIMILARITY: Belongs to the delta endotoxin family.  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC -----  
 CC EMBL; M98544; AAA22354.1; -;  
 CC EMBL; X62821; CAA44633.1; -;  
 CC EMBL; L36338; AAC36999.1; -;  
 CC EMBL; L49391; AAB00958.1; -;  
 CC EMBL; Y08920; CAA70124.1; -;  
 CC EMBL; L39815; L39815; -;  
 CC PIR; S25383; S25383.  
 CC HSSP; P02965; IC1Y.  
 CC InterPro; IPR001178; Endotoxin.  
 CC InterPro; IPR005638; endotoxin C.  
 CC InterPro; IPR005639; endotoxin N.  
 CC InterPro; IPR008979; Gal bind like.  
 CC Pfam; PF03944; Endotoxin\_C; 1.  
 CC Pfam; PF00555; Endotoxin\_M; 1.  
 CC Pfam; PF03945; Endotoxin\_N; 1.  
 CC Sporulation; Toxin.  
 KW FT VARIANT 159 159 K -> R (in strain 61).  
 FT VARIANT 233 233 D -> Y (in strain JHCC4835 and strain HD-  
 FT VARIANT 443 443 A -> V (in strain AB98).  
 FT VARIANT 711 712 -KQ -> NE (in strain HD-1 and strain 61).  
 SQ SEQUENCE 719 AA; 81216 MW; 3627E5A6C25DAFF5 CRC64;  
 Query Match 99.9%; Score 3756; DB 1; Length 719;  
 Best Local Similarity 99.9%; Pred. No. 1.1e-252;  
 Matches 718; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MKLNQDKHQSSNAKVDKISTDSLKNETDIELQNHEDCLKXSEYENVEPVSASTI 60  
 Db 1 MKLNQDKHQSSNAKVDKISTDSLKNETDIELQNHEDCLKXSEYENVEPVSASTI 60  
 QY 61 QTGIGIAGKILGTLPVPPAGQVASYLSFTLGLWPKGNQWEIFMEHVEEIIINQKISTYA 120  
 Db 61 QTGIGIAGKILGTLPVPPAGQVASYLSFTLGLWPKGNQWEIFMEHVEEIIINQKISTYA 120  
 QY 121 RNKALTDLKGDLALAVYHDSLESWVGNNRNNRARSVVKVQVIALLELMFVKLPSFAVSG 180  
 Db 121 RNKALTDLKGDLALAVYHDSLESWVGNNRNNRARSVVKVQVIALLELMFVKLPSFAVSG 180  
 QY 181 EEPVLLPIVAQAANLHLLLRDASIFGKEWGLSSSEISTFTYNNRQVERAGDSDHCVKWYS 240  
 Db 181 EEPVLLPIVAQAANLHLLLRDASIFGKEWGLSSSEISTFTYNNRQVERAGDSDHCVKWYS 240  
 QY 241 TGLNLRGNTNAESWRYNQFRDMLTLMVLDLVALPFSYDTQMPYIKTTAQLTRVYTDAI 300  
 Db 241 TGLNLRGNTNAESWRYNQFRDMLTLMVLDLVALPFSYDTQMPYIKTTAQLTRVYTDAI 300  
 QY 301 GTVHPHPSFTSTWYNNNAPSFAEAAVRNPHLLDLEQVTIYSLSRNSNTQYNNMW 360  
 Db 301 GTVHPHPSFTSTWYNNNAPSFAEAAVRNPHLLDLEQVTIYSLSRNSNTQYNNMW 360  
 QY 361 GGHKLEFRITGGTLNISTOGSTNTSINPVLPTSDRYRTESLAGLNLFTQPVNGVPR 420

Db 361 GGHKLEFRITGGTLNISTOGSTNTSINPVLPTSDRYRTESLAGLNLFTQPVNGVPR 420  
 QY 421 VDFHWKFVTHPIASDNFFYVPGVIGITQLQDSNELPPEATGQPNYESYSHRLSHIGLIS 480  
 Db 421 VDFHWKFVTHPIASDNFFYVPGVIGITQLQDSNELPPEATGQPNYESYSHRLSHIGLIS 480  
 QY 481 ASHVKALVYSWTHRSADRNTNTPNSITQIPLVKAFNLSGGAUVRGPGFTGGDLIRTN 540  
 Db 481 ASHVKALVYSWTHRSADRNTNTPNSITQIPLVKAFNLSGGAUVRGPGFTGGDLIRTN 540  
 QY 541 TGTFGDIRVNIINPPPAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDDLYK 600  
 Db 541 TGTFGDIRVNIINPPPAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDDLYK 600  
 QY 601 TRRTVGFTTFFSFLDVQSTFTTICAWNFSSGNGVYIDRFEFVPEVTEYAEYDFEKAQEKV 660  
 Db 601 TRRTVGFTTFFSFLDVQSTFTTICAWNFSSGNGVYIDRFEFVPEVTEYAEYDFEKAQEKV 660  
 QY 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVESLSDEFYLDKRELFEIVKAKQLHIERNM 719  
 Db 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVESLSDEFYLDKRELFEIVKAKQLHIERNM 719  
 RESULT 2  
 Q6X181 PRELIMINARY; PRT; 719 AA.  
 AC Q6X181;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Cry1I.  
 OS Name=cry1I;  
 OS Bacillus thuringiensis.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 CX NCBI\_TaxID=1428;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Espindola R., Lemos M.V.F., Lemos E.G.M., Sena J.A.D.;  
 RL Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AY262167; AAP86782.1; -;  
 DR InterPro; IPR001178; Endotoxin.  
 DR InterPro; IPR005638; endotoxin C.  
 DR InterPro; IPR005639; endotoxin N.  
 DR InterPro; IPR008979; Gal bind like.  
 DR Pfam; PF03944; Endotoxin\_C; 1.  
 DR Pfam; PF00555; Endotoxin\_M; 1.  
 DR Pfam; PF03945; Endotoxin\_N; 1.  
 SQ SEQUENCE 719 AA; 81216 MW; 3627E5A6C25DAFF5 CRC64;  
 Query Match 99.9%; Score 3756; DB 2; Length 719;  
 Best Local Similarity 99.9%; Pred. No. 1.1e-252;  
 Matches 718; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MKLNQDKHQSSNAKVDKISTDSLKNETDIELQNHEDCLKXSEYENVEPVSASTI 60  
 Db 1 MKLNQDKHQSSNAKVDKISTDSLKNETDIELQNHEDCLKXSEYENVEPVSASTI 60  
 QY 61 QTGIGIAGKILGTLPVPPAGQVASYLSFTLGLWPKGNQWEIFMEHVEEIIINQKISTYA 120  
 Db 61 QTGIGIAGKILGTLPVPPAGQVASYLSFTLGLWPKGNQWEIFMEHVEEIIINQKISTYA 120  
 QY 121 RNKALTDLKGDLALAVYHDSLESWVGNNRNNRARSVVKVQVIALLELMFVKLPSFAVSG 180  
 Db 121 RNKALTDLKGDLALAVYHDSLESWVGNNRNNRARSVVKVQVIALLELMFVKLPSFAVSG 180  
 QY 181 EEPVLLPIVAQAANLHLLLRDASIFGKEWGLSSSEISTFTYNNRQVERAGDSDHCVKWYS 240  
 Db 181 EEPVLLPIVAQAANLHLLLRDASIFGKEWGLSSSEISTFTYNNRQVERAGDSDHCVKWYS 240  
 QY 241 TGLNLRGNTNAESWRYNQFRDMLTLMVLDLVALPFSYDTQMPYIKTTAQLTRVYTDAI 300  
 Db 241 TGLNLRGNTNAESWRYNQFRDMLTLMVLDLVALPFSYDTQMPYIKTTAQLTRVYTDAI 300

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QY 301 GTVHPHPSFTSTWYNNAPSAIEAAVVRNPHLLDFLEQVTIYSLSSWSNTQYNNMW 360
DB 301 GTVHPHPSFTSTWYNNAPSAIEAAVVRNPHLLDFLEQVTIYSLSSWSNTQYNNMW 360
QY 361 GGHKLBRFTTGGTILNISTQGSTWTSINPVTLPFTSRDVRVYTESLAGNLFLTPQVNGVPR 420
DB 361 GGHKLBRFTTGGTILNISTQGSTWTSINPVTLPFTSRDVRVYTESLAGNLFLTPQVNGVPR 420
QY 421 VDFHKKFVTHPIASDNFYFGYAGIGTQLOSDSNELPPEATGQPNYESYSHRLSHIGLIS 480
DB 421 VDFHKKFVTHPIASDNFYFGYAGIGTQLOSDSNELPPEATGQPNYESYSHRLSHIGLIS 480
QY 481 ASHVKALVYSWTHRSADRTNTIIPNSITQIPLVKAFNLSSGAAVVRGPFTGGDILRRTN 540
DB 481 ASHVKALVYSWTHRSADRTNTIIPNSITQIPLVKAFNLSSGAAVVRGPFTGGDILRRTN 540
QY 541 TGTFGDIRVNIINPPFAQRYRIRYASTTDLOFHTSINGKAINQGNFSAATMNRGEDLDYK 600
DB 541 TGTFGDIRVNIINPPFAQRYRIRYASTTDLOFHTSINGKAINQGNFSAATMNRGEDLDYK 600
QY 601 TFRVGTFTTFFSFLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDPEKAQEKV 660
DB 601 TFRVGTFTTFFSFLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDPEKAQEKV 660
QY 661 TALFTSTNPRGLKTDVKDHYDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719
DB 661 TALFTSTNPRGLKTDVKDHYDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 3
AAP86782 PRELIMINARY; PRT; 719 AA.
ID AAP86782;
AC AAP86782; (TREMBLrel. 27, Created)
DT 02-MAR-2004 (TREMBLrel. 27, Last sequence update)
DR 02-MAR-2004 (TREMBLrel. 27, Last annotation update)
DE CRYII.
GN CRYII.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=T01.328;
RA Espindola R., Lemos M.V.F., Lemos E.G.M., Sena J.A.D.;
RT "Complete sequence of cryII gene of isolate T01.328 from Bacillus
RL thuringiensis from Cubatao (SP - Brazil) soil.";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY262167; AAP86782.1; -.
DR ENBL; AY262167; AAP86782.1; -.
SQ SEQUENCE 719 AA; 81216 MW; 3627E5A6C25DAFF5 CRC64;

Query Match 99.9%; Score 3756; DB 2; Length 719;
Best Local Similarity 99.9%; Pred. No. 1.1e-252;
Matches 718; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINNHEDCLKMSEYENVEPVSASTI 60
DB 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINNHEDCLKMSEYENVEPVSASTI 60
QY 61 QTGIGIAGKILGTIGVPFAQVASLYSFLGELWPXGKNQWEIFMBHVEEIIINQKISTYA 120
DB 61 QTGIGIAGKILGTIGVPFAQVASLYSFLGELWPXGKNQWEIFMBHVEEIIINQKISTYA 120
QY 121 RNKALTDKLGIDALAVYHDSLSWGVRNNTARSVVKVQYIALEIMFVKQLPSFAVSG 180
DB 121 RNKALTDKLGIDALAVYHDSLSWGVRNNTARSVVKVQYIALEIMFVKQLPSFAVSG 180
QY 181 EEPVLLPIYAAANLHLLLRDASIIFGKEWGLSSSEISTFYNQVRAGDYSBHCWKVYS 240
DB 181 EEPVLLPIYAAANLHLLLRDASIIFGKEWGLSSSEISTFYNQVRAGDYSBHCWKVYS 240

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QY 241 TGLNNLRGTNAESWVRYNQFRDMDTLMVLDLVALPPSYDTQWPIKTTAQLTREYITDAI 300
DB 241 TGLNNLRGTNAESWVRYNQFRDMDTLMVLDLVALPPSYDTQWPIKTTAQLTREYITDAI 300
QY 301 GTVHPHPSFTSTWYNNAPSAIEAAVVRNPHLLDFLEQVTIYSLSSWSNTQYNNMW 360
DB 301 GTVHPHPSFTSTWYNNAPSAIEAAVVRNPHLLDFLEQVTIYSLSSWSNTQYNNMW 360
QY 361 GGHKLBRFTTGGTILNISTQGSTWTSINPVTLPFTSRDVRVYTESLAGNLFLTPQVNGVPR 420
DB 361 GGHKLBRFTTGGTILNISTQGSTWTSINPVTLPFTSRDVRVYTESLAGNLFLTPQVNGVPR 420
QY 421 VDFHKKFVTHPIASDNFYFGYAGIGTQLOSDSNELPPEATGQPNYESYSHRLSHIGLIS 480
DB 421 VDFHKKFVTHPIASDNFYFGYAGIGTQLOSDSNELPPEATGQPNYESYSHRLSHIGLIS 480
QY 481 ASHVKALVYSWTHRSADRTNTIIPNSITQIPLVKAFNLSSGAAVVRGPFTGGDILRRTN 540
DB 481 ASHVKALVYSWTHRSADRTNTIIPNSITQIPLVKAFNLSSGAAVVRGPFTGGDILRRTN 540
QY 541 TGTFGDIRVNIINPPFAQRYRIRYASTTDLOFHTSINGKAINQGNFSAATMNRGEDLDYK 600
DB 541 TGTFGDIRVNIINPPFAQRYRIRYASTTDLOFHTSINGKAINQGNFSAATMNRGEDLDYK 600
QY 601 TFRVGTFTTFFSFLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDPEKAQEKV 660
DB 601 TFRVGTFTTFFSFLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDPEKAQEKV 660
QY 661 TALFTSTNPRGLKTDVKDHYDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719
DB 661 TALFTSTNPRGLKTDVKDHYDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 4
Q93NJ5 PRELIMINARY; PRT; 719 AA.
ID Q93NJ5;
AC Q93NJ5; (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DR 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE CryIIa.
GN CryIIa.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RA Song F., Zhang J., Gu A., Huang D., Li G.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF373207; AAK66742.1; -.
DR HSSP; P02965; 1CIY.
DR GO; GO:0005102; P:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin C.
DR InterPro; IPR005639; endotoxin N.
DR InterPro; IPR008979; Gal bind like.
DR Pfam; PF03944; Endotoxin_C_1.
DR Pfam; PF03955; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
SQ SEQUENCE 719 AA; 81225 MW; CG29DF2C44827241 CRC64;

Query Match 99.8%; Score 3751; DB 2; Length 719;
Best Local Similarity 99.7%; Pred. No. 2.3e-252;
Matches 717; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINNHEDCLKMSEYENVEPVSASTI 60
DB 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINNHEDCLKMSEYENVEPVSASTI 60
QY 61 QTGIGIAGKILGTIGVPFAQVASLYSFLGELWPXGKNQWEIFMBHVEEIIINQKISTYA 120

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Db 61 QTGIGIAGKILGTLPVFPAGQVASISYLGILGELWPKGNQWEIFMEHVBEIINQKISTYA 120  
 QY 121 RNKALTDLKGGLDALAVYHDSLESWGNRNTRARSVVKQYIALELMFVKLPSPFAVSG 180  
 Db 121 RNKALTDLKGGLDALAVYHDSLESWGNRNTRARSVVKQYIALELMFVKLPSPFAVSG 180  
 QY 181 BEVPLLPPIYAQAANLHLLLDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHCVKWS 240  
 Db 181 BEVPLLPPIYAQAANLHLLLDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHCVKWS 240  
 QY 241 TGLNLRGTNAESWVRNQFRDMLVLDLVALPSPSYDTQMPYIKTTAQLTREYVTDI 300  
 Db 241 TGLNLRGTNAESWVRNQFRDMLVLDLVALPSPSYDTQMPYIKTTAQLTREYVTDI 300  
 QY 301 GTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTTIYSLLSWSNTQYNNMW 360  
 Db 301 GTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTTIYSLLSWSNTQYNNMW 360  
 QY 361 GGKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRYSAGLNLFLTOPVNGVPR 420  
 Db 361 GGKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRYSAGLNLFLTOPVNGVPR 420  
 QY 421 VDFHWKFTVTHPIASDNFYVPGYAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 Db 421 VDFHWKFTVTHPIASDNFYVPGYAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 QY 481 ASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRTN 540  
 Db 481 ASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRTN 540  
 QY 541 TGTFGDIRVNIAPPFAQRYRIRYASTDTLQFHTSINGKAINQGNFSATMNRGDLDYK 600  
 Db 541 TGTFGDIRVNIAPPFAQRYRIRYASTDTLQFHTSINGKAINQGNFSATMNRGDLDYK 600  
 QY 601 TFRTVGFTTPSFSDLVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDPEKAQEKV 660  
 Db 601 TFRTVGFTTPSFSDLVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDPEKAQEKV 660  
 QY 661 TALFTSTNPRGLKTDVKDHYDQVNLVSLSDSEFYLDKRELFEIVKYAKQLHIERNM 719  
 Db 661 TALFTSTNPRGLKTDVKDHYDQVNLVSLSDSEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 5  
 CS85796 PRELIMINARY; PRT; 719 AA.  
 ID CS85796  
 AC CS85796  
 DT 01-NOV-1998 (TREMELrel. 08, Created)  
 DT 01-NOV-1998 (TREMELrel. 08, Last sequence update)  
 DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)  
 DE Insecticidal protein.  
 GN Name=crv101;  
 OS Bacillus thuringiensis (subsp. kurstaki).  
 OG Plasmid large plasmid.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=29339;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-S101;  
 RA Zhong Q., Deng R., Long Q., Yuan M., Pang Y., Wang X.;  
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF067695; AAC7691.1;  
 DR HSSP; P02965; 1CIY.  
 DR GO; GO:0005102; F:receptor binding; IEA.  
 DR GO; GO:0006952; P:defense response; IEA.  
 DR GO; GO:0009405; P:pathogenesis; IEA.  
 DR InterPro; IPR001178; Endotoxin.  
 DR InterPro; IPR005638; Endotoxin C.  
 DR InterPro; IPR005639; Endotoxin N.  
 DR InterPro; IPR008979; Gal bind like.  
 DR Pfam; PF03944; Endotoxin C; 1.  
 DR Pfam; PF00555; Endotoxin M; 1.  
 DR Pfam; PF03945; Endotoxin N; 1.

KW Plasmid. 719 AA; 81230 MW; 42746D478359BBA7 CRC64;  
 SQ SEQUENCE  
 Query Match 99.7%; Score 3750; DB 2; Length 719;  
 Best Local Similarity 99.7%; Pred. No. 2.8e-252;  
 Matches 717; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 MKLKNQDKHQSFSSNAKVDKISTSLKNETDIELQINHEDCLKMSYENVEPFSASTI 60  
 Db 1 MKLKNQDKHQSFSSNAKVDKISTSLKNETDIELQINHEDCLKMSYENVEPFSASTI 60  
 QY 61 QTGIGIAGKILGTLPVFPAGQVASISYLGILGELWPKGNQWEIFMEHVBEIINQKISTYA 120  
 Db 61 QTGIGIAGKILGTLPVFPAGQVASISYLGILGELWPKGNQWEIFMEHVBEIINQKISTYA 120  
 QY 121 RNKALTDLKGGLDALAVYHDSLESWGNRNTRARSVVKQYIALELMFVKLPSPFAVSG 180  
 Db 121 RNKALTDLKGGLDALAVYHDSLESWGNRNTRARSVVKQYIALELMFVKLPSPFAVSG 180  
 QY 181 BEVPLLPPIYAQAANLHLLLDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHCVKWS 240  
 Db 181 BEVPLLPPIYAQAANLHLLLDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHCVKWS 240  
 QY 241 TGLNLRGTNAESWVRNQFRDMLVLDLVALPSPSYDTQMPYIKTTAQLTREYVTDI 300  
 Db 241 TGLNLRGTNAESWVRNQFRDMLVLDLVALPSPSYDTQMPYIKTTAQLTREYVTDI 300  
 QY 301 GTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTTIYSLLSWSNTQYNNMW 360  
 Db 301 GTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTTIYSLLSWSNTQYNNMW 360  
 QY 361 GGKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRYSAGLNLFLTOPVNGVPR 420  
 Db 361 GGKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRYSAGLNLFLTOPVNGVPR 420  
 QY 421 VDFHWKFTVTHPIASDNFYVPGYAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 Db 421 VDFHWKFTVTHPIASDNFYVPGYAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 QY 481 ASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRTN 540  
 Db 481 ASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRTN 540  
 QY 541 TGTFGDIRVNIAPPFAQRYRIRYASTDTLQFHTSINGKAINQGNFSATMNRGDLDYK 600  
 Db 541 TGTFGDIRVNIAPPFAQRYRIRYASTDTLQFHTSINGKAINQGNFSATMNRGDLDYK 600  
 QY 601 TFRTVGFTTPSFSDLVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDPEKAQEKV 660  
 Db 601 TFRTVGFTTPSFSDLVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDPEKAQEKV 660  
 QY 661 TALFTSTNPRGLKTDVKDHYDQVNLVSLSDSEFYLDKRELFEIVKYAKQLHIERNM 719  
 Db 661 TALFTSTNPRGLKTDVKDHYDQVNLVSLSDSEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 6  
 CAC85964 PRELIMINARY; PRT; 719 AA.  
 ID CAC85964  
 AC CAC85964  
 DT 02-MAR-2004 (TREMELrel. 27, Created)  
 DT 02-MAR-2004 (TREMELrel. 27, Last sequence update)  
 DT 02-MAR-2004 (TREMELrel. 27, Last annotation update)  
 DE Delta-endotoxin.  
 GN CRV11A.  
 OS Bacillus thuringiensis (subsp. kurstaki).  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;  
 OC Bacillus cereus group; Bacillus thuringiensis.  
 OX NCBI\_TaxID=29339;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BNS3;  
 RA Tounsi S., Zouari N., Jacua S.;



RT "Cloning and study of the expression of a novel cryIIa-type gene from  
 RT *Bacillus thuringiensis* subsp. *kurstaki*.";  
 RL J. Appl. Microbiol. 95:123-28(2003).  
 DR EMBL; AJ315121; CAC85964.1; -  
 SQ SEQUENCE 719 AA; 81203 MW; 867655A6C25DAF8 CRC64;

Query Match 99.7%; Score 3748; DB 2; Length 719;  
 Best Local Similarity 99.6%; Pred. No. 3.8e-252; Indels 0; Gaps 0;  
 Matches 716; Conservative 1; Mismatches 2;  
 Qy 1 M K L N Q D K H S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y N V E P F V S A S T I 60  
 Db 1 M K L N Q D K H S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y N V E P F V S A S T I 60  
 Qy 61 Q T G I G I A G K I L T G V P P A G V A S L Y S F I L G E L M P K G N Q W E I F M E H V E E I I N Q K I S T Y A 120  
 Db 61 Q T G I G I A G K I L T G V P P A G V A S L Y S F I L G E L M P K G N Q W E I F M E H V E E I I N Q K I S T Y A 120  
 Qy 121 R N K A L T D L K G L D A L A V Y H D S L E S W G N R N N T R A R S V V K S Q Y I A L E M F V Q K L P S F A V S G 180  
 Db 121 R N K A L T D L K G L D A L A V Y H D S L E S W G N R N N T R A R S V V K S Q Y I A L E M F V Q K L P S F A V S G 180  
 Qy 181 E E V P L L P I Y A Q A A N L H L L L D A S I F G K E W G L S S E I S T F Y N Q V E R A G D Y S D H C V K W Y S 240  
 Db 181 E E V P L L P I Y A Q A A N L H L L L D A S I F G K E W G L S S E I S T F Y N Q V E R A G D Y S D H C V K W Y S 240  
 Qy 241 T G L N L R G T N A E S W R Y N Q F R D M T L M V D L V A L F P S Y D T Q M Y P I K T T A Q L T R E V Y T D A I 300  
 Db 241 T G L N L R G T N A E S W R Y N Q F R D M T L M V D L V A L F P S Y D T Q M Y P I K T T A Q L T R E V Y T D A I 300  
 Qy 301 G T V H P H P S F T S T T W Y N N N A P S F G A I E A A V V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N W 360  
 Db 301 G T V H P H P S F T S T T W Y N N N A P S F G A I E A A V V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N W 360  
 Qy 361 G G H K L E P R T I G G L N I S T Q S T N T S I N P V L P T S R D V Y R T E S L A G L N L F L T Q P V N G V P R 420  
 Db 361 G G H K L E P R T I G G L N I S T Q S T N T S I N P V L P T S R D V Y R T E S L A G L N L F L T Q P V N G V P R 420  
 Qy 421 V D F H W K F V T H P I A S D N F Y P G Y G I G T Q L O D S E N L P P E A T G Q P N Y E S Y S H R L S H I G L I S 480  
 Db 421 V D F H W K F V T H P I A S D N F Y P G Y G I G T Q L O D S E N L P P E A T G Q P N Y E S Y S H R L S H I G L I S 480  
 Qy 481 A S H V K A L Y S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G G D I L R R T N 540  
 Db 481 A S H V K A L Y S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G G D I L R R T N 540  
 Qy 541 T G T F G D I R V N I N P P P A Q R Y R I R Y A S T T D L Q P H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 600  
 Db 541 T G T F G D I R V N I N P P P A Q R Y R I R Y A S T T D L Q P H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 600  
 Qy 601 T F R T V G T T P F S F L D V Q S T T I G A W N F S S G N E V Y I D R I E F V P V E V T Y E A E Y D F E K A Q E K V 660  
 Db 601 T F R T V G T T P F S F L D V Q S T T I G A W N F S S G N E V Y I D R I E F V P V E V T Y E A E Y D F E K A Q E K V 660  
 Qy 661 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K Y A K O L H I E R N M 719  
 Db 661 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K Y A K O L H I E R N M 719

## RESULT 7

Q8KY61 PRELIMINARY; PRT; 719 AA.  
 AC Q8KY61;  
 DT 01-OCT-2002 (T-EMBLrel. 22, Created)  
 DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)  
 DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)  
 DE CRY.  
 OS *Bacillus thuringiensis*.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1428;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Porcar M., Martinez C., Caballero P.;

## RESULT 8

Q9F0P8 PRELIMINARY; PRT; 719 AA.  
 ID Q9F0P8  
 AC Q9F0P8;

RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF278797; AAM73516.1; -  
 DR FIR; B42459; B42459.  
 DR HSSP; P02965; 1CIY.  
 DR GO; GO:0005102; F:receptor binding; IEA.  
 DR GO; GO:0006952; P:defense response; IEA.  
 DR GO; GO:0009405; P:pathogenesis; IEA.  
 DR InterPro; IPR001178; Endotoxin.  
 DR InterPro; IPR005638; endotoxin\_C.  
 DR InterPro; IPR008979; endotoxin\_N.  
 DR Pfam; PF03944; Endotoxin\_C; 1-  
 DR Pfam; PF0555; Endotoxin\_C; 1-  
 DR Pfam; PF03945; Endotoxin\_N; 1.  
 SQ SEQUENCE 719 AA; 80984 MW; 84F1287246264473 CRC64;

Query Match 96.3%; Score 3621; DB 2; Length 719;  
 Best Local Similarity 96.1%; Pred. No. 2.7e-243;  
 Matches 691; Conservative 12; Mismatches 16; Indels 0; Gaps 0;

Qy 1 M K L N Q D K H S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y N V E P F V S A S T I 60  
 Db 1 M K L N Q D K H S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K I S E Y N V E P F V S A S T I 60  
 Qy 61 Q T G I G I A G K I L T G V P P A G V A S L Y S F I L G E L M P K G N Q W E I F M E H V E E I I N Q K I S T Y A 120  
 Db 61 Q T G I G I A G K I L T G V P P A G V A S L Y S F I L G E L M P K G N Q W E I F M E H V E E I I N Q K I S T Y A 120  
 Qy 121 R N K A L T D L K G L D A L A V Y H D S L E S W G N R N N T R A R S V V K S Q Y I A L E M F V Q K L P S F A V S G 180  
 Db 121 R N K A L T D L K G L D A L A V Y H D S L E S W G N R N N T R A R S V V K S Q Y I A L E M F V Q K L P S F A V S G 180  
 Qy 181 E E V P L L P I Y A Q A A N L H L L L D A S I F G K E W G L S S E I S T F Y N Q V E R A G D Y S D H C V K W Y S 240  
 Db 181 E E V P L L P I Y A Q A A N L H L L L D A S I F G K E W G L S S E I S T F Y N Q V E R A G D Y S D H C V K W Y S 240  
 Qy 241 T G L N L R G T N A E S W R Y N Q F R D M T L M V D L V A L F P S Y D T Q M Y P I K T T A Q L T R E V Y T D A I 300  
 Db 241 T G L N L R G T N A E S W R Y N Q F R D M T L M V D L V A L F P S Y D T L V Y P I K T T S Q L T R E V Y T D A I 300  
 Qy 301 G T V H P H P S F T S T T W Y N N N A P S F A I E A A V V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N W 360  
 Db 301 G T V H P N A S F A S T T W N N N A P S F T T E S A V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N W 360  
 Qy 361 G G H K L E P R T I G G L N I S T Q S T N T S I N P V L P T S R D V Y R T E S L A G L N L F L T Q P V N G V P R 420  
 Db 361 G G H R L E P R T I G G L N T S T Q S T N T S I N P V L P T S R D V Y R T E S L A G L N L F L T Q P V N G V P R 420  
 Qy 421 V D F H W K F V T H P I A S D N F Y P G Y G I G T Q L O D S E N L P P E A T G Q P N Y E S Y S H R L S H I G L I S 480  
 Db 421 V D F H W K F V T H P I A S D N F Y P G Y G I G T Q L O D S E N L P P E T T G Q P N Y E S Y S H R L S H I G L I S 480  
 Qy 481 A S H V K A L Y S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G G D I L R R T N 540  
 Db 481 A S H V K A L Y S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G G D I L R R T N 540  
 Qy 541 T G T F G D I R V N I N P P P A Q R Y R I R Y A S T T D L Q P H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 600  
 Db 541 T G T F G D I R V N I N P P P A Q R Y R I R Y A S T T D I Q P H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 600  
 Qy 601 T F R T V G T T P F S F L D V Q S T T I G A W N F S S G N E V Y I D R I E F V P V E V T Y E A E Y D F E K A Q E K V 660  
 Db 601 T F R T V G T T P F S F D V Q S T T I G A W N F S S G N E V Y I D R I E F V F V E V T Y E A E Y D F E K A Q E K V 660  
 Qy 661 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K Y A K O L H I E R N M 719  
 Db 661 T A L F T S T N P G L K T N V T E Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K Y A K O L H I E R N M 719

01-MAR-2001 (TRENBLrel. 16, Created)  
 01-MAR-2001 (TRENBLrel. 16, Last sequence update)  
 01-MAR-2004 (TRENBLrel. 26, Last annotation update)  
 CRYII.  
 DE Name=crvII;  
 OS Bacillus thuringiensis.  
 OG Plasmid pBRC19.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1428;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BT007;  
 RX MEDLINE=22837682; PubMed=12957903;  
 RA Song F., Zhang J., Gu A., Wu Y., Han L., He K., Chen Z., Yao J.,  
 Hu Y., Li G., Huang D.;  
 RT "Identification of cryII-type genes from Bacillus thuringiensis  
 strains and characterization of a novel cryII-type gene.";  
 RL Appl. Environ. Microbiol. 69:5207-5211(2003).  
 DR EMBL; AF211190; AAG43526.1; -.  
 DR HSP; P02965; 1C1Y.  
 DR GO; GO:0005102; P:receptor binding; IEA.  
 DR GO; GO:0006932; P:defense response; IEA.  
 DR GO; GO:0009405; P:pathogenesis; IEA.  
 DR InterPro; IPR001178; Endotoxin.  
 DR InterPro; IPR005638; endotoxin C.  
 DR InterPro; IPR008979; Gal bind like.  
 DR Pfam; PF03944; Endotoxin\_C; 1.  
 DR Pfam; PF00555; Endotoxin\_M; 1.  
 DR Pfam; PF03945; Endotoxin\_N; 1.  
 KW Plasmid.  
 SQ SEQUENCE 719 AA; 81024 MW; 7E17481922C435B6 CRC64;  
 Query Match 94.3%; Score 3547; DB 2; Length 719;  
 Best Local Similarity 93.5%; Pred. No. 3.8e-238;  
 Matches 672; Conservative 26; Mismatches 21; Indels 0; Gaps 0;  
 1 M K L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y E N V P F V S A S T I 60  
 1 M K L K N P D K H Q S L S S N A K V D K I A T D S L K N E T D I E L K N I N H E D F L R M S E H S E I D P F V S A S T I 60  
 61 Q T G I G I A K I L G T L G V P A G Q A S I S Y F I L G E L P K G K N O E I F M E H V E E I L I N K I S T Y A 120  
 61 Q T G I G I A K I L G T L G V P A G Q A S I S Y F I L G E L P K G K S Q W E I F M E H V E E I L I N K I S T Y A 120  
 121 R N K A L T D L K G L G D A L A V H D S L E S V G N R N N T R A S V V K S Q I A L E L M F V Q L P S F A V S G 180  
 121 R N I A L A D L K G L G D A L A V H S L E S W I K R N N A R A T S V V K S Q I A L E L L F V Q L P S F A V S G 180  
 181 E V P L P T I Y A Q A N L H L L L D R A S I F G K E W L S S E I S T F P N Q V E R A G Y S D H C V K W Y S 240  
 181 E V P L P T I Y A Q A N L H L L L D R A S V F G K E W L S S Q I S T F P N Q V E R T S D Y S D H C V K W Y S 240  
 241 T G L N L R G T N A E S W R Y N Q F R D M T L M V L D L V A L P P S Y D T Q M Y P I K T T A Q L T R E V Y T D A I 300  
 241 T G L N L R G T N A E S W R Y N Q F R K D M T L M V L D L I A L P P S Y D T L V Y P I K T T S Q L T R E V Y T D A I 300  
 301 G T V H P H P S T T T W N N A P S F A E A V R N P H L L D F L E Q V T T Y S L L S R W S N T Q Y N W M 360  
 301 G T V H P N A S F A S T T W N N A P S F A S E A V R N P H L L D F L E Q V T T Y S L L S R W S N T Q Y N W M 360  
 361 G G H K L E F T I G T L N I S T Q S T N T S I N P V T L P F T S R D V Y R T E S L A G L N L F T Q P V N G V P R 420  
 361 G G H R L E F T I G V L N T S T Q S T N T S I N P V T L P F T S R D V Y R T E S L A G L N L F T Q P V N G V P R 420  
 421 V D F H W K F V T H P I A S D N F Y P G V I G T Q L Q D S E N E L P P E A T G Q N Y S Y S H R L S H I G L I S 480  
 421 V D F H W K F A T L P I A S D N F Y L G V A G V T Q L Q D S E N E L P P E T T G Q N Y S Y S H R L S H I G L I S 480  
 481 A S H V K A L V Y S W T H R S A D R N T I E P N S I T Q I P L V A F N L S S G A A V V R G P C F T G G D I L R T N 540  
 481 A S H V K A L V Y S W T H R S A D R N T I E P N S I T Q I P L V A F N L S S G A A V V R G P C F T G G D I L R T N 540

541 T G T F G D I R V N I P P P A Q R Y R V I R Y A S T T D L Q F H T S I N G K A I N Q N F S A T M N R G E D L D Y K 600  
 541 T G T F G D I R V N I P P P A Q R Y R V I R Y A S T T D L Q F H T S I N G K A I N Q N F S A T M N R G E D L D Y K 600  
 601 T P R T V G F T T P F S F L D V Q S T F T I G A W N F S S G N E V I D R I E F V P V E V T Y E A E V D F F K A Q E K V 660  
 601 T P R T V G F T T P F S F S D V Q S T F T I G A W N F S S G N E V I D R I E F V P V E V T Y E A E V D F F K A Q E K V 660  
 661 T A L F T S T N P R G L K T D V K D Y H I D Q V S L N V E S L S D E F Y L D E K E L F E I V K Y A Q I H E R N M 719  
 661 T A L F T S T N P R G L K T D V K D Y H I D Q V S L N V E S L S D E F Y L D E K E L F E I V K Y A Q I H E R N M 719

RESULT 9  
 CLIB BACTE STANDARD; PRT; 719 AA.  
 AC Q45709;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE pesticidal crystal protein cryIIb (insecticidal delta-endotoxin  
 DE CryII(b)) (crystalline entomocidal protoxin) (81 kDa crystal protein).  
 GN Name=cryIIb; Synonyms=cryII(b), cryV, cryV465;  
 OS Bacillus thuringiensis (subsp. entomocidus).  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1436;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BP465;  
 RX MEDLINE=95314293; PubMed=7793960;  
 RA Shin B.-S., Park S.-H., Choi S.-K., Xoo B.T., Lee S.T., Kim J.I.;  
 RT "Distribution of cryV-type insecticidal protein genes in Bacillus  
 RT thuringiensis and cloning of cryV-type genes from Bacillus  
 RT thuringiensis subsp. kurstaki and Bacillus thuringiensis subsp.  
 RT entomocidus.";  
 RL Appl. Environ. Microbiol. 61:2402-2407(1995).  
 CC -!- FUNCTION: Promotes colloid osmotic lysis by binding to the midgut  
 CC epithelial cells of certain coleopteran and lepidopteran species.  
 CC Active on Plutella xylostella but not on Bombyx mori.  
 CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during  
 CC sporulation and is accumulated both as an inclusion and as part of  
 CC the spore coat.  
 CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-  
 CC terminus.  
 CC -!- SIMILARITY: Belongs to the delta endotoxin family.  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC EMBL; U07642; AAA82114.1; -.  
 DR PIR; I40590; I40590.  
 DR HSP; P02965; 1C1Y.  
 DR InterPro; IPR001178; Endotoxin.  
 DR InterPro; IPR005638; endotoxin C.  
 DR InterPro; IPR005639; endotoxin\_N.  
 DR InterPro; IPR008979; Gal bind like.  
 DR Pfam; PF03944; Endotoxin\_C; 1.  
 DR Pfam; PF00555; Endotoxin\_M; 1.  
 DR Pfam; PF03945; Endotoxin\_N; 1.  
 KW Sporulation; Toxin.  
 SQ SEQUENCE 719 AA; 81295 MW; E8210ABEA97688E CRC64;  
 Query Match 93.5%; Score 3516; DB 1; Length 719;  
 Best Local Similarity 92.8%; Pred. No. 5.4e-236;  
 Matches 667; Conservative 31; Mismatches 21; Indels 0; Gaps 0;  
 1 M K L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y E N V P F V S A S T I 60

Db 1 MRLKNDPDKHQLSSNAKVDKIATDSLKNETDIELKNNMNNEDYLRMSHESIDPFSASTI 60  
 QY 61 QTGIGIAGKILGTGVFPAGQVASYSLFGLWPKGKNQWEIEMFHEVVEEIIQKISTYA 120  
 Db 61 QTGIGIAGKILGTGVFPAGQVASYSLFGLWPKGKNQWEIEMFHEVVEEIIQKISTYA 120  
 QY 121 RNKALTDLKGLDALAVVHDSLESWGVRNRRNTRARSVVKQYIALELMFVKLPSPFAVSG 180  
 Db 121 RNKALSRLRGLGDALAVVHDSLESWGVRNRRNTRARSVVKQYIALELMFVKLPSPFAVSG 180  
 QY 181 BEVPLPIYAQAANLHLLLRDASIFGKWLSSSEISTFNROVERAGYSYHCHVKWYS 240  
 Db 181 BEVPLPIYAQAANLHLLLRDASIFGKWLSSSEISTFNROVERAGYSYHCHVKWYS 240  
 QY 241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALFPYSYDTOMYPIKTAQLTREVTYDAI 300  
 Db 241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALFPYSYDTOMYPIKTAQLTREVTYDAI 300  
 QY 301 GTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDFLQVITYISLLSRWSNTQYNNMW 360  
 Db 301 GTVHPNOAFSTWYNNAPSFSAIEAAVVRNPHLLDFLQVITYISLLSRWSNTQYNNMW 360  
 QY 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRITESLAGNLNLTQPVNGVPR 420  
 Db 361 GGHLESPIGALNTSTQGSTNTSINPVTLPFTSRDVRITESLAGNLNLTQPVNGVPR 420  
 QY 421 VDFHWKFTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDFLQVITYISLLSRWSNTQYNNMW 480  
 Db 421 VDFHWKFTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDFLQVITYISLLSRWSNTQYNNMW 480  
 QY 481 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 540  
 Db 481 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 540  
 QY 541 TGTFGDIRVNINPPPAQRYRIRYASTTDLPQHTSINGKAINQGNFSAATNRGDLDYK 600  
 Db 541 TGTFGDIRVNINPPPAQRYRIRYASTTDLPQHTSINGKAINQGNFSAATNRGDLDYK 600  
 QY 601 TFRVVGFTTTPSFSDVOSTTIGAWNFSSNEVYIDRIEFVPEVTEAEYDEKQAKV 660  
 Db 601 TFRVVGFTTTPSFSDVOSTTIGAWNFSSNEVYIDRIEFVPEVTEAEYDEKQAKV 660  
 QY 661 TALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDEFYLDKRELFVYKAKQIHIERNM 719  
 Db 661 TALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDEFYLDKRELFVYKAKQIHIERNM 719

## RESULT 10

CLID\_BACTU STANDARD; PRT; 719 AA.  
 AC Q9XDLI;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Pesticidal crystal protein cryII (insecticidal delta-endotoxin  
 DE CryII(d) (Crystalline entomocidal protoxin) (81 kDa crystal protein).  
 GN Name=cryIId; Synonyms=cryII(d), NRCryV;  
 OS Bacillus thuringiensis.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1428;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BR30;  
 RX MEDLINE=20374042; PubMed=10919402;  
 RA Choi S.-K., Shin B.-S., Kong E.-M., Rho H.-M., Park S.-H.;  
 RT "Cloning of a new Bacillus thuringiensis cryII-type crystal protein  
 RL gene".  
 RL Curr. Microbiol. 41:65-69(2000).  
 CC -!- FUNCTION: Promotes colicoidosmotic lysis by binding to the midgut  
 CC epithelial cells of many lepidopteran larvae. Active on Plutella  
 CC xylostella and on Bombyx mori.  
 CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during  
 CC sporulation and is accumulated both as an inclusion and as part of

CC the spore coat.  
 CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-terminus.  
 CC -!- SIMILARITY: Belongs to the delta endotoxin family.  
 CC -----  
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 CC or send an email to license@isb-sib.ch).  
 CC -----  
 CC EMBL; AF047579; AAD44366.1; --  
 DR HSSP; P02965; 1CIV.  
 DR InterPro; IPR001178; Endotoxin.  
 DR InterPro; IPR005638; endotoxin\_C.  
 DR InterPro; IPR005639; endotoxin\_N.  
 DR InterPro; IPR008979; Gal\_bind\_like.  
 DR Pfam; PF03944; Endotoxin\_C; 1.  
 DR Pfam; PF03945; Endotoxin\_N; 1.  
 DR Sporulation; Toxin.  
 KW SEQUENCE 719 AA; 81403 MW; F335F5689D3B0C45 CRC64;  
 SQ  
 Query Match 90.2%; Score 3393; DB 1; Length 719;  
 Best Local Similarity 89.7%; Pred. No. 2e-227;  
 Matches 645; Conservative 35; Mismatches 39; Indels 0; Gaps 0;  
 QY 1 MRLKNDPDKHQLSSNAKVDKIATDSLKNETDIELKNNMNNEDYLRMSHESIDPFSASTI 60  
 Db 1 MRLKNDPDKHQLSSNAKVDKIATDSLKNETDIELKNNMNNEDYLRMSHESIDPFSASTI 60  
 QY 61 QTGIGIAGKILGTGVFPAGQVASYSLFGLWPKGKNQWEIEMFHEVVEEIIQKISTYA 120  
 Db 61 QTGIGIAGKILGTGVFPAGQVASYSLFGLWPKGKNQWEIEMFHEVVEEIIQKISTYA 120  
 QY 121 RNKALTDLKGLDALAVVHDSLESWGVRNRRNTRARSVVKQYIALELMFVKLPSPFAVSG 180  
 Db 121 RNKALTDLKGLDALAVVHDSLESWGVRNRRNTRARSVVKQYIALELMFVKLPSPFAVSG 180  
 QY 181 BEVPLPIYAQAANLHLLLRDASIFGKWLSSSEISTFNROVERAGYSYHCHVKWYS 240  
 Db 181 BEVPLPIYAQAANLHLLLRDASIFGKWLSSSEISTFNROVERAGYSYHCHVKWYS 240  
 QY 241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALFPYSYDTOMYPIKTAQLTREVTYDAI 300  
 Db 241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALFPYSYDTOMYPIKTAQLTREVTYDAI 300  
 QY 301 GTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDFLQVITYISLLSRWSNTQYNNMW 360  
 Db 301 GTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDFLQVITYISLLSRWSNTQYNNMW 360  
 QY 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRITESLAGNLNLTQPVNGVPR 420  
 Db 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRITESLAGNLNLTQPVNGVPR 420  
 QY 421 VDFHWKFTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDFLQVITYISLLSRWSNTQYNNMW 480  
 Db 421 VDFHWKFTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDFLQVITYISLLSRWSNTQYNNMW 480  
 QY 481 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 540  
 Db 481 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 540  
 QY 541 TGTFGDIRVNINPPPAQRYRIRYASTTDLPQHTSINGKAINQGNFSAATNRGDLDYK 600  
 Db 541 TGTFGDIRVNINPPPAQRYRIRYASTTDLPQHTSINGKAINQGNFSAATNRGDLDYK 600  
 QY 601 TFRVVGFTTTPSFSDVOSTTIGAWNFSSNEVYIDRIEFVPEVTEAEYDEKQAKV 660  
 Db 601 TFRVVGFTTTPSFSDVOSTTIGAWNFSSNEVYIDRIEFVPEVTEAEYDEKQAKV 660

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661 TALTSTNPRGLKTDVQYHIDQVSNLVSLSDFYLDEKRELFEIVKYAKQLHIERNM 719
661 TALTSTNPRGLKTDVQYHIDQVSNLVSLSDFYLDEKRELFEIVKYAKQLHIERNM 719

RESULT 11
CIBB_BACTU
ID CIBB_BACTU STANDARD; PRT; 719 AA.
AC 087404;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pesticidal crystal protein cryIIc (insecticidal delta-endotoxin
DE CryII(c)) (Crystalline entomocidal protoxin) (81 kDa crystal protein).
GN Name=cryIIc; Synonyms=cryII(c);
OS Bacillus thuringiensis.
OC Bacterioidetes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C18 / Egypt;
RA Osman Y.A., Makkour M.A., Bulla L.A. Jr.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut
CC epithelial cells of insects.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -!- SIMILARITY: Belongs to the delta endotoxin family.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC
CC EMBL; AF056933; AAC62933.1; -.
CC HSP; P02965; 1CIY.
CC InterPro; IPR001178; Endotoxin.
CC InterPro; IPR005638; endotoxin C.
CC InterPro; IPR005639; endotoxin N.
CC InterPro; IPR008979; Gal_bind_Like.
CC Pfam; PF03944; Endotoxin C; 1.
CC Pfam; PF00555; Endotoxin M; 1.
CC Pfam; PF03945; Endotoxin N; 1.
CC Plasmid; Sporulation; Toxin.
CC KW SEQUENCE 719 AA; 81210 MW; 8370B3F06B905DFP CRC64;
CC
Query Match 89.7%; Score 3373; DB 1; Length 719;
Best Local Similarity 89.7%; Pred. No. 4.9e-226;
Matches 645; Conservative 33; Mismatches 41; Indels 0; Gaps 0;

QY 1 MKLKNQDHQSFPSSNAKVDKISTDSLKNETDIELQNIHEDCLMKSEYENVEPFSASTI 60
DB 1 MKLKNPDKHQTLSSNAKVDKATDSLKNETDIELKMNEDYLRMSEHSIDPFVSASTI 60

QY 61 QTGIGIAGKILGTLPVAGQVASYLSYFGLWLPKGNQWEIFMHEVVEIINOKISTYA 120
DB 61 QTGIGIAGKILGTLPVPPGQIASYLSYFGLWLPKGSQWEIFMHEVVEIINRKISTYA 120

QY 121 RNKALTDLKGLDALAVHDSLESWGNNRNPARSVVKSOVIALELMFVKLPSFAVSG 180
DB 121 RNKALTDLKGLDALAVHDSLESWGNNRNPARSVVKVNNQVIALELMFVKLPSFAVSG 180

QY 181 BEVPLLPYIAQANLHLLLRDASIFGKEWGLSSSEISTFYNNQVERAGSDHCWKYS 240
DB 181 BEVPLLPYIAQANLHLLLRDASIFKNGGLSASEISTFYNNQVERTRDYSYHCWKNN 240

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241 TGLANLRTGNAESWRYNQFRDMTLMVLDLVALFPSYDTOMYPIKTAQJLTREVYTDAL 300
241 TGLANLRTGNAESWRYNQFRDMTLMVLDLVALFPSYDTOMYPIKTAQJLTREVYTDAL 300

QY 301 GTVPHPHSFTSTWYNNNAPSFSAEAAVVRNPPLLDLEQVTVIYSLLSRWSNTQYMMNW 360
DB 301 GTVPHPHSFTSTWYNNNAPSFSAEAAVVRNPPLLDLEQVTVIYSLLSRWSNTQYMMNW 360

QY 361 GGHKLEFRTIGGTNLNISTOGSTNTSINPVTLPFTSRDVRVYTESLAGNLFTOPVNGVPR 420
DB 361 GGHKLEFRTIGGTNLNISTOGSTNTSINPVTLPFTSRDVRVYTESLAGNLFTOPVNGVPR 420

QY 421 VDFHKKFVTHPIASDNFYVGVGTQDQSENELPPEATGQPNYESYSHRLSHIGLIS 480
DB 421 VDFHKKFVTHPIASDNFYVGVGTQDQSENELPPEATGQPNYESYSHRLSHIGLIS 480

QY 481 ASHVXALVYSWTHRSADRNTIETPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRTN 540
DB 481 ASHVXALVYSWTHRSADRNTIETPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRTN 540

QY 541 TGTFGDIRVNIINPFAQRYRVRIRYASTTDQFHTSINGKAINQGNFSATMNRGDLDYK 600
DB 541 TGTFGDIRVNIINPFAQRYRVRIRYASTTDQFHTSINGKAINQGNFSATMNRGDLDYK 600

QY 601 TERTVGTFTTFFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVFEVTVYEAEDFEKAQKV 660
DB 601 TERTVGTFTTFFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVFEVTVYEAEDFEKAQKV 660

QY 661 TALFTSTNPRGLKTDVQYHIDQVSNLVSLSDFYLDEKRELFEIVKYAKQLHIERNM 719
DB 661 TALFTSTNPRGLKTDVQYHIDQVSNLVSLSDFYLDEKRELFEIVKYAKQLHIERNM 719

RESULT 12
CIBB_BACTU STANDARD; PRT; 1229 AA.
AC Q45739;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pesticidal crystal protein cryIbB (insecticidal delta-endotoxin
DE CryIb(b)) (Crystalline entomocidal protoxin) (140 kDa crystal protein).
DE Name=cryIbB; Synonyms=cryIb(b), cryE15;
GN Bacillus thuringiensis.
OC Bacterioidetes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NREL B-21110 / EG5847;
RA Donovan W.P., Tan Y., Jany C.S., Gonzalez J.M. Jr.;
RT "Bacillus thuringiensis cryet4 and cryet5 toxin genes and proteins
RT toxic to lepidopteran insects.";
RL Patent number US5322687, 21-JUN-1994.
CC -!- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut
CC epithelial cells of many lepidopteran larvae.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -!- SIMILARITY: Belongs to the delta endotoxin family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; L32020; AAA2344.1; -.
CC HSP; P02965; 1CIY.
CC InterPro; IPR001178; Endotoxin.

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DR	InterPro; IPR005638; endotoxin C.	OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
DR	InterPro; IPR005639; endotoxin N.	OX	NCBI_TaxID=1441;
DR	InterPro; IPR008979; Gal bind like.	RN	SEQUENCE FROM N.A.
DR	Pfam; PF03944; Endotoxin_C; 1.	RA	Bishop A.H., Bone E.J., Ellar D.J.;
DR	Pfam; PF00555; Endotoxin_M; 1.	RT	"Cloning of novel Bacillus thuringiensis delta-endotoxin.";
DR	Pfam; PF03945; Endotoxin_N; 1.	RL	Submitted (NOV-1994) to the EMBL/GenBank/DDDB databases.
KW	Sporeulation; Toxin.	CC	-!- FUNCTION: Promotes colloidomotic lysis by binding to the midgut epithelial cells of insects.
SQ	SEQUENCE 1229 AA; 139769 MW; A4C949DB675C3269 CRC64;	CC	-!- DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of the spore coat.
	Query Match 65.0%; Score 2445.5; DB 1; Length 1229;	CC	-!- MISCELLANEOUS: Toxic segment of the protein is located in the N-terminus.
	Best Local Similarity 65.6%; Pred. No. 4.2e-161;	CC	-!- SIMILARITY: Belongs to the delta endotoxin family.
	Matches 470; Conservative 92; Mismatches 138; Indels 17; Gaps 6;	CC	-----
QY	13 SSNAKVDKISTDSLKN-ETDIELQ-NINHEDCIKMSEYENVEPVSASTQTGIGTAGKI 70	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
Db	7 NENEIINALSPTVNSPSTQNMSPDARIEDSLCAEVNNDIPFVSASTVQTGINAGRI 66	CC	-----
QY	71 LGTLGVPPAGQVASYFLIGELWPKGNOWEIMFHEVEEIIINOKISTYARNKALTDLKG 130	CC	EMBL; Z46442; CAA86568.1; .
Db	67 LGVLGVPPAGQVASYFLIGELWPKGNOWEIMFHEVEEIIINOKISTYARNKALTDLKG 126	DR	HSSP; P02965; 1CIY
QY	131 LGDALAVYHDSLEWGNRNTRARSVVKQYQIALELMFVQKLPSPFAVSGEEVPLPIYA 190	DR	InterPro; IPR001178; Endotoxin.
Db	127 LGRGYSYQQALETWLDNRNDARSRSIILERYVALELDITTAIPFRIRNEEVPFLMVA 186	DR	InterPro; IPR005638; endotoxin C.
QY	191 QAANLHLLLRDASIFGKMGSLSSSEISTFYNRQVERAGDYSDHCVKWYSTGLNNLRGTN 250	DR	InterPro; IPR005639; endotoxin N.
Db	187 QAANLHLLLRDASIFGKMGSLSSSEISTFYNRQVERAGDYSDHCVKWYSTGLNNLRGTN 246	DR	InterPro; IPR008979; Gal bind like.
QY	251 AESWVRNQFRDMLVLDLVALFPSPYDTQMPYIKTTAQLTREYVYDAITGVHPHPSFT 310	DR	Pfam; PF03944; Endotoxin_C; 1.
Db	247 AESWLRYNQFRDMLVLDLVALFPSPYDTQMPYIKTTAQLTREYVYDAITGVHPHPSFT 306	DR	Pfam; PF00555; Endotoxin_M; 1.
QY	311 STTWNNNAPSFAIAEAVVRNPHLLDFLEQVITYSLLSWSNTQYMMWGHKLPFTI 370	DR	Pfam; PF03945; Endotoxin_N; 1.
Db	307 STWNNNAPSFAIAEAVVRNPHLLDFLEQVITYSLLSWSNTQYMMWGHKLPFTI 366	KW	Sporeulation; Toxin.
QY	371 GGTINISTQGST-NTSINPVTLPFTSRDVRVYTESLAGNLFLTPQVNGVPRVDFHWKFTV 429	SQ	SEQUENCE 1233 AA; 140451 MW; 7318382413529F21 CRC64;
Db	367 GGTINTSTQGLTNTNISINPVTLPFTSRDVRVYTESLAGNLFLTPQVNGVPRVDFHWKFTV 422		Query Match 65.0%; Score 2445.5; DB 1; Length 1233;
QY	430 HPIASDNFYYPG-----YVGIGTQODSENELPPEATQGPNYESYSHLSHIGLISAS 482		Best Local Similarity 65.6%; Pred. No. 4.2e-161;
Db	423 --INPQNIYERGATTSYQYQGVIGIQLFDSSETLPETTERPNYESYSHLSHIGLIS 480		Matches 470; Conservative 92; Mismatches 138; Indels 17; Gaps 6;
QY	483 HVKALVYSWTHRSADRNTIENPSITQIPLVKAFNLSSGAAVRGGFTGCDILRRTNIG 542	QY	13 SSNAKVDKISTDSLKN-ETDIELQ-NINHEDCIKMSEYENVEPVSASTQTGIGTAGKI 70
Db	481 TLRAVYVSWTHRSADRNTIENPSITQIPLVKAFNLSSGAAVRGGFTGCDILRRTNIG 540	Db	7 NENEIINALSPTVNSPSTQNMSPDARIEDSLCAEVNNDIPFVSASTVQTGINAGRI 66
QY	543 TFGDIRVNIINPPAQRVVRIRYASTDLOFHTSINGKALNOGNFSAIMNRGDDLYKTF 602	QY	71 LGTLGVPPAGQVASYFLIGELWPKGNOWEIMFHEVEEIIINOKISTYARNKALTDLKG 130
Db	541 TFGDIRVNIINPPAQRVVRIRYASTDLOFHTSINGKALNOGNFSAIMNRGDDLYKTF 600	Db	67 LGVLGVPPAGQVASYFLIGELWPKGNOWEIMFHEVEEIIINOKISTYARNKALTDLKG 126
QY	603 RTVGFTTPFSLDQVQFTTGANNSSGNEVYIDRIEFVPEVETVYAEYDFEKAQEKVTA 662	QY	131 LGDALAVYHDSLEWGNRNTRARSVVKQYQIALELMFVQKLPSPFAVSGEEVPLPIYA 190
Db	601 RTAGFTTPFSLDQVQFTTGANNSSGNEVYIDRIEFVPEVETVYAEYDFEKAQEKVTA 659	Db	127 LGRGYSYQQALETWLDNRNDARSRSIILERYVALELDITTAIPFRIRNEEVPFLMVA 186
QY	663 LFTSTNPRGLKTDVYKHIDQVNLVBSLSEDFEYLDKRELPIVKYAKQLHIERNM 719	QY	191 QAANLHLLLRDASIFGKMGSLSSSEISTFYNRQVERAGDYSDHCVKWYSTGLNNLRGTN 250
Db	660 LFTSTNPRGLKTDVYKHIDQVNLVBSLSEDFEYLDKRELPIVKYAKQLHIERNM 716	Db	187 QAANLHLLLRDASIFGKMGSLSSSEISTFYNRQVERAGDYSDHCVKWYSTGLNNLRGTN 246
RESULT 13		QY	251 AESWVRNQFRDMLVLDLVALFPSPYDTQMPYIKTTAQLTREYVYDAITGVHPHPSFT 310
CIBC BACTM	STANDARD; PRT; 1233 AA.	Db	247 AESWLRYNQFRDMLVLDLVALFPSPYDTQMPYIKTTAQLTREYVYDAITGVHPHPSFT 306
ID	CIBC BACTM	QY	311 STTWNNNAPSFAIAEAVVRNPHLLDFLEQVITYSLLSWSNTQYMMWGHKLPFTI 370
AC	Q45774;	Db	307 STWNNNAPSFAIAEAVVRNPHLLDFLEQVITYSLLSWSNTQYMMWGHKLPFTI 366
DT	30-MAY-2000 (Rel. 39, Created)	QY	371 GGTINISTQGST-NTSINPVTLPFTSRDVRVYTESLAGNLFLTPQVNGVPRVDFHWKFTV 429
DT	30-MAY-2000 (Rel. 39, Last sequence update)	Db	367 GGTINTSTQGLTNTNISINPVTLPFTSRDVRVYTESLAGNLFLTPQVNGVPRVDFHWKFTV 422
DT	05-JUN-2004 (Rel. 44, Last annotation update)	QY	430 HPIASDNFYYPG-----YVGIGTQODSENELPPEATQGPNYESYSHLSHIGLISAS 482
DE	Pesticidal crystal protein cryIbC (insecticidal delta-endotoxin)	Db	423 --INPQNIYERGATTSYQYQGVIGIQLFDSSETLPETTERPNYESYSHLSHIGLIS 480
DE	CryIb(c) (crystalline entomocidal protoxin) (140 kDa crystal protein).	QY	483 HVKALVYSWTHRSADRNTIENPSITQIPLVKAFNLSSGAAVRGGFTGCDILRRTNIG 542
GN	Names=cryIbC; Synonyms=cryIb(c), cryIbC;	Db	481 TLRAVYVSWTHRSADRNTIENPSITQIPLVKAFNLSSGAAVRGGFTGCDILRRTNIG 540
OS	Bacillus thuringiensis (subsp. morrisoni).	QY	543 TFGDIRVNIINPPAQRVVRIRYASTDLOFHTSINGKALNOGNFSAIMNRGDDLYKTF 602
		Db	541 TFGDIRVNIINPPAQRVVRIRYASTDLOFHTSINGKALNOGNFSAIMNRGDDLYKTF 600
		QY	603 RTVGFTTPFSLDQVQFTTGANNSSGNEVYIDRIEFVPEVETVYAEYDFEKAQEKVTA 662
		Db	601 RTAGFTTPFSLDQVQFTTGANNSSGNEVYIDRIEFVPEVETVYAEYDFEKAQEKVTA 659
		QY	663 LFTSTNPRGLKTDVYKHIDQVNLVBSLSEDFEYLDKRELPIVKYAKQLHIERNM 719
		Db	660 LFTSTNPRGLKTDVYKHIDQVNLVBSLSEDFEYLDKRELPIVKYAKQLHIERNM 716

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Db 481 TLRAVYVSWTHRSADRTNIGPNIQTQPLVKALNLSGVTVVGGPGFTGGDILRRNTG 540
QY 543 TFGDIRVNNPFAQRYVRIRYASTTDLQPHSTINGKAINQGNFSATMARGEDLDYKTF 602
Db 541 TFGDIRLNNVPLSQRYVRIRYASTTDLQPHSTINGKAINQGNFSATMARGEDLDYKTF 600
QY 603 RTVGFTTFFSFLDVQSTTCIGAMFSSGNEVYIDRIEFPVVEVYEAEDYFKAQEKVTA 662
Db 601 RTAGFSTFPFNLAQSTFTLGAQSFEN-QEYVIDRVEFPVPAEVTFAEYDLERAQKAVNA 659
QY 663 LFTSTNPRGLKTDVNDYHIDQVSNLVESLSDEFYLDKRELFYVKAQKQLHIERNM 719
Db 660 LFTSTNPRRLKTDVTDYHIDQVSNLVACLSDEFCLDEKRELFYVKAQKQLSDERNL 716

RESULT 14
Q93T75 PRELIMINARY; PRT; 1228 AA.
AC Q93T75;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Delta-endotoxin CryIa2.
GN Name=cryIa2;
OS Bacillus thuringiensis (subsp. entomocidus).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1436;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HD-9;
RA Mat Isa M.N., Abdullah M.A.F., Mahadi N.M.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF363025; AAK51084.1;
DR HSSP; P07130; 1DLC.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin C.
DR InterPro; IPR005639; endotoxin N.
DR Pfam; PF03944; Endotoxin C; 1.
DR Pfam; PF00555; Endotoxin M; 1.
DR Pfam; PF03945; Endotoxin N; 1.
SQ SEQUENCE 1228 AA; 139620 MW; 3DA2A4DBF59C95C3 CRC64;

Query Match 60.6%; Score 2277.5; DB 2; Length 1228;
Best Local Similarity 62.7%; Pred. NO. 2.1e-149;
Matches 449; Conservative 80; Mismatches 162; Indels 25; Gaps 6;

QY 23 TDSLKNEFDIELQNLNH-----EDLKMSEVENVEPVSASTIQTGIGIAGKI 70
Db 2 TSNRRKNEINAVSNHSAQWDLDPDARIEDSLCAEGNIDPPVSASTVGTGINIAGRI 61
QY 71 LGTLGVPPAGQVASYLSPILGELMPKGNQWEIEMHEVEETINQKISTYANKALTDLKG 130
Db 62 LGVLGVPPAGQVASYLSPILGELMPKGNQWEIEMHEVEETINQKISTYANKALTDLKG 121
QY 131 LGDALAVHDSLSVWGNVNNTRASVYKSYOIALELMFVQKLPSPFVSGVEEVPPLPIA 190
Db 132 LGDSFRAYCQSLDLEWNRDARTSRVLTQVIALELDPLNAPLFAIRNVEPPLMVIYA 181
QY 191 QAAHLHLLLRDASTFGKWLSSSEISTFTYNNQVERAGDYSRCHVWYSTGLANLRGTN 250
Db 182 QAAHLHLLLRDASTFGKWLSSSEISTFTYNNQVERAGDYSRCHVWYSTGLANLRGTN 241
QY 251 ABSWRYNQFRDMLVLDLVALPSPYDTQWPKITTAQLTREVYDTAIGTVHPHSFT 310
Db 242 AASWRYNQFRDMLVLDLVALPSPYDTQWPKITTAQLTREVYDTAIGTVHPHSFT 299
QY 311 STTWNNNAPSFAEAAAVRNPHLLDFLEQVITYSLLSRNSNTQYMMWGGHKLFRPTI 370

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Db 300 SWNNYNNAPSFAEAAAIRSPHLLDFLEQVITYSASSRWSNTHMTYWRGHTIQSRPI 359
QY 371 GGTLMISTGNTGNTGNTGNTGNTGNTGNTGNTGNTGNTGNTGNTGNTGNTGNTGNTG 428
Db 360 GGLLNTSHGANTGNTGNTGNTGNTGNTGNTGNTGNTGNTGNTGNTGNTGNTGNTGNT 416
QY 429 THP-----IASNFYVPGVIGTQLODSENELPPEATGQPNYSESHRLSHIGLISASH 483
Db 417 TNPQISDRGTANYSQP-YESPLQKDSSETLPPETTERPNEYSESHRLSHIGLISASH 475
QY 484 VKALVYVSWTHRSADRTNIGPNIQTQPLVKALNLSGVTVVGGPGFTGGDILRRNTG 543
Db 476 VNVFVSWTHRSADRTNIGPNIQTQPLVKALNLSGVTVVGGPGFTGGDILRRNTG 535
QY 544 FGDIRVNNPFAQRYVRIRYASTTDLQPHSTINGKAINQGNFSATMARGEDLDYKTF 603
Db 536 FGPVIRVTVNGPLTQRYIGFRYASTVDFDFVSRGGTTVNNFRFLRTVNSGDELKYNFV 595
QY 604 TVGFTTFFSFLDVQSTTCIGAMFSSGNEVYIDRIEFPVVEVYEAEDYFKAQEKVTA 663
Db 596 RRAFTTFFTQIQTQPLVKALNLSGVTVVGGPGFTGGDILRRNTG 655
QY 664 FSTNPRGLKTDVNDYHIDQVSNLVESLSDEFYLDKRELFYVKAQKQLHIERNM 719
Db 656 FNTNPRRLKTDVTDYHIDQVSNLVACLSDEFCLDEKRELFYVKAQKQLSDERNL 711

RESULT 15
C1BA_BACTK STANDARD; PRT; 1228 AA.
ID AC P05517; Q45731;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 05-JUN-2004 (Rel. 44, Last annotation update)
DE Pesticidial crystal protein cryIaB (insecticidal delta-endotoxin
DE CryIaB(a)) (crystalline entomocidical protoxin) (140 kDa crystal protein).
GN Name=cryIaB; Synonyms=cryIa(a), cryA4;
OS Bacillus thuringiensis (subsp. kurstaki), and
OS Bacillus thuringiensis (subsp. entomocidus).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=29339, 1436;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.kurstaki; STRAIN=HD-2;
RX MEDLINE=88203216; PubMed=3362680;
RA Brizzard B.L., Whiteley H.R.;
RT "Nucleoside sequence of an additional crystal protein gene cloned from
RT Bacillus thuringiensis subsp. thuringiensis."
RL Nucleic Acids Res. 16:2723-2723 (1988).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.entomocidus; STRAIN=HD-110;
RA Soetaert P.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Promotes colloid-osmotic lysis by binding to the midgut
CC epithelial cells of insects.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -!- SIMILARITY: Belongs to the delta endotoxin family.
CC
CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC
CC EMBL; X06711; CAA29898.1; -
CC EMBL; X95704; CAA65003.1; -
DR

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DR PIR; S00873; S00873.
DR HSP; P07130; 1DLC.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal bind like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
DR Sporulation; Toxin.
KW VARIANT
FT 150 Y -> H (in strain HD-110).
SQ SEQUENCE 1228 AA; 139647 MW; C8E3A19F5D98575 CRC64;

Query Match      60.5%; Score 2276.5; DB 1; Length 1228;
Best Local Similarity 62.7%; Pred. No. 2.5e-149;
Matches 449; Conservative 80; Mismatches 162; Indels 25; Gaps 6;

QY 23 TDSLKNETDIELQNIH-----EDCLKMSEYENVEFPVSASITQTGIGIAGKI 70
Db 1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
2 TSNRKNENEINAVSNHSAQMDLLPDARIEDSLCIAEGNNIDPFVSASTVQTGINIAGRI 61

QY 71 LGTLGVFPAGQVASLYSFI LGELWPKGNQWEIFMEHVEIINOKISTVARNKALTDLKG 130
Db 1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
62 LGVLGVFPAGQLASFYFV LGELWPKGRDQWEIFLEHVEQLINQITENARNTALARIQG 121

QY 131 LGDALAVYHDSLSWGNRNNTARSVVKSOYIALELMFVKLPSPAVSGEEVPLPIYA 190
Db 1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
122 LGDSFRAYQGSLEDWLENRDADRTSRVLTQYIALELDFLNAMPLFAIRNQEVPLLMVYA 181

QY 191 QANLHLLLRDASIFGKEWGLSSSEISTFYNQVRERAGDYSDHCVKWYSTGLNNLRGTN 250
Db 1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
182 QANLHLLLRDASLFGSEFGLTSQELQRYERQVETRDYSCYVWNTGLNSLRGTN 241

QY 251 AESWRYNQPRRDMTLMVLDAVLFPSYDTQMPYIKTTAQLTREVTYDAIGTVHPHPSFT 310
Db 1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
242 AASWRYNQPRDLTLGVLDLVALFPSYDRTYPTINTSAQLTREVTYDAIGAT--GVNMA 299

QY 311 STTWYNNAPSPAIAEAIVNPHLLDFLEQVITYLSLRSWNTQYNNWGGHKLFPRTI 370
Db 1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
300 SMWYNNAPSPAIAEAIAIRSPHLLDFLEQLTIFSSASSRWNTNRYMVRGHTIQSRPI 359

QY 371 GGTINISTOGSTNTSINPVTLPFTSRDVRVTSIAGLNLP--LTQPVNGVPRVDFHWKFV 428
Db 1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
360 GGLNTSTHGATNTSINPVTLPFASRDVYRTESYAGVLLWGIYLEPIHGVTYRNF-- 416

QY 429 THP-----IASDNFYPGYVGIGTQLQDSNELPPPEATQOPNYESYSHRSLSHIGLISAH 483
Db 1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
417 TNPQNISDRGTANYSQP-YESPLQLKXSETLPETTERPNYESYSHRSLSHIGIILQSR 475

QY 484 VKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNTTGT 543
Db 1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
476 VNPVYSWTHRSADRTNTIGPNEITQIPWKASELPFGTIVVRGPGFTGGDILRRNTTGG 535

QY 544 FGIIRVNINPPFAQRVVRIRYASTTDLQPHTSINGKAINQGNFSATMARGEDLDYKTFR 603
Db 1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
536 FGIIRVTNGLTQRYRIGPRYASTVDPPFVSRRGGTTVNNFRFLRTMNSGDCLKYGNFV 595

QY 604 TVGFTTFPSLDVQSFTTIGAWNPFSSGNEVYIDRIEFVPVETVYAEYDFEKAQKVTAL 663
Db 1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
596 RRAFTPTFTQIQDIRTSIQGLSGNGEYIDKIEIIPVTATFEAYDLERAQAEAVNAL 655

QY 664 FTSTNPRGLKTDVKDHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719
Db 1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
656 FTNTNPRRLKTDVTDVHIDQVSNLVSLSDEFCLDEKRELLEKVKYAKRLSDERNL 711
```

Search completed: October 28, 2004, 18:30:02  
Job time : 106.579 secs





GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 28, 2004, 18:05:43 ; Search time 19.191 Seconds  
(without alignments)  
3604.811 Million cell updates/sec

Title: US-10-019-823B-57  
Perfect score: 3760  
Sequence: 1 MLKNQDKHQSFSSNAKVDK.....KRELFEIVKYAKQLHIERNM 719

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3756	99.9	719	2 I39815	insecticidal prote
2	3747	99.7	719	2 S25383	parasporal crystal
3	3739	99.4	719	2 I39814	insecticidal prote
4	3516	93.5	719	2 I40590	cryV465 protein -
5	2276.5	60.5	1228	2 S00873	parasporal crystal
6	1900	50.5	380	2 B42459	hypothetical prote
7	1494	39.7	1157	1 S49247	parasporal crystal
8	1482.5	39.4	1166	2 S32845	parasporal crystal
9	1472	39.1	1155	2 A26513	parasporal crystal
10	1469	39.1	1174	2 S32649	parasporal crystal
11	1465	39.0	1155	2 JD0002	parasporal crystal
12	1465	39.0	1156	2 A29125	parasporal crystal
13	1458.5	38.8	934	2 A22798	parasporal crystal
14	1457.5	38.8	1176	2 JT0241	parasporal crystal
15	1451.5	38.6	1176	2 JC2219	parasporal crystal
16	1448	38.5	1155	2 S02134	parasporal crystal
17	1447.5	38.5	1176	2 A22617	parasporal crystal
18	1447.5	38.5	1176	2 S02215	parasporal crystal
19	1447.5	38.5	1181	2 A41052	parasporal crystal
20	1444	38.4	1155	2 I39838	parasporal crystal
21	1358	36.1	1174	2 A42559	parasporal crystal
22	1353	36.0	1138	2 A48944	parasporal crystal
23	1339.5	35.6	1156	2 A29838	parasporal crystal
24	1329.5	35.4	823	2 S04181	parasporal crystal
25	1320.5	35.1	1189	2 S00944	parasporal crystal
26	1310	34.8	1154	2 S39536	parasporal crystal
27	1270	33.8	1171	2 I40572	parasporal crystal
28	1270	33.8	1171	2 A37829	parasporal crystal
29	1261	33.5	1176	2 A48970	parasporal crystal

30	1238	32.9	1160	2 S32647	parasporal crystal
31	1223.5	32.5	1165	2 S11446	parasporal crystal
32	1207.5	32.1	655	2 JC7140	protoxin - Bacilli
33	1195	31.8	1172	2 S32689	parasporal crystal
34	1186	31.5	1160	2 I40589	parasporal crystal
35	1161.5	30.9	1178	1 USBSXH	parasporal crystal
36	1161	30.9	1177	2 A49785	parasporal crystal
37	1154	30.7	652	2 A27323	parasporal crystal
38	1135	30.2	659	2 S10228	parasporal crystal
39	1104.5	29.4	652	2 I39811	parasporal crystal
40	984	26.2	649	1 JHO261	parasporal crystal
41	933	24.8	618	2 S11445	parasporal crystal
42	889	23.6	1156	2 S19306	parasporal crystal
43	827	22.0	1136	1 USBS81	parasporal crystal
44	691.5	18.4	934	2 B29838	parasporal crystal
45	666	17.7	1180	2 I39870	parasporal crystal

ALIGNMENTS

RESULT 1

I39815  
insecticidal protein cryV - Bacillus thuringiensis  
C:Species: Bacillus thuringiensis  
C:Date: 19-Jul-1996 #sequence revision 19-Jul-1996 #text change 09-Jul-2004  
C:Accession: I39815

R:Gleave, A.P.; Williams, R.; Hedges, R.J.  
Appl. Environ. Microbiol. 59, 1683-1687, 1993

A:Title: Screening by polymerase chain reaction of Bacillus thuringiensis serotypes for iensis subsp. kurstaki.

A:Reference number: I39815; MUID:93298009; PMID:8517758  
A:Accession: I39815

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-719 <RES>

A:Cross-references: UNIPROT:Q45752; GB:M98544; NID:gl42767; PIDN:AAA22354.1; PID:gl42768

C:Genetics:

A:Gene: cryV

C:Superfamily: parasporal crystal protein

Query Match 99.9%; Score 3756; DB 2; Length 719;  
Best Local Similarity 99.9%; Pred. No. 9.8e-256;  
Matches 718; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	MLKNQDKHQSFSSNAKVDKISTSLKNETDIELQNIHEDCLKMSYEYENVEPFSASTI	60
DB	1	MLKNQDKHQSFSSNAKVDKISTSLKNETDIELQNIHEDCLKMSYEYENVEPFSASTI	60
QY	61	QTGIGIAGKILGTGVPFAGQVASYLSYFILGELPKGNQWEIPEHVEEIIINQKISTYA	120
DB	61	QTGIGIAGKILGTGVPFAGQVASYLSYFILGELPKGNQWEIPEHVEEIIINQKISTYA	120
QY	121	RNKALTDLKLGDALAVYHDSLESWVGNNRNRARSVVKSOYIALELMFVQKLPFAVSG	180
DB	121	RNKALTDLKLGDALAVYHDSLESWVGNNRNRARSVVKSOYIALELMFVQKLPFAVSG	180
QY	181	EVPLLPPIYAQAANUHLHLLLRDASIFGKENGSLSSSEISTFYNNQVERAGDYSDHCWKYS	240
DB	181	EVPLLPPIYAQAANUHLHLLLRDASIFGKENGSLSSSEISTFYNNQVERAGDYSDHCWKYS	240
QY	241	TGLNNLRGTNAESWRYNQFRDMDTLMVLVDFVPSYDTQWPIKTTAQLTREYVTDAI	300
DB	241	TGLNNLRGTNAESWRYNQFRDMDTLMVLVDFVPSYDTQWPIKTTAQLTREYVTDAI	300
QY	301	GTVHPHPSTFTTNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMMNW	360
DB	301	GTVHPHPSTFTTNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMMNW	360
QY	361	GGHKLFEFTIGTLLNISTQGSTNTSINPVTLPFTSRDYVRTESLAGNLFLTQPVNGVPR	420
DB	361	GGHKLFEFTIGTLLNISTQGSTNTSINPVTLPFTSRDYVRTESLAGNLFLTQPVNGVPR	420

QY 421 VDFHWKFTVTHPIASDNFYPCYVIGIGTQLODSENELPPEATGQPNVYESYSHRLSHIGLIS 480  
DB 421 VDFHWKFTVTHPIASDNFYPCYVIGIGTQLODSENELPPEATGQPNVYESYSHRLSHIGLIS 480  
QY 481 ASHVKALVSWTHRSADRTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILARTN 540  
DB 481 ASHVKALVSWTHRSADRTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILARTN 540  
QY 541 TGTGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMRGSDLDYK 600  
DB 541 TGTGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMRGSDLDYK 600  
QY 601 TFRVVGFTTPSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEVYEAEDFEKAQEKV 660  
DB 601 TFRVVGFTTPSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEVYEAEDFEKAQEKV 660  
QY 661 TALFTSTNPRGLKTDVVDYHIDQVSNLVESLSDFFYLDEKRELFEIVKYAKQLHIERNM 719  
DB 661 TALFTSTNPRGLKTDVVDYHIDQVSNLVESLSDFFYLDEKRELFEIVKYAKQLHIERNM 719  
RESULT 2  
S25383  
parasporal crystal protein cryIIa1 - Bacillus thuringiensis  
N:Alternate names: delta-endotoxin; parasporal crystal protein cryV  
C:Species: Bacillus thuringiensis  
C:Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 09-Jul-2004  
C:Accession: S25383  
R:Taylor, R.; Tippett, J.; Gibb, G.; Pella, S.; Pike, D.; Jordan, L.; Ely, S.  
Mol. Microbiol. 6, 1211-1217, 1992  
A:Title: Identification and characterization of a novel Bacillus thuringiensis delta-end  
A:Reference number: S25383; MUID:92269582; PMID:1598820  
A:Accession: S25383  
A:Molecule type: DNA  
A:Residues: 1-719 <TAI>  
A:Cross-references: UNIPROT:Q45752; EMBL:X62821; NID:940289; PID:CAA44633.1; PID:940290  
C:Genetics:  
A:Gene: cryV  
C:Superfamily: parasporal crystal protein  
C:Keywords: delta-endotoxin  
Query Match 99.7%; Score 3747; DB 2; Length 719;  
Best Local Similarity 99.7%; Pred. No. 4.2e-255;  
Matches 717; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 MKLKNQDKHQSFSNAKVDKISTDSLNKNETDIELQNIHEDCLKMSYENVEPVSASTI 60  
DB 1 MKLKNQDKHQSFSNAKVDKISTDSLNKNETDIELQNIHEDCLKMSYENVEPVSASTI 60  
QY 61 QTGIGIAGKILGTGVPFAGQVASYLSPILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
DB 61 QTGIGIAGKILGTGVPFAGQVASYLSPILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
QY 121 RNKALTDLKGDLAVYHDSLESVWGNRNNTRASSVVKSVQYIALELMFVQKLPFAVSG 180  
DB 121 RNKALTDLKGDLAVYHDSLESVWGNRNNTRASSVVKSVQYIALELMFVQKLPFAVSG 180  
QY 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFFYNQVERAGDYSYHCVKWS 240  
DB 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFFYNQVERAGDYSYHCVKWS 240  
QY 241 TGLNLRGTNAESWRYNQFRDMLVLDLVALPSPYDTQMPYIKTTAQLTREYVTDAL 300  
DB 241 TGLNLRGTNAESWRYNQFRDMLVLDLVALPSPYDTQMPYIKTTAQLTREYVTDAL 300  
QY 301 GTVHPHPSFTSTTWNNNAPSFAEAAVVRNPHLLDLEQVTIYSLSRWSNTQYNNMW 360  
DB 301 GTVHPHPSFTSTTWNNNAPSFAEAAVVRNPHLLDLEQVTIYSLSRWSNTQYNNMW 360  
QY 361 GGHKLEFRITIGTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFLTPQVNGVPR 420  
DB 361 GGHKLEFRITIGTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFLTPQVNGVPR 420

QY 421 VDFHWKFTVTHPIASDNFYPCYVIGIGTQLODSENELPPEATGQPNVYESYSHRLSHIGLIS 480  
DB 421 VDFHWKFTVTHPIASDNFYPCYVIGIGTQLODSENELPPEATGQPNVYESYSHRLSHIGLIS 480  
QY 481 ASHVKALVSWTHRSADRTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILARTN 540  
DB 481 ASHVKALVSWTHRSADRTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILARTN 540  
QY 541 TGTGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMRGSDLDYK 600  
DB 541 TGTGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMRGSDLDYK 600  
QY 601 TFRVVGFTTPSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEVYEAEDFEKAQEKV 660  
DB 601 TFRVVGFTTPSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEVYEAEDFEKAQEKV 660  
QY 661 TALFTSTNPRGLKTDVVDYHIDQVSNLVESLSDFFYLDEKRELFEIVKYAKQLHIERNM 719  
DB 661 TALFTSTNPRGLKTDVVDYHIDQVSNLVESLSDFFYLDEKRELFEIVKYAKQLHIERNM 719  
RESULT 3  
I39814  
insecticidal protein cryVI - Bacillus thuringiensis  
C:Species: Bacillus thuringiensis  
C:Date: 19-Jul-1996 #sequence\_revision 19-Jul-1996 #text\_change 26-Aug-1999  
C:Accession: I39814  
R:Shin, B.S.; Park, S.H.; Choi, S.K.; Koo, B.T.; Lee, S.T.; Kim, J.I.  
Appl. Environ. Microbiol. 61, 2402-2407, 1995  
A:Title: Distribution of cryVI-type insecticidal protein genes in Bacillus thuringiensis  
tomocidus.  
A:Reference number: I39814; MUID:95314293; PMID:7793960  
A:Accession: I39814  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-719 <RES>  
A:Cross-references: GB:I36338; NID:9540281; PIDN:AA36999.1; PID:9540282  
C:Genetics:  
A:Gene: cryVI  
C:Superfamily: parasporal crystal protein  
Query Match 99.4%; Score 3739; DB 2; Length 719;  
Best Local Similarity 99.4%; Pred. No. 1.5e-254;  
Matches 715; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
QY 1 MKLKNQDKHQSFSNAKVDKISTDSLNKNETDIELQNIHEDCLKMSYENVEPVSASTI 60  
DB 1 MKLKNQDKHQSFSNAKVDKISTDSLNKNETDIELQNIHEDCLKMSYENVEPVSASTI 60  
QY 61 QTGIGIAGKILGTGVPFAGQVASYLSPILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
DB 61 QTGIGIAGKILGTGVPFAGQVASYLSPILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
QY 121 RNKALTDLKGDLAVYHDSLESVWGNRNNTRASSVVKSVQYIALELMFVQKLPFAVSG 180  
DB 121 RNKALTDLKGDLAVYHDSLESVWGNRNNTRASSVVKSVQYIALELMFVQKLPFAVSG 180  
QY 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFFYNQVERAGDYSYHCVKWS 240  
DB 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFFYNQVERAGDYSYHCVKWS 240  
QY 241 TGLNLRGTNAESWRYNQFRDMLVLDLVALPSPYDTQMPYIKTTAQLTREYVTDAL 300  
DB 241 TGLNLRGTNAESWRYNQFRDMLVLDLVALPSPYDTQMPYIKTTAQLTREYVTDAL 300  
QY 301 GTVHPHPSFTSTTWNNNAPSFAEAAVVRNPHLLDLEQVTIYSLSRWSNTQYNNMW 360  
DB 301 GTVHPHPSFTSTTWNNNAPSFAEAAVVRNPHLLDLEQVTIYSLSRWSNTQYNNMW 360  
QY 361 GGHKLEFRITIGTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFLTPQVNGVPR 420  
DB 361 GGHKLEFRITIGTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFLTPQVNGVPR 420

QY 421 VDFHKKFVTHPIASDNFYYPGYGIGTQLODSENELPPEATGPNVYESYSHRLSHIGLIS 480  
DB 421 VDFHKKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGPNVYESYSHRLSHIGLIS 480  
QY 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGDIILRTN 540  
DB 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGDIILRTN 540  
QY 541 TGFEGDIRVNIINPPFAQRYRVRIRYASTTDLQPHTSINGKAINQGNFSAATMNRGDDLYK 600  
DB 541 TGFEGDIRVNIINPPFAQRYRVRIRYASTTDLQPHTSINGKAINQGNFSAATMNRGDDLYK 600  
QY 601 TERTVGTTPPSFLDVQSTFTIGAMNFSNGNEVYIDRIEFVPVEVTEAEYDEFEKAQEKV 660  
DB 601 TERTVGTTPPSFLDVQSTFTIGAMNFSNGNEVYIDRIEFVPVEVTEAEYDEFEKAQEKV 660  
QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFYVYAKQIHIERNM 719  
DB 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFYVYAKQIHIERNM 719

RESULT 4  
I40590  
cryV465 protein - Bacillus thuringiensis  
C/Species: Bacillus thuringiensis  
C/Date: 12-Aug-1996 #sequence\_revision 12-Aug-1996 #text\_change 09-Jul-2004  
C/Accession: I40590  
R/Shin, B.S.; Park, S.H.; Choi, S.K.; Koo, B.T.; Lee, S.T.; Kim, J.I.  
Appl. Environ. Microbiol. 61, 2402-2407, 1995  
A/Title: Distribution of cryV-type insecticidal protein genes in Bacillus thuringiensis  
tomocidus.  
A/Reference number: I39814; MUID: 95314293; PMID: 7793960  
A/Accession: I40590  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-719 <RES>  
A/Cross-references: UNIPROT:Q45709; EMBL:U07642; NID:g467234; PIDN:AAA82114.1; PID:g4672  
C/Genetics:  
A/Gene: cryV465  
C/Superfamily: parasporal crystal protein

Query Match 93.5%; Score 3516; DB 2; Length 719;  
Best Local Similarity 92.8%; Pred. No. 7.le-239;  
Matches 667; Conservative 31; Mismatches 21; Indels 0; Gaps 0;  
..

QY 1 MKLKNQKHQSFSSNAKVKISTDLSKNETDIELQNIHEDCLKNSEYENVEPFSASTI 60  
DB 1 MKLKNPDKHQSLSNAKVKIATDLSKNETDIELKNMNEDEYLRMSEHESIDPFVSASTI 60  
QY 61 QTGIGIAGKILGTLGVPPAGVASLYSFIILGELWPKGKQWEIFMEHVVEIINOKISTYA 120  
DB 61 QTGIGIAGKILGTLGVPPAGQIASLYSFIILGELWPKGSQWEIFMEHVVEIINOKILTIA 120  
QY 121 RNKALTDLKLGDALAYYHDSLESVGNRNNTARSVYKSYQIYALBELMFVQKLPFAVSG 180  
DB 121 RNKALSDLRLGDALAYVHESLESVGNRNNTARSVYKQYIYALBELMFVQKLPFAVSG 180  
QY 181 EEVPLPIYAQAANLHLLILDASIFCKEWGLSSSEISTFYNQVERAGDYSCHVKWYS 240  
DB 181 EEVPLPIYAQAANLHLLILDASIFCKEWGLSSSEISTFYNQVERAGDYSCHVKWYN 240  
QY 241 TGLNLRGTNAESVVRVYQFRDMTLMVLIDVALFPSSYDTQMPYIKTTAQLTREVYTDAL 300  
DB 241 TGLNLRGTNAESVVRVYQFRDMTLMVLIDVALFPSSYDTQMPYIKTTAQLTREVYTDAL 300  
QY 301 GTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWNSQTQNNMW 360  
DB 301 GTVHPNQAFSTTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWNSQTQNNMW 360  
QY 361 GCHKLEPRTIGGLINISTQGSTNTSINPVTLPFTSRDVRVYTESLAGNLFLTQPVNGVPR 420  
DB 361 GCHRLSERPIGGLINISTQGSTNTSINPVTLPFTSRDVRVYTESLAGNLFLTQPVNGVPR 420

QY 421 VDFHKKFVTHPIASDNFYYPGYGIGTQLODSENELPPEATGPNVYESYSHRLSHIGLIS 480  
DB 421 VDFHKKFPTLPASDNFYPLVAGYGTQLODSENELPPTTQPNYESYSHRLSHIGLIS 480  
QY 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGDIILRTN 540  
DB 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGDIILRTN 540  
QY 541 TGFEGDIRVNIINPPFAQRYRVRIRYASTTDLQPHTSINGKAINQGNFSAATMNRGDDLYK 600  
DB 541 TGFEGDIRVNIINPPFAQRYRVRIRYASTTDLQPHTSINGKAINQGNFSAATMNRGDDLYK 600  
QY 601 TERTVGTTPPSFLDVQSTFTIGAMNFSNGNEVYIDRIEFVPVEVTEAEYDEFEKAQEKV 660  
DB 601 TERTVGTTPPSFLDVQSTFTIGAMNFSNGNEVYIDRIEFVPVEVTEAEYDEFEKAQEKV 660  
QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFYVYAKQIHIERNM 719  
DB 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFYVYAKQIHIERNM 719

RESULT 5  
S00873  
parasporal crystal protein cryBa1 - Bacillus thuringiensis subsp. thuringiensis  
N/Alternate names: parasporal crystal protein cryA4  
C/Species: Bacillus thuringiensis subsp. thuringiensis  
C/Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 09-Jul-2004  
C/Accession: S00873  
R/Brizzard, B.L.; Whiteley, H.R.  
Nucleic Acids Res. 16, 2723-2724, 1988  
A/Title: Nucleotide sequence of an additional crystal protein gene cloned from Bacillus t  
A/Reference number: S00873; MUID: 89203216; PMID: 3362680  
A/Accession: S00873  
A/Molecule type: DNA  
A/Residues: 1-1228 <BRI>  
A/Cross-references: UNIPROT:P05517; EMBL:X06711; NID:g40264; PIDN:CAA29898.1; PID:g58094  
C/Genetics:  
A/Gene: cryA4  
A/Start codon: TTG  
C/Superfamily: parasporal crystal protein  
C/Keywords: delta-endotoxin

Query Match 60.5%; Score 2276.5; DB 2; Length 1228;  
Best Local Similarity 62.7%; Pred. No. 2e-151;  
Matches 449; Conservative 80; Mismatches 162; Indels 25; Gaps 6;  
..

QY 23 TDSLKNETDIELQNIH-----EDCLKNSEYENVEPFSASTIQTGIGIAGKI 70  
DB 2 TSNRNKNEIINAVSNHSAQMDLLPDARIEDSLCIAEGNIDDPFVSASTVQTGINIAGRI 61  
QY 71 LGTLGVPPAGVASLYSFIILGELWPKGKQWEIFMEHVVEIINOKISTYARKALTDLKG 130  
DB 62 LGVLGVPPAGQLASLYSFLVGLWPRGRDQWEIFLEHVEQLINQOITENARNTALARLQG 121  
QY 131 LGDALAVYHDSLESVGNRNNTARSVYKSYQIYALBELMFVQKLPFAVSGEVPPLPIYA 190  
DB 122 LGDSFRAVYQSSLEDWLENDADARTSVLYQYVIALELDLFLNAPLFAIRNOEVPPLMUYA 181  
QY 191 QAANLHLLLRDASIFCKEWGLSSSEISTFYNQVERAGDYSCHVKWYSYGLNLRGTN 250  
DB 182 QAANLHLLLRDASIFGSEFGLTSGEIQRYVERQVERTRDYSYCVIEWYNTGLNSLRGTN 241  
QY 251 AESWRYNQFRDMTLMVLIDVALFPSSYDTQMPYIKTTAQLTREVYTDALGTVHPHPSFT 310  
DB 242 AASWRYNQFRDRLTLGVLDLVALFPSSYDTTRYINTYSAQLTREVYTDALGAT--GVNMA 299  
QY 311 STTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWNSQTQNNMWGCHKLEPRTI 370  
DB 300 SMWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWNSQTQNNMWGCHKLEPRTI 359  
QY 371 GGLTINISTQGSTNTSINPVTLPFTSRDVRVYTESLAGNLFLTQPVNGVPRVDFHKKFV 428  
DB 360 GGLTINISTQGSTNTSINPVTLPFTSRDVRVYTESLAGNLFLTQPVNGVPRVDFHKKFV 416



Db 709 YGHDKXKMLLEAVRAAKRLSRNL 732

## RESULT 8

S32645  
parasporeal crystal protein crylGal - Bacillus thuringiensis  
C:Species: Bacillus thuringiensis  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
C:Accession: S32645  
R/Lambert, B.  
submitted to the EMBL Data Library, April 1993  
A:Reference number: S32645  
A:Accession: S32645  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1166 <LAM>  
A:Cross-references: UNIPROT:Q45746; EMBL:Z22510; NID:g295861; PIDN:CAA80233.1; PID:g2958  
C:Superfamily: parasporeal crystal protein  
C:Keywords: delta-endotoxin

Query Match 39.4%; Score 1482.5; DB 2; Length 1166;  
Best Local Similarity 46.2%; Pred. No. 1.1e-95;  
Matches 326; Conservative 97; Mismatches 207; Indels 75; Gaps 16;  
QY 41 DCLKMEYE---NVEPPFVSASTIQGIGIAGKILGTGVFPAGQVASYSPILGELWPK 36  
DB 13 NCLNPESEIFNARNNSFGVLVSQSSGL---TFLEAAVPEAGFALGFDIINGAL--- 66  
QY 97 GKQWEIFMEHVEEINQKISTYARKALTDLKGDLALAVHDSLESVWGRNNTPRS 156  
DB 67 GVDQWLSFLRQIEQLIRQIELEARNRATAILTGLSSSYLYVEALREWENDPNPASOE 126  
QY 157 VVKSOYALMLFMFVKLPSPAVSGEVPPLPIYAQAANLHLLLRDASIFGKEMGLSSSE 216  
DB 127 RVTRRLTDDAIVTGLTPIARNLEVNLSVTQAANLHLLLRDAVFGKRWGLTOAN 186  
QY 217 ISTFYNRQERAGDYSDHCVKYSTGLNNLRGNAESWRYNQFRDMTLMVLVALPP 276  
DB 187 IEDLYRLTNSIQEYSDHCARWYNQGLNEIGGISR---RYLDFQDLTAISVLDIVALPP 242  
QY 277 SYDTQWPIKTAQLREVYTDAL--GTVHPHPSFTSTWYNNNAPSFSAIEAAVVRNH 334  
DB 243 NYDIRTYPIQSQLREIYTSFVWAGNI-----NFGLSIANVLRAHP 285  
QY 335 LLDPLEQVITYSLLSRWSNTQYNNMGHKLERTIG-GTLN-----ISTQGSTNTS 385  
DB 286 LMDFDIRVIYTSVR--STPY---WAGHEVISRTGQGGQNEIRFPLYGVAANAEPVY 340  
QY 386 INPVTLPFTSRDVRYES-----LAGNLFLTPQVNGVPRVDFHWKFTVHTPIASDNFY 439  
DB 341 IRETGFTDEORQYRARSRYVSPRSQGFSLVDAVG-----FLT--IFSASVSY 388  
QY 440 PGVVGIGTQLQDSENELPPEATQOPNYESYSHRLSHIGLISAS-----HVKALVYSWTR 494  
DB 389 RNFGFNT---DIIDEPIEGTDP--FTGSHRLCHVGFLASSPFFISQVAPAFISWTR 443  
QY 495 SADRTNTIENSIITQIPLVKAFNLSGAAVVRGPGFTGGDILRTNTGTGDIRVNINPP 554  
DB 444 SATLTNTIADPVTQIPLVKAFNLSGATVKGPGFTGGDILRTNTVNGSPGDMRVNITAP 503  
QY 555 PAQRYRIRYASTDLQFHTSINGKAINQGNFSATMNRGCDLYKTERVGTGTTTPESEL 614  
DB 504 LSQRYRIRYASTDLQFHTSINGKAINQGNFSATMNRGCDLYKTERVGTGTTTPESEL 563  
QY 615 DVOSTFTIGAWNFSNGNEVIDRIEFVPEVYEAEDFEKAQEKYALTFTSTNPRGLKT 674  
DB 564 DANSTFTIGAFGSPNNEVIDRIEFVPAEVTFAEYDLEKAQKAVNALFTSSNQGLKT 623  
QY 675 DVKDYHIDQVSNLVESLSDEFYLDKEKRELFEIVKYAKQLHIERNM 719  
DB 624 DVTDYHIDKYSNLVVECLSDFECLDEKRELSEKVKHAKRLSDERNL 668

## RESULT 9

A26513  
parasporeal crystal protein - Bacillus thuringiensis (strain aizawai)  
C:Species: Bacillus thuringiensis  
C:Date: 11-Mar-1988 #sequence\_revision 11-Mar-1988 #text\_change 09-Jul-2004  
C:Accession: A26513  
R/Oeda, K.; Oshie, K.; Shimizu, M.; Nakamura, K.; Yamamoto, H.; Nakayama, H.;  
Gene 53, 113-119, 1987  
A:Title: Nucleotide sequence of the insecticidal protein gene of Bacillus thuringiensis  
A:Reference number: A26513; MUID:87248103; PMID:3297927  
A:Accession: A26513  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1155 <OED>  
A:Cross-references: UNIPROT:P06578; GB:M16463; NID:g143098; PIDN:AAA22551.1; PID:g143099  
C:Superfamily: parasporeal crystal protein  
C:Keywords: delta-endotoxin

Query Match 39.1%; Score 1472; DB 2; Length 1155;  
Best Local Similarity 44.4%; Pred. No. 6e-95;  
Matches 315; Conservative 113; Mismatches 227; Indels 54; Gaps 12;  
QY 36 NINHEDCUKMEYENVE-PFVSASTIQG-----IGIAGKILGTGVFPAGQVASYLS 87  
DB 4 NPNINECIYPNCLSNPEVEVLGGERIETGTPIDISLSLTQFLISEF-VPGAGFVLGVD 62  
QY 88 FILGELWPKGNQWEIFMEHVEEINQKISTYARKALTDLKGDLALAVHDSLESWVG 147  
DB 63 IHWGIF---GPSQMDAFVUQIEQLNQRIEFPARNOAISRLGSLNLYQIYAEFREWEA 119  
QY 148 NRNNTTRASVVKSYQIALLELMFVKLPSPAVSGEVPPLPIYAQAANLHLLLRDASIFG 207  
DB 120 DPTNPALREEMRIQFDMNSALTITAIPLFAVONYQVPLSVVQAANLHLSVLDRSVFVG 179  
QY 208 KEMGLSSSEISTFYNRQERAGDYSDHCVKYSTGLNNLRGNAESWRYNQFRDMTLM 267  
DB 180 QRWGPDAAITNSRYNDLTRLIGNYTDHARVWYNTGLERWGPDSRDWIRYQFRELTLT 239  
QY 268 VLDLVALPSPYDTPMYPIKTTAQLREVYTDALGTVHPHPSFTSTWYNNNAPSFSAIEA 327  
DB 240 VLDIVSLFPNVDSTRTYPIRTVSQLTREIYTNPV-----LENFDGGSFRALAQ 285  
QY 328 AV---VRNPHLLDFLEQVITYSLLSR-----WSNTQYNNM---WGHKLEPFTIGGTLNIS 377  
DB 286 GIEGSIKPSHLMIDILNSITITTDARGEYVWSGHQIMASPVGSGPEFTFPLYGTMGNA 345  
QY 378 TQGSTNTINPVTLPFTSRDVRYESLAGNLFLTPQVNGVPRVDFHWKFTVHTPIASDNF 437  
DB 346 PQORIVAQIGQVTRTSLSTLYRRFPNIGIN---NQLSVLDTGTEFAYG-----TSSNL 396  
QY 438 YYPGVGIGTQLQDSENELPPEATQOPNYESYSHRLSHIGLI-----SASHVKALVYS 490  
DB 397 PSAVYKSGT--VDSLDEIPQNNNPPRQGFSHRLSHVMSFRSGFSNVSYSIIRAPMFS 454  
QY 491 WTHRSADRTNTIENSIITQIPLVKAFNLSGAAVVRGPGFTGGDILRTNTGTGDIRVN 550  
DB 455 WTHRSAEFNIIIPSSQITQIPLTSTNLGSGTSVVGKPGFTGGDILRTNISFGQSTLRN 514  
QY 551 INPPPAQRYRIRYASTDLQFHTSINGKAINQGNFSATMNRGCDLYKTERVGTGTTT 610  
DB 515 ITAPLSQRYRIRYASTTNLQFHTSIDGRPINQGNFSATMSSGSLNQSQSFRTVGTFTT 574  
QY 611 PSFLDQSTFTIGAWNFSNGNEVIDRIEFVPEVYEAEDFEKAQEKYALTFTSTNPR 670  
DB 575 FNFSNGSVFTLSAHVFNSENGNEVIDRIEFVPAEVTFAEYDLEKAQKAVNALFTSSNQI 634  
QY 671 GLKTDVYHIDQVSNLVESLSDEFYLDKEKRELFEIVKYAKQLHIERNM 719  
DB 635 GLKTDVYHIDQVSNLVVECLSDFECLDEKRELSEKVKHAKRLSDERNL 683

## RESULT 10

S32649

Parasporal crystal protein cryIpa3 - Bacillus thuringiensis

C:Species: Bacillus thuringiensis  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
C:Accession: S32649  
R:Lambert, B.

submitted to the EMBL Data Library, April 1993

A:Reference number: S32645

A:Accession: S32649

A>Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-1174 <LAM>

A:Cross-references: UNIPROT:Q45749; EMBL:Z22512; NID:G295865; PIDN:CAA80235.1; PID:G2958

C:Superfamily: parasporal crystal protein

C:Keywords: delta-endotoxin

Query Match : 39.1%; Score 1469; DB 2; Length 1174;  
Best Local Similarity 44.8%; Pred. No. 9.9e-95;  
Matches 325; Conservative 103; Mismatches 202; Indels 96; Gaps 17;

QY	36	NINHE---	DCLKMEYENVPFVSASTIQIGIA-GKILGTGVFPAGQVASYFIL	90
DB	4	NIQOCVPYNCISNPEVILSEESTGELPLDISLTRELLSEFFVGVGAFGLPLDIW	63	
QY	91	GELMPKGNQNEIMEHVEEIIINQISTYARKALTDLKGGLDALAVYHDSLSWGNGN	150	
DB	64	GFITP---SEWSLFLOTEQIEQRIETLERNRAITTLRLGLADSEYVLEALREWEENP	120	
QY	151	NTRASVVKSOYIALELMFVKLPSFAVSGEVEPLPIYAQAANHLHLLLRDASIFGKEW	210	
DB	121	NAQLREVRIFANTDDALITAINNFLTSEIFLPSVYVQAANHLSLRDVSGQGW	180	
QY	211	GLSSEISTFYNQVERAGDYSCHVKWYSTGLNLRGTNAESVRYVRRDMLTMLVD	270	
DB	181	GLDIATVNNHYNRLINLHRYTECHLDYNGLENLGRGTQWSRNFRRRLTLTVD	240	
QY	271	LVALFBSYDTQYPIKTAQTLREVYDAIGTVHPHPSFTSTWYNNAPS-PSAEAAV	329	
DB	241	IVALFPNDARAYPIQTSQTREIYTSV--IEDSP-----VSANIENGFRNREFG-	290	
QY	330	VRNPHLLDFLEQVTIYSLSEWSNTQYNNMGGHKLFRITGGTFLNISTQSTNTSINPV	389	
DB	291	VRPHLMDPMN-----SLFVTAETVRSGTVMGHLV-----SSRTAGNPI	331	
QY	390	TLPP-----TSRDYVRRESLACGLNFLTQPVNGVPRVDFHWKVTHTPIAS	434	
DB	332	NFIYGFNPGGAIWIADDEPRPYRT-----LSDPV-----FVRGFGN	371	
QY	435	DNFYPGYVGIGTQLQ-----DSENELPPEATGQPNYBSYSHRLSHI----	476	
DB	372	PH-YVLGLRGVAFQQTGNHTRTFRNSGTIDSLDEIPQDNGAPNDYSHVNLHVTFR	430	
QY	477	--GLISASHV-KALVYSWTHRSADRTNIPNSITQIPLVKAFNLSSGAIVRGPGFTG	533	
DB	431	WPGIAGSDSWRAPFMSFWTHRSADRTNIINPNIITQIPAVKAKHNLSSGTVVRGPGFTG	490	
QY	534	DILARTNTGDIRVNNPFAQRYVRIRYASTDLOPHTSINGKAINQGNFSATMNR	593	
DB	491	DLARTNTGTPADIRVNLITGLSORVYVRIRYASTDLOPFTINGSVNQGQFQTMNR	550	
QY	594	GEDLDYKTRFVGTTPFPFLDVOSTTTIGAMPSSGNEVIYDRIEFPVPEVTEAEYDF	653	
DB	551	GGNLESGNFRTAGFTSPFSNAQSTETTLGTQAFSN-QEYVIDRIEFPVPAEVTFAESDL	609	
QY	654	EKAQEKYALTSTNPGLKTDVKDHYHDOVSNLAVESLSDSEYLDKRELFEIVKYAKOL	713	
DB	610	ERAGANVALFTSTSQLGLKINTVGTGHIHQVSNLVACLSDPEFLDKRELSEKVKAKRL	669	
QY	714	HIERNM	719	
DB	670	SDKRN	675	

RESULT 11

JD0002

Parasporal crystal protein cryIab3 - Bacillus thuringiensis

C:Species: Bacillus thuringiensis  
C:Date: 28-Dec-1987 #sequence\_revision 28-Dec-1987 #text\_change 09-Jul-2004  
C:Accession: A90025; A91560; A90955; S14555; A24172; A29043; JD0002  
R:Kondo, S.; Tamura, N.; Kunitate, A.; Hattori, M.; Akashi, A.; Ohmori, I.

Agric. Biol. Chem. 51, 455-463, 1987

A:Title: Cloning and nucleotide sequencing of two insecticidal delta-endotoxin genes from  
A:Reference number: A90025

A:Accession: A90025

A:Molecule type: mRNA

A:Residues: 1-1155 <KON>

A:Cross-references: UNIPROT:P06578

A:Experimental source: subsp. kurstaki

R:Geiser, M.; Schweitzer, S.; Grimm, C.

Gene 48, 109-118, 1986

A:Title: The hypervariable region in the genes coding for entomopathogenic crystal protei  
A:Reference number: A91560; MUID:87163505; PMID:3557124

A:Accession: A91560

A:Molecule type: DNA

A:Residues: 1-1155 <GEI>

A:Cross-references: GB:M15271; NID:G143123; PIDN:AAA22561.1; PID:G143124

A:Experimental source: subsp. kurstaki

R:Wabiko, H.; Raymond, K.C.; Bulla Jr., L.A.

DNA 5, 305-314, 1986

A:Title: Bacillus thuringiensis entomocidal protoxin gene sequence and gene product anal  
A:Reference number: A90955; MUID:86300092; PMID:3743328

A:Accession: A90955

A:Molecule type: DNA

A:Residues: 1-1155 <WAB>

A:Cross-references: GB:M13898; NID:G142719; PIDN:AAA22330.1; PID:G142720

A:Experimental source: subsp. berliner

R:Chak, K.F.; Jen, J.C.

submitted to the EMBL Data Library, October 1990

A:Description: Complete nucleotide sequence and expression in Escherichia coli of a cry  
A:Reference number: S14555

A:Accession: S14555

A:Molecule type: DNA

A:Residues: 1-1155 <CHA>

A:Cross-references: EMBL:X54939; NID:G40272; PIDN:CAA38701.1; PID:G40273

R:Hofte, H.; de Grave, H.; Seurinck, J.; Jansens, S.; Mahillon, J.; Ampe, C.; Vandekerck  
Eur. J. Biochem. 161, 273-280, 1986

A:Title: Structural and functional analysis of a cloned delta endotoxin of Bacillus thuri  
A:Reference number: A26461; MUID:87054026; PMID:3023091

A:Accession: A26461

A:Molecule type: DNA

A:Residues: 1-730, 'L', 732-784, 'R', 786-1155 <HOF>

A:Cross-references: GB:X04698; NID:G40254; PIDN:CAA28405.1; PID:G40255

A:Experimental source: strain berliner 1715

C:Comment: This toxin is lethal to the larvae of lepidopterans and dipterans.

C:Genetics:

A:Gene: cry-1-2; bt2

C:Superfamily: parasporal crystal protein

C:Keywords: delta-endotoxin

F:82-586/Product: toxic peptide #status predicted <XP>

F:82-300/Region: toxic #status predicted

F:300-586/Region: insecticidal #status predicted

Query Match : 39.0%; Score 1465; DB 2; Length 1155;

Best Local Similarity 44.5%; Pred. No. 1.8e-94;

Matches 316; Conservative 112; Mismatches 226; Indels 56; Gaps 13;

QY 36 NINHEDECLKMEYENVE-PFVSASTIQIG-----IGIACKILGTGVFPAGOVASIYS 87

DB 4 NPNINECPYNCISNPEVEVLGGERIETGTPIDISLTQFLSEF-VPGAGFVLGLVD 62

QY 88 FILGELWPKGNQNEIMEHVEEIIINQISTYARKALTDLKGGLDALAVYHDSLSWG 147

DB 63 IIWGIF--GPSQMDAFLVQIEQLINQRIEERFARNQAIISRLGLESLNYQIYAESFREWEA 119

QY 148 NNNTRASVVKSVQVIALELMFVKLPSFAVSGEVEPLPIYAQAANHLHLLLRDASIFG 207

Db	120	DPFNPALREEMRIQFNDMNSALTTPAIFAVQNTQVPLLSVYQAAALHLSVLURDVSFVG	179
Qy	208	KEWGLSSSISTFYNRQVERAGYSDCHCVKYSYGLNLRCTNAESWVRNQFRRDWTLM	267
Db	180	QRWGPDAAITNSRYNDLRELIGNYTDHAVRYNTGLERWGPDSRDWIRYNQFRELTLT	239
Qy	268	VLDLVALPFSYDTOMYPKTKTAQLTREYVYTDAGTWHPHPSFTSTTWYNNNAESP	323
Db	240	VLDIVSLFNYDSRTYPIRTVSQLTREIYTNV	285
Qy	324	ATEAAVVRPHLLDFLEOVTIYSLLSR	376
Db	286	GIEGS-IRSFHLMJLINSITTYDAHREYVWSGHQIWASPVGSPGPEFPFLPYCTMGNA	344
Qy	377	STQGSNTNTGPNVTLPTFSRQVYRTESLAGNLFLTPQVNGVPRVDPHKVTHPIASON	436
Db	345	APQOIRVAILOGGVYRTISSTLYRPPFNIGIN	395
Qy	437	FYYPGVVGITQLQDSENELPEATQPNYSYSHRLSHITGLI	489
Db	396	LPSAVTRKSGT	453
Qy	490	SWTHRSADRTNTEPNSITQIPLVKAFNLSCGAAVRGPGTGGDILERTNTGFGDIRV	549
Db	454	SWIHRSAEFNNIIPSSQITQIPLTKSTNLGSGTSVVKGPGTGGDILRRTPSQISTLAV	513
Qy	550	NINPPAQRYRIRYASTTDLOFHTSINGKALINQGFSAFMNKGEDLDYKTRPTVGFTT	609
Db	514	NITAPLUSQRYRIRYASTTNLOFHTSDGPRINQGNFSAFMSSGSLQSGSPRTVGFTT	573
Qy	610	PFSELDVQGTFTIGAWNTSSGNEVVYDRIEFPVPEVTVEAEYDPEKAQKVTAFLTSTNP	669
Db	574	PNFNSGSSVFTLSAHVFNSGNEVVYDRIEFPVPAEVTVEAEYDLERAQKAVNELFTSSNQ	633
Qy	670	RLKUTDXYDHIDQVSNLVESLDSFFYLDEKRELFELIVKYAKQLHIERNM	719
Db	634	IGLKTVDVTHIDQVSNLVESLDSDFLDEKRELSKVYGAKRLLSDSRNI	683

RESULT 12

A29125  
parasporal crystal protein Bt2 - *Bacillus thuringiensis* subsp. *kurstaki* (strain HD-1)  
C:Species: *Bacillus thuringiensis* subsp. *kurstaki*  
C:Date: 15-Dec-1988 #sequence\_revision 15-Dec-1988 #text\_change 09-Jul-2004  
C:Accession: A29125  
R:Fischhoff, D.A.; Bowdish, K.S.; Perlak, F.J.; Marrone, P.G.; McCormick, S.M.; Niederman  
Bio/Technology 5, 807-813, 1987  
A:Title: Insect tolerant transgenic tomato plants.  
A:Reference number: A29125  
A:Accession: A29125  
A:Status: not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-1156 <FIS>  
A:Cross-references: UNIPROT:Q9P296; UNIPROT:Q9J721  
C:Superfamily: parasporal crystal protein  
C:Keywords: delta-endotoxin

Qy 208 KEWGLSSSEISTFYNRQVERAGDYSCHCVKVSYSTGLNNLRGNAESWVRYNQPRRDWTLM 267  
:  
Db 180 QRWGFDAAATINSRVNDILTRLLIGNYTHDAVRMYNTGLERVMGPSRSDRWIRYNQPERELTLT 239  
:  
Qy 268 VLDLVALPPSYDTQWPKTKTAQLREVVTDAIGTVHPHPSFTSTTWYNNAPSF-----S 323  
:  
Db 240 VLDIVSLFPNVDSTRYPARTVSQLREIYNPV-----LENDFGSFRGSAQ 285  
:  
Qy 324 AIEAAVVRPHLLDPLEQVTIYSLLSR----WSNTQYMMN---WGCHKLEFRTIGTGLNI 376  
:  
Db 286 GIEGS-IRSPHLMDILNSITIVTDAHRGEYYWSGHQIMASPVGFSGPEFTFFPLYGTWGN 344  
:  
Qy 377 STQGTSINPVLPTFSRDVRYTESLAGNLFLTQPVNGVPRVDHFHKFVTHPIASDN 436  
:  
Db 345 APQORIVAQLGGVVRTLSTLYRRFPNIGIN--NQQLSVLDGTEFAYG-----TSSN 395  
:  
Qy 437 FYYPGYVGIGTQLODSENELPEATGQNYESYSHRLSHIGLI-----SASHVKALVY 489  
:  
Db 396 LPSAVYRKSGT--VDSDLDEIPQNNNVPRQGFSHRLSHVSMFRSCFNSSVSIIRAPMF 453  
:  
Qy 490 SWTHRSADRTNIENPSITQPLVKAFNLSSGAADVGRGFTGGDILLRINTTCTFGDIRV 549  
:  
Db 454 SWIHRSAEFNNII PSSQITQPLTKSTNLGSGTSVVGPGFTGGDILLRTPSQIGISLRV 513  
:  
Qy 550 NINPFPAQRVRYRYASTTDLQFHTSINGKAINQGNFSATWNRGEDLDYKKFRTVGFETT 609  
:  
Db 514 NITAPLSORYRVRIYASTTNLQFHTSIDGRPINQGNFSATWSSGSLNQSFGSPRTVGFETT 573  
:  
Qy 610 PFSFLDVOSTTTIGAWNFSSGNEVVIDRIEFVPVEVTEAEYDFEKAQKVTLAFTSTNP 669  
:  
Db 574 PFNFSGSSVSTLSAHVNSGNEVVIDRIEFVPAEVTFAEYDLERAQKAVNELFTSSNQ 633  
:  
Qy 670 RGLKTDVKDKYHDQVSNLVESLSDFYLDEKKELFETVKYAKOLHIERNM 719  
:  
Db 634 IGLKTDTVTDYHIDQVSNLVESCLDSDFCLDEKKElsekvkhakrlsderml 683  
:  
  
RESULT 13  
A22798  
parasporal crystal protein - Bacillus thuringiensis  
C:Species: Bacillus thuringiensis  
C>Date: 23-Aug-1987 #sequence\_revision 23-Aug-1987 #text\_change 09-Jul-2004  
C:Accession: A22798  
R:Shibano, Y.; Yanagata, A.; Nakamura, N.; Iizuka, T.; Sugisaki, H.; Takanami, M.  
Gene 34, 243-251, 1985  
A:Title: Nucleotide sequence coding for the insecticidal fragment of the Bacillus thuringiensis var. israelensis delta-endotoxin gene  
A:Reference number: A22798; PMID:85232070; PMID:2989108  
A:Accession: A22798  
A:Molecule type: DNA  
R:Residues: 1-334 <SH1>  
A:Cross-references: UNIPROT:Q9SV8; GB:M10917; NID:gl43100; PIDN:AAA22552.1; PID:g551713  
C:Comment: The authors translated the codon ACA for residue 264 as Ser.  
C:Superfamily: parasporal crystal protein  
C:Keywords: delta-endotoxin

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Db 180 QRWGFAATINSRYNDLRLIGNYTDYAVRWYNTGLERWVGPSDRDWRVYNQFRRELTLT 239
QY 268 VLDLVALPSPDYDTQWYPIKTTAQLTRVYVYDAIGTVHHPHSFTSTWYNNAPSFSAIEA 327
Db 240 VLDLVALPSPDYDSRRYPPIRTVSQLTRVYVYV-----LENFDSFRGMAQ 285
QY 328 AV---VRNPFLDLFLEQVYIYSLRSWNTQYMMWGGHKLFRITGGT---LNIQTQS 381
Db 286 RIEQNIQPHLMDILNRIITVTDVHRG-----FNWMSGHQITASPVGFGPEFAFPLFGN 340
QY 382 TWTINPVTLPSTRDVRVRESL-----AGLNFLTPQVNGVPRVDFHKKFVTHPI 432
Db 341 AGNAAPPVVLVSLTGLGIFRLLSSPLRYRIILGSGPN---NQELFVLDGTEFSASLTNL 397
QY 433 ASDNFYFPGYVIGIGTQQLQDSNELPPEATGPNYESYSHRLSHIGLISAS-----HVKAL 487
Db 398 PSTIYRQGTV-----DSLVDVIPPQDQNSVPPRAGFSHRLSHVMTLSQAAGAVYTLRAP 450
QY 488 VYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVRPGFTGGDILRRWTGTFGDI 547
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QY 548 RVNINPPPAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDDLYKTFRTVGF 607
Db 511 RVNITAPLSQRYRVRIRYASTTNLQFHTSIDGRPINQGNFSAATMSSGSLQSGSFRIVGF 570
QY 608 TTPSFELDVQSTFTIGAWNFSSGNEVYIDRIEFVVPVEVYEAEDYFKAQEKYVLTFTST 667
Db 571 TTPNFNSGSSVFTLSAHFVNSGNEVYIDRIEFVPAEVTPEAEYDLERAQKAVNELFTSS 630
QY 668 NPGRLKTDVKDHYIDQVSNLVESLSDREYLDKELPEIVKYAKQLHIERNM 719
Db 631 NOIGLKTVDYDHYIDQVSNLVESLSDREYLDKELPEIVKYAKQLHIERNM 682

RESULT 14
JT0241
parasporal crystal protein - Bacillus thuringiensis (strain aizawai IPL7)
N:Alternate names: 135K insecticidal protein
C:Species: Bacillus thuringiensis
C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C:Accession: JT0241
R:Shimizu, M.; Oshie, K.; Nakamura, K.; Takada, Y.; Oeda, K.; Ohkawa, H.
A:Title: Cloning and expression in Escherichia coli of the 135-KDa insecticidal protein
A:Reference number: JT0241
A:Accession: JT0241
A:Molecule type: DNA
A:Residues: 1-1176 <SHI>
A:Cross-references: UNIPROT:P02965
A:Note: b. thuringiensis aizawai IPL7 produces similar 130K and 135K insecticidal proteins
C:Comment: The 135K protein has insecticidal activity against Plutella xylostella larvae
C:Superfamily: parasporal crystal protein
C:Keywords: delta-endotoxin

Query Match 38.8%; Score 1457.5; DB 2; Length 1176;
Best Local Similarity 43.7%; Pred. No. 6.4e-94;
Matches 311; Conservative 118; Mismatches 222; Indels 61; Gaps 12;

QY 36 NINHEDCIKMSEYENVE-PFVSASTIQG-----IGIAGKILGTGVFPAGQVSLYS 87
Db 4 NPNIKECIPYCNLSNPEVEVLGGERIETGYTPIDISLTQFLSEP-VPGAGFVLGLVD 62
QY 88 FILGELWPKGNQWEIFMEHVEEINQKISTYARKKALTDLKGLGDALAVYHDSLESWVG 147
Db 63 IIWGIF---GPSQWDAFLVQIEQLINQRIEFARNQAIISRLGSLNLIYIYASFREWEA 119
QY 148 NRNNTARSVVKSVQVIALELMFVQKLPSFVSGEVPELPIYQAANLHLLLRDASIFG 207
Db 120 DPTNPALEEMRIQFNDMNSALTTPAIFLVAVNQYQVPLLSVYVQAANLHLSVLDSVFG 179
QY 208 KEWGLSSSEISTFYNRQVERAGDYSCHVKWYSYGLNLRGNTNAESWVRYNQFRDWTLM 267
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Db 180 QRWGFAATINSRYNDLRLIGNYTDYAVRWYNTGLERWVGPSDRDWRVYNQFRRELTLT 239
QY 268 VLDLVALPSPDYDTQWYPIKTTAQLTRVYVYDAIGTVHHPHSFTSTWYNNAPSFSAIEA 327
Db 240 VLDLVALPSPDYDSRRYPPIRTVSQLTRVYVYV-----LENFDSFRGMAQ 285
QY 328 AV---VRNPFLDLFLEQVYIYSLRSWNTQYMMWGGHKLFRITGGT---LNIQTQS 381
Db 286 RIEQNIQPHLMDILNRIITVTDVHRG-----FNWMSGHQITASPVGFGPEFAFPLFGN 340
QY 382 TWTINPVTLPSTRDVRVRESL-----AGLNFLTPQVNGVPRVDFHKKFVTHPI 432
Db 341 AGNAAPPVVLVSLTGLGIFRLLSSPLRYRIILGSGPN---NQELFVLDGTEFSASLTNL 397
QY 433 ASDNFYFPGYVIGIGTQQLQDSNELPPEATGPNYESYSHRLSHIGLISAS-----HVKAL 487
Db 398 PSTIYRQGTV-----DSLVDVIPPQDQNSVPPRAGFSHRLSHVMTLSQAAGAVYTLRAP 450
QY 488 VYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVRPGFTGGDILRRWTGTFGDI 547
Db 451 TFSWQHRSABEFNNIIPSSQITQIPLTKSTNLGSGTSVVGFGFTGGDILRRTPGQISTL 510
QY 548 RVNINPPPAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDDLYKTFRTVGF 607
Db 511 RVNITAPLSQRYRVRIRYASTTNLQFHTSIDGRPINQGNFSAATMSSGSLQSGSFRIVGF 570
QY 608 TTPSFELDVQSTFTIGAWNFSSGNEVYIDRIEFVVPVEVYEAEDYFKAQEKYVLTFTST 667
Db 571 TTPNFNSGSSVFTLSAHFVNSGNEVYIDRIEFVPAEVTPEAEYDLERAQKAVNELFTSS 630
QY 668 NPGRLKTDVKDHYIDQVSNLVESLSDREYLDKELPEIVKYAKQLHIERNM 719
Db 631 NOIGLKTVDYDHYIDQVSNLVESLSDREYLDKELPEIVKYAKQLHIERNM 682

RESULT 15
JC2219
parasporal crystal protein cryIaA - Bacillus thuringiensis
C:Species: Bacillus thuringiensis
C>Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
C:Accession: JC2219
R:Udayasuriyan, V.; Nakamura, A.; Mori, H.; Masaki, H.; Uozumi, T.
Biosci. Biotechnol. Biochem. 58, 830-835, 1994
A:Title: Cloning of a new cryIa(a) gene from Bacillus thuringiensis strain FU-2-7 and ana
A:Reference number: JC2219; MUID:94289859; PMID:7764972
A:Accession: JC2219
A:Molecule type: DNA
A:Residues: 1-1176 <UDA>
A:Cross-references: UNIPROT:Q45736; DBJ:D17518; NID:G506190; PIDN:BA04468.1; PID:G5357f
C:Genetics:
A:Gene: cryIa(a)
C:Superfamily: parasporal crystal protein
C:Keywords: delta-endotoxin

Query Match 38.6%; Score 1451.5; DB 2; Length 1176;
Best Local Similarity 43.5%; Pred. No. 1.7e-93;
Matches 310; Conservative 118; Mismatches 223; Indels 61; Gaps 12;

QY 36 NINHEDCIKMSEYENVE-PFVSASTIQG-----IGIAGKILGTGVFPAGQVSLYS 87
Db 4 NPNIKECIPYCNLSNPEVEVLGGERIETGYTPIDISLTQFLSEP-VPGAGFVLGLVD 62
QY 88 FILGELWPKGNQWEIFMEHVEEINQKISTYARKKALTDLKGLGDALAVYHDSLESWVG 147
Db 63 IIWGIF---GPSQWDAFLVQIEQLINQRIEFARNQAIISRLGSLNLIYIYASFREWEA 119
QY 148 NRNNTARSVVKSVQVIALELMFVQKLPSFVSGEVPELPIYQAANLHLLLRDASIFG 207
Db 120 DPTNPALEEMRIQFNDMNSALTTPAIFLVAVNQYQVPLLSVYVQAANLHLSVLDSVFG 179
QY 208 KEWGLSSSEISTFYNRQVERAGDYSCHVKWYSYGLNLRGNTNAESWVRYNQFRDWTLM 267
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Db 180 QRMGDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSRDRWVYNQFRRELTILT 239
Qy 268 VLDLVALFPSPYDTQMPYIKTAQITREYVYDAIGTVHPHPSFTTWWANNAPSPSAIEA 327
Db 240 VLDLVALFNSYDSRRYPITVSCUTREIYTNPV-----LENFDGSPFGMAQ 285
Qy 328 AV---VRNPHLLDFLEQVITYSLLSRWSTNQYNNMGHKLERTIGGT---LNISTQGS 381
Db 286 RIEQNIRQPHLMILNSIITYTDVHRG-----FNYWGHQITASPVGFSQPEFAFELFCN 340
Qy 382 TMTSINPVLPTFSRDRVYRTESL-----AGLNLFLTQPVNGVPRVDFHKKFVTHFI 432
Db 341 AGNAAPPVLVSLGGLGIFRTLSSPLXRIILGSGPN---NQELFVLDGTGTFGASLTNL 397
Qy 433 ASDNFYYPGVGIGTQLQDSENELPPEATGCPNYESYSHRLSHIGLISAS-----HVKAL 487
Db 398 PSTIYQRGTV-----DSLVDIPQDNSVPPRAGFSHRLSHVTLMSQAAGAVYTLRAP 450
Qy 488 VYSWTHRSADRTNTIENSTIQPLVKAFNLSSGAAVVRGPGTGGDILERRINTGTGDI 547
Db 451 TFSWQHRSAEFNNIIPSSQITQPLTKSTNLGSGTGVKGPFTGGDILERTSPGQISTL 510
Qy 548 RVNINPPFAQRYRIRYASTTLOPHTSINGKAINQGNFSATMNGEDLDYKTFETVGF 607
Db 511 RVNITAPLSQRYRIRYASTTLOPHTSIDGRPINQGNFSATMNGSGSNLQSGSFRTVGF 570
Qy 608 TTPFSLDVQSTFTIGAMNFSNGEYVIDRIEFVPEVTEYAEYDPEKAQEKVTLFTST 667
Db 571 TTPFNFSNGSVFTLSAHVFNSEYVIDRIEFVPAEVTFAEYDLERAQKAVNELFTSS 630
Qy 668 NPREGLKTDVXDYHIDQVSNLVECLSDFEFLDEXRELFEIVKYAKQLHIERNM 719
Db 631 NQIGLKTVDYDHYHIDQVSNLVECLSDFEFLDEXRELFEIVKYAKQLHIERNL 692

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Search completed: October 28, 2004, 18:31:55  
 Job time : 22.191 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 28, 2004, 18:10:58 ; Search time 65.6795 Seconds  
(without alignments)  
3549.224 Million cell updates/sec

Title: US-10-019-823b-57  
Perfect score: 3760  
Sequence: 1 MKLKNQDKHQSFSSNAKVDK.....KRELEIVKXQLHIERNM 719

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1370721 seqs, 324215800 residues

Total number of hits satisfying chosen parameters: 1370721

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:  
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2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
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20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3756	99.9	719	17 US-10-782-020-10	Sequence 10, Appl
2	3756	99.9	719	17 US-10-782-141-8	Sequence 8, Appl
3	3756	99.9	719	17 US-10-782-096-10	Sequence 10, Appl
4	3756	99.9	719	17 US-10-782-570-7	Sequence 7, Appl
5	3472.5	92.4	710	14 US-10-428-961-42	Sequence 42, Appl
6	2277.5	60.6	1228	16 US-10-809-953-10	Sequence 10, Appl
7	2264.5	60.2	1207	10 US-09-988-462-7	Sequence 7, Appl
8	2186.5	58.2	1227	14 US-10-428-961-63	Sequence 63, Appl
9	2171.5	57.8	1186	9 US-09-826-660-23	Sequence 23, Appl
10	2115	56.2	1228	14 US-10-428-961-38	Sequence 38, Appl
11	2115	56.2	1228	15 US-10-614-524-2	Sequence 2, Appl
12	1932.5	51.4	643	9 US-09-826-660-25	Sequence 25, Appl
13	1724.5	45.9	1167	14 US-10-089-678-1	Sequence 1, Appl

14	1680.5	44.7	653	14	US-10-428-961-6	Sequence 6, Appl
15	1669.5	44.4	1157	17	US-10-782-141-16	Sequence 16, Appl
16	1669.5	44.4	1157	17	US-10-782-096-17	Sequence 17, Appl
17	1669.5	44.4	1157	17	US-10-782-570-13	Sequence 13, Appl
18	1510	40.2	1206	13	US-10-032-717-2	Sequence 2, Appl
19	1510	40.2	1206	14	US-10-414-637-2	Sequence 2, Appl
20	1510	40.2	1206	15	US-10-606-320-2	Sequence 2, Appl
21	1510	40.2	1206	17	US-10-746-914-2	Sequence 4, Appl
22	1494	39.7	1210	13	US-10-032-717-4	Sequence 4, Appl
23	1494	39.7	1210	14	US-10-414-637-4	Sequence 4, Appl
24	1494	39.7	1210	15	US-10-606-320-4	Sequence 4, Appl
25	1494	39.7	1210	17	US-10-746-914-4	Sequence 4, Appl
26	1487.5	39.6	1156	14	US-10-099-285-72	Sequence 72, Appl
27	1487.5	39.6	1156	14	US-10-428-961-28	Sequence 28, Appl
28	1465	39.0	1155	9	US-09-756-643-2	Sequence 2, Appl
29	1465	39.0	1155	10	US-09-988-462-9	Sequence 9, Appl
30	1465	39.0	1155	14	US-10-136-998A-2	Sequence 2, Appl
31	1465	39.0	1177	14	US-10-035-060-6	Sequence 6, Appl
32	1465	39.0	1181	10	US-09-988-462-11	Sequence 11, Appl
33	1465	39.0	1181	10	US-09-988-462-13	Sequence 13, Appl
34	1465	39.0	1181	10	US-09-988-462-15	Sequence 15, Appl
35	1465	39.0	1181	10	US-09-988-462-17	Sequence 17, Appl
36	1465	39.0	1181	10	US-09-988-462-28	Sequence 28, Appl
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38	1465	39.0	1181	14	US-10-136-998A-8	Sequence 8, Appl
39	1465	39.0	1181	14	US-10-136-998A-10	Sequence 10, Appl
40	1465	39.0	1181	14	US-10-136-998A-12	Sequence 12, Appl
41	1460	38.8	1177	14	US-10-035-060-2	Sequence 2, Appl
42	1458	38.8	1177	14	US-10-035-060-8	Sequence 8, Appl
43	1457	38.8	1177	14	US-10-102-469-24	Sequence 24, Appl
44	1447.5	38.5	1176	17	US-10-782-141-6	Sequence 6, Appl
45	1447.5	38.5	1176	17	US-10-782-096-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1  
US-10-782-020-10  
; Sequence 10, Application US/10782020  
; Publication No. US20040197916A1  
; GENERAL INFORMATION:  
; APPLICANT: Carozzi, Nadine  
; APPLICANT: Hargiss, Tracy  
; APPLICANT: Koziel, Michael G.  
; APPLICANT: Duck, Nicholas B.  
; APPLICANT: Carr, Brian  
; TITLE OF INVENTION: AXMI-004, A Delta-Endotoxin Gene and  
; TITLE OF INVENTION: Methods for Its Use  
; FILE REFERENCE: 045600/274139  
; CURRENT APPLICATION NUMBER: US/10/782,020  
; CURRENT FILING DATE: 2004-02-19  
; PRIOR APPLICATION NUMBER: 60/448,810  
; PRIOR FILING DATE: 2003-02-20  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 719  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
US-10-782-020-10

Query Match	99.9%	Score	3756	DB	17	Length	719
Best Local Similarity	99.9%	Pred. No.	4.5e-308				
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Db	1	MKLKNQDKHQSFSSNAKVDKISTDS	1	MKLKNQDKHQSFSSNAKVDKISTDS	1	MKLKNQDKHQSFSSNAKVDKISTDS	1
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Db	61	QTGIGAGKILGTIGVFFAGQVSLYSF	61	QTGIGAGKILGTIGVFFAGQVSLYSF	61	QTGIGAGKILGTIGVFFAGQVSLYSF	61

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 181 EEPVLLPIYAQAANLHLLLRDASIFGKDWGLSSSEISTFYNRQVERAGDYSDHCVKWYS 240  
 181 EEPVLLPIYAQAANLHLLLRDASIFGKDWGLSSSEISTFYNRQVERAGDYSDHCVKWYS 240  
 241 TGLNLRGNTNAESWRYNQFRDMTLMVLDLVALFPSYDTQMPYIKTTAQLTREVYTDI 300  
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RESULT 2

US-10-782-141-8  
 ; Sequence 8, Application US/10782141  
 ; Publication No. US20040197917A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Carozzi, Nadine  
 ; APPLICANT: Hargiss, Tracy  
 ; APPLICANT: Kozziel, Michael G.  
 ; APPLICANT: Duck, Nicholas B.  
 ; APPLICANT: Carr, Brian  
 ; TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and  
 ; TITLE OF INVENTION: Methods for Its Use  
 ; FILE REFERENCE: 045600/274143  
 ; CURRENT APPLICATION NUMBER: US/10782,141  
 ; CURRENT FILING DATE: 2004-02-20  
 ; PRIOR APPLICATION NUMBER: 60/448, 632  
 ; PRIOR FILING DATE: 2003-02-20  
 ; NUMBER OF SEQ ID NOS: 23  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 8  
 ; LENGTH: 719  
 ; TYPE: PRT  
 ; ORGANISM: Bacillus thuringiensis  
 US-10-782-141-8

Query Match 99.9%; Score 3756; DB 17; Length 719;  
 Best Local Similarity 99.9%; Pred. No. 4.5e-308;  
 Matches 718; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 MLKNQDKHQSFSNAKVDKISTDSLKNETDIELQNIHEDCLMKSEYENVEPVSASTI 60  
 61 QTGIGTAGKILGTILGVPFAGQVASLXSFILGELWPKGNQWEIFMEHVBEIINQKISTVA 120  
 61 QTGIGTAGKILGTILGVPFAGQVASLXSFILGELWPKGNQWEIFMEHVBEIINQKISTVA 120  
 121 RNKALDGLGDLALAVYHDSLESWGNNRNRARSVVKSQYIALELMPVQKLPFAVSG 180  
 121 RNKALDGLGDLALAVYHDSLESWGNNRNRARSVVKSQYIALELMPVQKLPFAVSG 180  
 181 EEPVLLPIYAQAANLHLLLRDASIFGKDWGLSSSEISTFYNRQVERAGDYSDHCVKWYS 240  
 181 EEPVLLPIYAQAANLHLLLRDASIFGKDWGLSSSEISTFYNRQVERAGDYSDHCVKWYS 240  
 241 TGLNLRGNTNAESWRYNQFRDMTLMVLDLVALFPSYDTQMPYIKTTAQLTREVYTDI 300  
 241 TGLNLRGNTNAESWRYNQFRDMTLMVLDLVALFPSYDTQMPYIKTTAQLTREVYTDI 300  
 301 GTVHPHPSFTSTWYNNAPSAIEAAVVRNPHLLDFLEQVTTIYSLSRWSNTQYNNMW 360  
 301 GTVHPHPSFTSTWYNNAPSAIEAAVVRNPHLLDFLEQVTTIYSLSRWSNTQYNNMW 360  
 361 GGHKLEFRITGTLNISTOGSNTSINPVTLPFTSRDVRVYTESLAGLNLFTQPVNGVPR 420  
 361 GGHKLEFRITGTLNISTOGSNTSINPVTLPFTSRDVRVYTESLAGLNLFTQPVNGVPR 420  
 421 VDFHMKFVTHPIASDNFYYPGVGIGTQLODSENLPPPEATQPNYESYSHRLSHIGLIS 480  
 421 VDFHMKFVTHPIASDNFYYPGVGIGTQLODSENLPPPEATQPNYESYSHRLSHIGLIS 480  
 481 ASHVKALVSWTHRSADRNTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
 481 ASHVKALVSWTHRSADRNTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
 541 TGTGDIRVNIINPPFAQRYRVRIRVASTTDLQFHTSINGKAINQGNFSATNMRGEDLDYK 600  
 541 TGTGDIRVNIINPPFAQRYRVRIRVASTTDLQFHTSINGKAINQGNFSATNMRGEDLDYK 600  
 601 TERTVGFTTPSFQVSTFTIGAMNFGSGNEVYIDRIEFVPEVVEYAEYDPEKAQEKV 660  
 601 TERTVGFTTPSFQVSTFTIGAMNFGSGNEVYIDRIEFVPEVVEYAEYDPEKAQEKV 660  
 661 TALFTSTNPRGLKTDVKDHYDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719  
 661 TALFTSTNPRGLKTDVKDHYDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 3

US-10-782-096-10  
 ; Sequence 10, Application US/10782096  
 ; Publication No. US20040210964A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Carozzi, Nadine  
 ; APPLICANT: Hargiss, Tracy  
 ; APPLICANT: Kozziel, Michael G.  
 ; APPLICANT: Duck, Nicholas B.  
 ; APPLICANT: Carr, Brian  
 ; TITLE OF INVENTION: AXMI-009, A Delta-Endotoxin Gene and  
 ; TITLE OF INVENTION: Methods for Its Use  
 ; FILE REFERENCE: 045600/274148  
 ; CURRENT APPLICATION NUMBER: US/10782,096  
 ; CURRENT FILING DATE: 2004-02-19  
 ; PRIOR APPLICATION NUMBER: 60/448, 633  
 ; PRIOR FILING DATE: 2003-02-20  
 ; NUMBER OF SEQ ID NOS: 23  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 10  
 ; LENGTH: 719  
 ; TYPE: PRT  
 ; ORGANISM: Bacillus thuringiensis  
 US-10-782-096-10

Query Match 99.9%; Score 3756; DB 17; Length 719;

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Best Local Similarity 99.9%; Pred. No. 4.5e-308;
Matches 718; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 M K L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y N V E P F V S A S T I 60
Db 1 M K L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y N V E P F V S A S T I 60

QY 61 Q T G I G A G K I L G T L G V P F A G V A S L Y S F I L G E L W P K G N Q W E I F M E H V E E I I N Q I S T Y A 120
Db 61 Q T G I G A G K I L G T L G V P F A G V A S L Y S F I L G E L W P K G N Q W E I F M E H V E E I I N Q I S T Y A 120

QY 121 R N K A L T D L K G L G D A L A V Y H D S L E S W G N R N N T R A R S V V K S Y I A L E L M F V Q K L P S F A V S G 180
Db 121 R N K A L T D L K G L G D A L A V Y H D S L E S W G N R N N T R A R S V V K S Y I A L E L M F V Q K L P S F A V S G 180

QY 181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S E I S T F Y N Q V E R A G D Y S D H C V K W Y S 240
Db 181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S E I S T F Y N Q V E R A G D Y S D H C V K W Y S 240

QY 241 T G L N L R G T N A E S W R Y N Q F R D M T L M V L D L V A L P S Y D T Q M Y P I K T T A Q L T R E V Y T D A I 300
Db 241 T G L N L R G T N A E S W R Y N Q F R D M T L M V L D L V A L P S Y D T Q M Y P I K T T A Q L T R E V Y T D A I 300

QY 301 G T V H P H P S F T S T T W Y N N N A P S F S A I E A A V V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N W 360
Db 301 G T V H P H P S F T S T T W Y N N N A P S F S A I E A A V V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N W 360

QY 361 G G H K L E F R T I G G T L N I S T Q S T N T S I N P V T L P F T S R D V Y T E S L A G L N L F L T O P V N G V P R 420
Db 361 G G H K L E F R T I G G T L N I S T Q S T N T S I N P V T L P F T S R D V Y T E S L A G L N L F L T O P V N G V P R 420

QY 421 V D F H W K F V T H P I A S D N F Y P G Y A G I G T Q L D S E N E L P P E A T G Q P N Y E S Y S H R L S H I G L I S 480
Db 421 V D F H W K F V T H P I A S D N F Y P G Y A G I G T Q L D S E N E L P P E A T G Q P N Y E S Y S H R L S H I G L I S 480

QY 481 A S H V K A L V Y S W T H S A D R T N T I E N S I T Q I P L V K A F N L S S G A A V V R G P F T G D I L R T N 540
Db 481 A S H V K A L V Y S W T H S A D R T N T I E N S I T Q I P L V K A F N L S S G A A V V R G P F T G D I L R T N 540

QY 541 T G T F G D I R V N I N P P A Q R Y R V I R Y A S T D L Q F H T S I N G K A I N Q G N F S A T M W R G E D L D Y K 600
Db 541 T G T F G D I R V N I N P P A Q R Y R V I R Y A S T D L Q F H T S I N G K A I N Q G N F S A T M W R G E D L D Y K 600

QY 601 T F R V G F T T P S F L D V Q S T F T I G A W N F S S G N E V I D R I E F V P V E V T Y E A E Y D F E K A Q E K V 660
Db 601 T F R V G F T T P S F L D V Q S T F T I G A W N F S S G N E V I D R I E F V P V E V T Y E A E Y D F E K A Q E K V 660

QY 661 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K Y A K Q L H I E R N M 719
Db 661 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K Y A K Q L H I E R N M 719

RESULT 4
US-10-782-570-7
; Sequence 7, Application US/10782570
; Publication No. US20040210965A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-007, A Delta-Endotoxin Gene and
; TITLE OF INVENTION: Methods for Its Use
; FILE REFERENCE: 045600/274144
; CURRENT APPLICATION NUMBER: US/10/782,570
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: 60/448,812
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 719
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; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-782-570-7

Query Match 99.9%; Score 3756; DB 17; Length 719;
Best Local Similarity 99.9%; Pred. No. 4.5e-308;
Matches 718; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 M K L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y N V E P F V S A S T I 60
Db 1 M K L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y N V E P F V S A S T I 60

QY 61 Q T G I G A G K I L G T L G V P F A G V A S L Y S F I L G E L W P K G N Q W E I F M E H V E E I I N Q I S T Y A 120
Db 61 Q T G I G A G K I L G T L G V P F A G V A S L Y S F I L G E L W P K G N Q W E I F M E H V E E I I N Q I S T Y A 120

QY 121 R N K A L T D L K G L G D A L A V Y H D S L E S W G N R N N T R A R S V V K S Y I A L E L M F V Q K L P S F A V S G 180
Db 121 R N K A L T D L K G L G D A L A V Y H D S L E S W G N R N N T R A R S V V K S Y I A L E L M F V Q K L P S F A V S G 180

QY 181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S E I S T F Y N Q V E R A G D Y S D H C V K W Y S 240
Db 181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S E I S T F Y N Q V E R A G D Y S D H C V K W Y S 240

QY 241 T G L N L R G T N A E S W R Y N Q F R D M T L M V L D L V A L P S Y D T Q M Y P I K T T A Q L T R E V Y T D A I 300
Db 241 T G L N L R G T N A E S W R Y N Q F R D M T L M V L D L V A L P S Y D T Q M Y P I K T T A Q L T R E V Y T D A I 300

QY 301 G T V H P H P S F T S T T W Y N N N A P S F S A I E A A V V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N W 360
Db 301 G T V H P H P S F T S T T W Y N N N A P S F S A I E A A V V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N W 360

QY 361 G G H K L E F R T I G G T L N I S T Q S T N T S I N P V T L P F T S R D V Y T E S L A G L N L F L T O P V N G V P R 420
Db 361 G G H K L E F R T I G G T L N I S T Q S T N T S I N P V T L P F T S R D V Y T E S L A G L N L F L T O P V N G V P R 420

QY 421 V D F H W K F V T H P I A S D N F Y P G Y A G I G T Q L D S E N E L P P E A T G Q P N Y E S Y S H R L S H I G L I S 480
Db 421 V D F H W K F V T H P I A S D N F Y P G Y A G I G T Q L D S E N E L P P E A T G Q P N Y E S Y S H R L S H I G L I S 480

QY 481 A S H V K A L V Y S W T H S A D R T N T I E N S I T Q I P L V K A F N L S S G A A V V R G P F T G D I L R T N 540
Db 481 A S H V K A L V Y S W T H S A D R T N T I E N S I T Q I P L V K A F N L S S G A A V V R G P F T G D I L R T N 540

QY 541 T G T F G D I R V N I N P P A Q R Y R V I R Y A S T D L Q F H T S I N G K A I N Q G N F S A T M W R G E D L D Y K 600
Db 541 T G T F G D I R V N I N P P A Q R Y R V I R Y A S T D L Q F H T S I N G K A I N Q G N F S A T M W R G E D L D Y K 600

QY 601 T F R V G F T T P S F L D V Q S T F T I G A W N F S S G N E V I D R I E F V P V E V T Y E A E Y D F E K A Q E K V 660
Db 601 T F R V G F T T P S F L D V Q S T F T I G A W N F S S G N E V I D R I E F V P V E V T Y E A E Y D F E K A Q E K V 660

QY 661 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K Y A K Q L H I E R N M 719
Db 661 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K Y A K Q L H I E R N M 719

RESULT 5
US-10-428-961-42
; Sequence 42, Application US/10428961
; Publication No. US20030237111A1
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Chu, Chih-Rei
; APPLICANT: Donovan, William P.
; APPLICANT: Gilmer, Amy J.
; APPLICANT: Rupar, Mark J.
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin
; FILE REFERENCE: MECO201--1
; CURRENT APPLICATION NUMBER: US/10/428,961
; CURRENT FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: 09/661,322
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; PRIOR FILING DATE: 2000-09-13  
 ; PRIOR APPLICATION NUMBER: 60/153,995  
 ; PRIOR FILING DATE: 1999-09-15  
 ; NUMBER OF SEQ ID NOS: 63  
 ; SOFTWARE: Patent in version 3.2  
 ; SEQ ID NO 42  
 ; LENGTH: 710  
 ; TYPE: PRT  
 ; ORGANISM: Bacillus thuringiensis  
 ; FEATURE:  
 ; NAME/KEY: misc.feature  
 ; LOCATION: (2007..(200)  
 ; OTHER INFORMATION: The 'Xaa' at location 200 stands for any naturally occurring amino acid  
 US-10-428-961-42

Query Match 92.4%; Score 3472.5; DB 14; Length 710;  
 Best Local Similarity 92.4%; Pred. No. 4e-284;  
 Matches 664; Conservative 15; Mismatches 31; Indels 9; Gaps 1;

QY	1	MLKQDKHQSPSSNAKVDKISTDLKNETDIELQNHEDCLKSEYENVEPFSASTI	60
DB	1	MKSQKQNHQSLSNATVDKXFTGSLNNTTELQNFH-----EGIEPFSVSTI	51
QY	61	QTGIGIAGKILGTLGVPPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA	120
DB	52	QTGIGIAGKILGTLGVPPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA	111
QY	121	RNKALTDLGLDGLAVVHDSLESVGNRNTRASSVVKSOVIALELMFVQKLPSFVAVSG	180
DB	112	RNKALADLGLDGLAVVHDSLESVGNRNTRASSVVKSOVIALELMFVQKLPSFVAVSG	171
QY	181	EBVPLPIYAQANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDSDCHVKWYS	240
DB	172	EBVPLPIYAQANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDSDCHVKWYN	231
QY	241	TGLNLRGNTNAESWRYNQFRDMLTMDLVALPSSYDTOMYPIKTTAQLTREVYTDI	300
DB	232	TGLNLGMNAESWRYNQFRDMLTMDLVALPSSYDTOMYPIKTTAQLTREVYTDI	291
QY	301	GVVHPHPSFTSTWYNNNAPSFAEAAVVRNPHLLDLEQVTIYSLSRWSNTQYNNW	360
DB	292	GVVHPHPSFTSTWYNNNAPSFAEAAVVRNPHLLDLEQVTIYSLSRWSNTQYNNW	351
QY	361	GGHKLFEFTIGTLMISTQGSTNTSINPVTLPFTSRDVRYSAGLNLFTQPVNGVPR	420
DB	352	GGHKLFEFTIGTLMISTQGSTNTSINPVTLPFTSRDVRYSAGLNLFTQPVNGVPR	411
QY	421	VDPHKVFTHPTASDNFYYPGVGIGTOLQDSENELPPEATGQPNYESYSHRLSHIGLIS	480
DB	412	VDPHKVFTHPTASDNFYYPGVGIGTOLQDSENELPPEATGQPNYESYSHRLSHIGLIS	471
QY	481	ASHVKALVSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN	540
DB	472	ASHVKALVSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN	531
QY	541	TCTFGDIRVNPFAQRYVRIRYASTDLOFHTSINGKAINQGNFSATNRCGEDLDYK	600
DB	532	TCTFGDIRVNPFAQRYVRIRYASTDLOFHTSINGKAINQGNFSATNRCGEDLDYK	591
QY	601	TPRTVGTTPFSFSDVQSTFTIGAMNFSGNEVYIDRIEFVPEVTEAEYDPEKAQSKV	660
DB	592	TPRTVGTTPFSFSDVQSTFTIGAMNFSGNEVYIDRIEFVPEVTEAEYDPEKAQBEV	651
QY	661	TALFTSTPRGLKTDVKDHYHDQVSNLVESLSDEFLDEKELFEIVKAKOLHIERNM	719
DB	652	TALFTSTPRGLKTDVKDHYHDQVSNLVESLSDEFLDEKELFEIVKAKOLHIERNM	710

RESULT 6  
 US-10-809-953-10  
 ; Sequence 10, Application US/10809953  
 ; Publication No. US20040181825A1  
 ; GENERAL INFORMATION:

; APPLICANT: Van Mellaert, Herman  
 ; APPLICANT: Botterman, Johan  
 ; APPLICANT: Van Rie, Jeroen  
 ; APPLICANT: Joos, Henk  
 ; TITLE OF INVENTION: RECOMBINANT PLANT EXPRESSING NON-COMPETITIVELY BINDING Bt INSECTIC  
 ; FILE REFERENCE: 021565-078  
 ; CURRENT APPLICATION NUMBER: US/10/809,953  
 ; CURRENT FILING DATE: 2004-03-26  
 ; PRIOR APPLICATION NUMBER: US/09/661,016  
 ; PRIOR FILING DATE: 2000-09-13  
 ; PRIOR APPLICATION NUMBER: PCT/EP90/00905  
 ; PRIOR FILING DATE: 1990-05-30  
 ; PRIOR APPLICATION NUMBER: GB 89401499.2  
 ; PRIOR FILING DATE: 1989-05-31  
 ; NUMBER OF SEQ ID NOS: 10  
 ; SOFTWARE: Patent in Ver. 2.0  
 ; SEQ ID NO 10  
 ; LENGTH: 1228  
 ; TYPE: PRT  
 ; ORGANISM: Bacillus thuringiensis  
 US-10-809-953-10

Query Match 60.6%; Score 2277.5; DB 16; Length 1228;  
 Best Local Similarity 62.7%; Pred. No. 8.8e-183;  
 Matches 449; Conservative 80; Mismatches 162; Indels 25; Gaps 6;

QY	23	TDSLKNETDIELQNH-----EDCLKSEYENVEPFSASTIQTGIGIAGKI	70
DB	2	TSNRKNEEIIINAVSHSACMDLLDPARIEDSLCTAEGNIDPFSVASTVQGINIAGRI	61
QY	71	LGLTGVPPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYARNKALTDLKG	130
DB	62	LGVLVFPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYARNKALTDLKG	121
QY	131	LGDALAVVHDSLESVGNRNTRASSVVKSOVIALELMFVQKLPSFVAVSGEVPVLLPIYA	190
DB	122	LGDSPRAYQOSLEDDWENRDDRATRSVLTQVIALELDFLNAFLPFAIRNQEVPLLMVYA	181
QY	191	QAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDSDCHVKWYSTGLNLRGTN	250
DB	182	QAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDSDCHVKWYSTGLNLRGTN	241
QY	251	ABSWRYNQFRDMLTMDLVALPSSYDTOMYPIKTTAQLTREVYTDIAGTVHHPST	310
DB	242	AASWRYNQFRDMLTMDLVALPSSYDTOMYPIKTTAQLTREVYTDIAGTVHHPST	299
QY	311	STTWYNNNAPSFAEAAVVRNPHLLDLEQVTIYSLSRWSNTQVMMNMGHKLFEFTI	370
DB	300	SMWYNNNAPSFAEAAVVRNPHLLDLEQVTIYSLSRWSNTQVMMNMGHKLFEFTI	359
QY	371	GGTFLNISTQGSTNTSINPVTLPFTSRDVRYSAGLNLFTQPVNGVPRVDPHFKV	428
DB	360	GGTFLNISTQGSTNTSINPVTLPFTSRDVRYSAGLNLFTQPVNGVPRVDPHFKV	416
QY	429	THP-----TASDNFYYPGVGIGTOLQDSENELPPEATGQPNYESYSHRLSHIGLISASH	483
DB	417	THPQNTSDRGNTANYSQP-YESPOLQKQSELPETTERPNERPYESYSHRLSHIGLISQSR	475
QY	484	VKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN	543
DB	476	VNVVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN	535
QY	544	FGDIRVNPFAQRYVRIRYASTDLOFHTSINGKAINQGNFSATNRCGEDLDYK	603
DB	536	FGDIRVNPFAQRYVRIRYASTDLOFHTSINGKAINQGNFSATNRCGEDLDYK	595
QY	604	TVGFTTPFSFSDVQSTFTIGAMNFSGNEVYIDRIEFVPEVTEAEYDPEKAQSKV	663
DB	596	TVGFTTPFSFSDVQSTFTIGAMNFSGNEVYIDRIEFVPEVTEAEYDPEKAQSKV	655
QY	664	FTSTNPRGLKTDVKDHYHDQVSNLVESLSDEFLDEKELFEIVKAKOLHIERNM	719

Db 656 FTNTPRLKTDVTDYHIDQVSNLVACLSDBFCLDEKRELEKVKYAKRLSDERNL 711

RESULT 7

US-09-988-462-7

; Sequence 7, Application US/09988462

; Publication No. US20030046726A1

GENERAL INFORMATION:

APPLICANT: Koziel, Michael G.

; Desai, Nalin M.

; Lewis, Kelly S.

; Kramer, Vance C.

; Warren, Gregory W.

; Evola, Stephen V.

; Crossland, Lyle D.

; Wright, Martha S.

; Merlin, Ellis J.

; Launis, Karen L.

TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED

; INSECTICIDAL ACTIVITY IN MAIZE

NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:

ADDRESSEE: Syngenta Biotechnology, Inc.

STREET: 3054 Cornwallis Road

CITY: Research Triangle Park

STATE: NC

COUNTRY: USA

ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/988,462

FILING DATE: 20-NO. US20030046726A1-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/547,422

FILING DATE: 11-APR-2000

APPLICATION NUMBER: US 08/459,504

FILING DATE: 02-JUN-1995

APPLICATION NUMBER: US 07/951,715

FILING DATE: 25-SEP-1992

APPLICATION NUMBER: US 07/772,027

FILING DATE: 04-OCT-1991

ATTORNEY/AGENT INFORMATION:

NAME: Meigs, J. Timothy

REGISTRATION NUMBER: 38,241

REFERENCE/DOCKET NUMBER: S-188051

TELECOMMUNICATION INFORMATION:

TELEPHONE: (919)541-8587

TELEFAX: (919)541-8689

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 1207 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 7:

US-09-988-462-7

Query Match 60.2%; Score 2264.5; DB 10; Length 1207;

Best Local Similarity 64.3%; Pred. No. 1.1e-181;

Matches 442; Conservative 78; Mismatches 154; Indels 13; Gaps 5;

QY 40 EDCIKXSEVNEPVSASTCTGTGAGKILGTVFPAGQVSLYFLLGELWPKGN 99

Db 10 EDSLCAAGNIDPVSASTVQTGINIAGRLGVLPFAGQLASTFSLVGLWPKGRD 69

QY 100 QWEIFMEHVEEIIQKISTYARNKALTDKGLDALAVYHDSLSWVGRNNTARSVK 159

Db 70 QWEIFLEHVEQLNQITENARNALTARLQGLGDSFRAYQQSLDNLNRRDARTRSVLY 129

QY 160 SOYIALELMFVQKLPSFAVSGSEVLLPIYQAANLHLLLRDASIFGKENGSLSSSEIST 219

Db 130 TQYIALELDFLNAFLFAIRNQEVLLMVYAQAANLHLLLRDASIFGSEFGTQSQEIQR 189

QY 220 FYNQOVERAGDYSDHCWKYSTGLANLGGTNAESVRYNQPRDMLVLDLVALFPSSYD 279

Db 190 YYERQVERTRDYSYCVIEWYNTGLNSLRGTNAASWRINQFRDLTLGVDLVALFPSSYD 249

QY 280 TQMPYIKTTAQLTREYVYTDAGTGVHPHPSFTTWTYNNNAPSFAIEAAVVRNPHLLDFL 339

Db 250 TRTYPINTSAQLTREYVYTDAGT--GVNMAWMYNNNAPSFAIEAAIRSPHLLDFL 307

QY 340 EQVTIYSLRSWSNTQYMMWCHLEKLEPRTIGTINISQSGTNTSINPVTLPFTSRDYY 399

Db 308 EQLTIFSSASSRWSNTRHMTYWRGHTIQSRPIGGGLNTSHGATNTSINPVTURFASRDYY 367

QY 400 RTESLAGLNLF--LTQPVNGVPRVDFHMKFVTHP-----IASDNFYYPGVYVIGTQLQDS 452

Db 368 RTESYAGVLLWGLYLEPIHGVTVRNF---TNPQNISDRGTANYSQP-YESPGQLKDS 423

QY 453 ENELPPEATGQPNYESYSHRLSHIGLISASHVKALVYSWTHRSADRTNIENSTIQIPL 512

Db 424 ETELPPETTERPNEYSYSHRLSHIGILQSRVNVFVYSWTHRSADRTNIGNRTIQIPM 483

QY 513 VKAFNLSSGAAVVRGPGFTGGDILRRNTGTGDIRVNIINPPFAQRYRVRIRYASTDLQ 572

Db 484 VKASELPQGTTVVRGPGFTGGDILRRNTGTGDIRVNIINPPFAQRYRVRIRYASTVDFD 543

QY 573 PHTSINGKAINQGNFSATVNRGEDLDYKTRFVTVGTFPTSPFDLDVQSTFTTIGAWNPFSSGNE 632

Db 544 FVSVRGGTTVNNFRFLRTMNSGDELKYGNFVRRATFTPTFTQIQDIIRTSIQGLSGNGE 603

QY 633 VYIDRIEFYFVETVYEAEDYDESKAOKVYALFTSTNPRGLKTDVXDYHIDQVSNLVESLS 692

Db 604 VYIDKIEIIPVTATFEAYDLELRAQAVNALFTNPRKLDVTDYHIDQVSNLVACL 663

QY 693 DEFYLDKEKLELFEIVKYAKQLHIERNM 719

Db 664 DEFCLDEKLELKVYAKRLSDERNL 690

RESULT 8

US-10-428-961-63

; Sequence 63, Application US/10428961

; Publication No. US20030237111A1

GENERAL INFORMATION:

; APPLICANT: Baum, James A.

; APPLICANT: Chu, Chih-Rei

; APPLICANT: Donovan, William P.

; APPLICANT: Gilmer, Amy J.

; APPLICANT: Rupar, Mark J.

; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin

; FILE REFERENCE: MECO201--1

; CURRENT APPLICATION NUMBER: US/10/428,961

; CURRENT FILING DATE: 2003-05-02

; PRIOR APPLICATION NUMBER: 09/661,322

; PRIOR FILING DATE: 2000-09-13

; PRIOR APPLICATION NUMBER: 60/153,995

; PRIOR FILING DATE: 1999-09-15

; NUMBER OF SEQ ID NOS: 63

; SOFTWARE: Patent in version 3.2

; SEQ ID NO 63

; LENGTH: 1227

; TYPE: PRT

; ORGANISM: Bacillus thuringiensis

US-10-428-961-63

Query Match 58.2%; Score 2186.5; DB 14; Length 1227;

Best Local Similarity 59.2%; Pred. No. 4.3e-175;

Matches 423; Conservative 105; Mismatches 173; Indels 13; Gaps 3;

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QY 13 SSNAKVDKISTDSLKN-----ETDIELQINIHEDCLMKSEYENVEPVFSASTIQTGIG 65
DB 7 NENEINAIISIPAVSHSQAOMLSTDAI-----EDSLCIAEGNNIDPFVSASTVQTGIN 61
QY 66 IAGKILGTGVFPAGQVASYFLIGELWPKGNQWEIEMEHVEEIIINOKISTYARNKAL 125
DB 62 IAGRILGLVGVFPAGQVASYFLIGELWPKGNQWEIEMEHVEEIIINOKISTYARNKAL 121
QY 126 TDLKGLGDALAVYHDSLESWGNRNTRARSVVKSOYIALELMFVQKLPSPAVSGSEVPL 185
DB 122 ARLOGGNGSFRAQQSLEDWENRDARTSRVLYTQYIALELDFNAMPLFAIRNQEVEPL 181
QY 186 LPIYAQAANLHLLLRDASIFGKEMGLSSSEISTFYNQVERAGDYSYDCHVKWYSTGLNN 245
DB 182 LMVYAQAANLHLLLRDASIFGSEFGLTSQEIQRVYERQVETREYSDYCARWYNTGLNN 241
QY 246 LRGTHAESVVRYNQPRDMTLMVLDFVALFPSYDTQMYPIKTTAQLTREYVTDAGTGVHP 305
DB 242 LRGTHAESVVRYNQPRDMTLMVLDFVALFPSYDTQMYPIKTTAQLTREYVTDAGTGVHP 301
QY 306 HPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMMGGHKL 365
DB 302 PSGFASSTWNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMMGGHKL 361
QY 366 EPTTIGTGLNISTQGSTNTSINPVLPTSRDYRTESLAGNLFLTOPVNGVPRVDHFW 425
DB 362 ESRTIRGSLSTHGTNTSINPVLPTSRDYRTESLAGNLFLTOPVNGVPRVDHFW 421
QY 426 KFTVPIASDNFYCYGVIGITQLODSENELPPEATGPNYESYSHRLSHGLISASHVK 485
DB 422 RNPNSLRGSLLYTIGYGVGTQDFSETELPETTERPNYESYSHRLSNILISGNTLR 481
QY 486 ALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVRGPGTGGDIIRNTWTFG 545
DB 482 APVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVRGPGTGGDIIRNTWTFG 541
QY 546 DIRVNIINPPFAQRYRIRYASITDLOPHTSINGKALINQGNFSAATMRGEBLDYKTRTV 605
DB 542 SMGLFNNTSLQRYRVRVRYAASQTMVLVTVGGSTTFDQGFPSMSANESLTSQSFRFA 601
QY 606 GFTTFFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQKVTAFT 665
DB 602 EPPVGISASGSQ-TAGISISNNAGRQTPHFDKIEPIPATLEABSDLERAKAVNALFT 660
QY 666 STNPRGLKTDVXDYHIDQVSNLVSLSDEFYLDKRELEFEIVKYAKOLHIERNM 719
DB 661 NTNPRRLKGTVDYDHYHIDEVSNLVACLSEDFCLDEKRELEFEIVKYAKOLHIERNM 714

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## RESULT 9

```

US-09-826-660-23
; Sequence 23, Application US/09826660
; Patent No. US20010026940A1
; GENERAL INFORMATION:
; APPLICANT: Cardineau, Guy A.
; APPLICANT: Stelman, Steven J.
; APPLICANT: Narva, Kenneth E.
; TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins
; CURRENT FILING DATE: 2001-04-05
; CURRENT APPLICATION NUMBER: US/09/826,660
; PRIOR APPLICATION NUMBER: 09/178,252
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: 60/065,215
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/076,445
; PRIOR FILING DATE: 1998-03-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 23
; LENGTH: 1186
; TYPE: PRT
; ORGANISM: Artificial Sequence

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; FEATURE:
; OTHER INFORMATION: Toxin encoded by synthetic B.t. gene
US-09-826-660-23

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Query Match 57.8%; Score 2171.5; DB 9; Length 1186;
Best Local Similarity 59.0%; Pred. No. 7.5e-174;
Matches 421; Conservative 108; Mismatches 172; Indels 13; Gaps 3;

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QY 13 SSNAKVDKISTDSLKN-----ETDIELQINIHEDCLMKSEYENVEPVFSASTIQTGIG 65
DB 7 NENEINAIISIPAVSHSQAOMLSTDAI-----EDSLCIAEGNNIDPFVSASTVQTGIN 61
QY 66 IAGKILGTGVFPAGQVASYFLIGELWPKGNQWEIEMEHVEEIIINOKISTYARNKAL 125
DB 62 IAGRILGLVGVFPAGQVASYFLIGELWPKGNQWEIEMEHVEEIIINOKISTYARNKAL 121
QY 126 TDLKGLGDALAVYHDSLESWGNRNTRARSVVKSOYIALELMFVQKLPSPAVSGSEVPL 185
DB 122 ARLOGGNGSFRAQQSLEDWENRDARTSRVLYTQYIALELDFNAMPLFAIRNQEVEPL 181
QY 186 LPIYAQAANLHLLLRDASIFGKEMGLSSSEISTFYNQVERAGDYSYDCHVKWYSTGLNN 245
DB 182 LMVYAQAANLHLLLRDASIFGSEFGLTSQEIQRVYERQVETREYSDYCARWYNTGLNN 241
QY 246 LRGTHAESVVRYNQPRDMTLMVLDFVALFPSYDTQMYPIKTTAQLTREYVTDAGTGVHP 305
DB 242 LRGTHAESVVRYNQPRDMTLMVLDFVALFPSYDTQMYPIKTTAQLTREYVTDAGTGVHP 301
QY 306 HPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMMGGHKL 365
DB 302 PSGFASSTWNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMMGGHKL 361
QY 366 EPTTIGTGLNISTQGSTNTSINPVLPTSRDYRTESLAGNLFLTOPVNGVPRVDHFW 425
DB 362 ESRTIRGSLSTHGTNTSINPVLPTSRDYRTESLAGNLFLTOPVNGVPRVDHFW 421
QY 426 KFTVPIASDNFYCYGVIGITQLODSENELPPEATGPNYESYSHRLSHGLISASHVK 485
DB 422 RNPNSLRGSLLYTIGYGVGTQDFSETELPETTERPNYESYSHRLSNILISGNTLR 481
QY 486 ALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVRGPGTGGDIIRNTWTFG 545
DB 482 APVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVRGPGTGGDIIRNTWTFG 541
QY 546 DIRVNIINPPFAQRYRIRYASITDLOPHTSINGKALINQGNFSAATMRGEBLDYKTRTV 605
DB 542 SMGLFNNTSLQRYRVRVRYAASQTMVLVTVGGSTTFDQGFPSMSANESLTSQSFRFA 601
QY 606 GFTTFFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQKVTAFT 665
DB 602 EPPVGISASGSQ-TAGISISNNAGRQTPHFDKIEPIPATLEABSDLERAKAVNALFT 660
QY 666 STNPRGLKTDVXDYHIDQVSNLVSLSDEFYLDKRELEFEIVKYAKOLHIERNM 719
DB 661 SSNQIGLKTVDYDHYHIDEVSNLVACLSEDFCLDEKRELEFEIVKYAKOLHIERNM 714

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## RESULT 10

```

US-10-428-961-38
; Sequence 38, Application US/10428961
; Publication No. US20030237111A1
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Chu, Chih-Rei
; APPLICANT: Donovan, William P.
; APPLICANT: Gilmer, Amy J.
; APPLICANT: Rupaar, Mark J.
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin
; FILE REFERENCE: Polynucleotides, Compositions, and Methods of Use (Amended)
; CURRENT FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: 09/661,322

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; PRIOR FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: 60/153,995
; PRIOR FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 38
; LENGTH: 1228
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-428-961-38

Query Match      56.2%; Score 2115; DB 14; Length 1228;
Best Local Similarity 59.5%; Pred. No. 4.7e-169;
Matches 424; Conservative 98; Mismatches 181; Indels 10; Gaps 7;

QY 13 SNAKVDKISTDSLNK-ETDIELQ-NINHEDCMKSEYENVEPVSASTIQTGIGIAGKI 70
DB 7 NENEINALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGINIAGRI 66
QY 71 LGTLGVFPAGOVASLYSFLGELWPKGNQWEIFMEHVEEIIINQISTYARNKALTDLKG 130
DB 67 LGVLGVFPAGQIASFYSLVGLWPRGRDQWEIFLEHVEQLINQITENARNALALAQ 126
QY 131 LGDALAVYHDSLESWGNRNTRARSVKQYIALELMFVQKLPSPAVSGEEVPLPIYA 190
DB 127 LGDSFRAYQQSLEDWLENRDDARTRSVLYTQYIALELDFLNAMPLFAIRNQEVPLLMVYA 186
QY 191 QAAHLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWYSTGLNNLRGTN 250
DB 187 QAAHLHLLLRDASIFGSEFGLTQEIQRYEYERQVEQTRDYSDYCVWYNTGLNSLRGTN 246
QY 251 AESWRYNQFRDMTLMVLVDLVALPSPYDTQMPYIKTTAQLTRVYTDATGTVHPHPSFT 310
DB 247 AASWRYNQFRDMLTGLVDLVALPSPYDTRTPINTSAQLTRVYTDATGAT--GVNMA 304
QY 311 STTWYNNAPSFAIEAAVVRNPHLLDLEQVITYSLSRWSNTQYMMWGGHKLERTI 370
DB 305 SMWYNNAPSFAIETAVIRSPHLLDLEQVITYSLSRWSATRHMTYWRGHTIQSRPI 364
QY 371 GGTINISQTGNTSINPVLTPFTSRDVRPESLAGNLF--LTQPVNGVPRVDFHWKFV 428
DB 365 GGLNTSTHGTNTSINPVLSPFSRDVYVWTSYAGVLLWGIYLEPIHGVPTRFNRNP 424
QY 429 --THPIASDNFYPGYVIGTQLODSENELPPEATGQPNYESYHRLSHIGLISASHVKA 486
DB 484 PYSWTHRSADRTNITSSDSITQIPLVKSFNLSGTSVVGSGFTGGDIIRTNVNGSVLS 543
QY 547 IRVNIINPPFAQRYVRIRYASTTDLOFHTSINGKAINQGNFSAATMNRGEBLDYKFTFTVG 606
DB 544 MGLNFNTSLQRYVRVRYAASQTMVLRTVVGSTTFDQGFPTMSANESLTSQSFRFAE 603
QY 607 FTTFPFLDVQSTTTIGAWNFSSGNEVYIDRIEFPVVEVTEAEYDEKAEQKVLTALFTS 666
DB 604 FPVGISAGSQ--TAGISISNAGSQTHFDKIEFIPITAFEAEDYDLERAQEAVALFTN 662
QY 667 TNPRGLKTDVXDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719
DB 663 TNPRRLKTDVTDYHIDQVSNLVACLSDSEFCLEKRELLEKVKYAKRLSDERNL 715

RESULT 11
US-10-614-524-2
; Sequence 2, Application US/10614524
; Publication No. US20040016020A1
; GENERAL INFORMATION:
; APPLICANT: Arnaut, Greta
; APPLICANT: Boets, Annemie
; APPLICANT: Daume, Nicole
; APPLICANT: Mathieu, Eva

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; APPLICANT: Vanneste, Stijn
; APPLICANT: Van Rie, Jeroen
; TITLE OF INVENTION: Insecticidal proteins from Bacillus thuringiensis.
; FILE REFERENCE: NEWBTSUS2
; CURRENT APPLICATION NUMBER: US/10/614,524
; CURRENT FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: US/09/739,243
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/173387
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1228
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-614-524-2

Query Match      56.2%; Score 2115; DB 15; Length 1228;
Best Local Similarity 59.5%; Pred. No. 4.7e-169;
Matches 424; Conservative 98; Mismatches 181; Indels 10; Gaps 7;

QY 13 SNAKVDKISTDSLNK-ETDIELQ-NINHEDCMKSEYENVEPVSASTIQTGIGIAGKI 70
DB 7 NENEINALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGINIAGRI 66
QY 71 LGTLGVFPAGOVASLYSFLGELWPKGNQWEIFMEHVEEIIINQISTYARNKALTDLKG 130
DB 67 LGVLGVFPAGQIASFYSLVGLWPRGRDQWEIFLEHVEQLINQITENARNALALAQ 126
QY 131 LGDALAVYHDSLESWGNRNTRARSVKQYIALELMFVQKLPSPAVSGEEVPLPIYA 190
DB 127 LGDSFRAYQQSLEDWLENRDDARTRSVLYTQYIALELDFLNAMPLFAIRNQEVPLLMVYA 186
QY 191 QAAHLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWYSTGLNNLRGTN 250
DB 187 QAAHLHLLLRDASIFGSEFGLTQEIQRYEYERQVEQTRDYSDYCVWYNTGLNSLRGTN 246
QY 251 AESWRYNQFRDMTLMVLVDLVALPSPYDTQMPYIKTTAQLTRVYTDATGTVHPHPSFT 310
DB 247 AASWRYNQFRDMLTGLVDLVALPSPYDTRTPINTSAQLTRVYTDATGAT--GVNMA 304
QY 311 STTWYNNAPSFAIEAAVVRNPHLLDLEQVITYSLSRWSNTQYMMWGGHKLERTI 370
DB 305 SMWYNNAPSFAIETAVIRSPHLLDLEQVITYSLSRWSATRHMTYWRGHTIQSRPI 364
QY 371 GGTINISQTGNTSINPVLTPFTSRDVRPESLAGNLF--LTQPVNGVPRVDFHWKFV 428
DB 365 GGLNTSTHGTNTSINPVLSPFSRDVYVWTSYAGVLLWGIYLEPIHGVPTRFNRNP 424
QY 429 --THPIASDNFYPGYVIGTQLODSENELPPEATGQPNYESYHRLSHIGLISASHVKA 486
DB 484 PYSWTHRSADRTNITSSDSITQIPLVKSFNLSGTSVVGSGFTGGDIIRTNVNGSVLS 543
QY 547 IRVNIINPPFAQRYVRIRYASTTDLOFHTSINGKAINQGNFSAATMNRGEBLDYKFTFTVG 606
DB 544 MGLNFNTSLQRYVRVRYAASQTMVLRTVVGSTTFDQGFPTMSANESLTSQSFRFAE 603
QY 607 FTTFPFLDVQSTTTIGAWNFSSGNEVYIDRIEFPVVEVTEAEYDEKAEQKVLTALFTS 666
DB 604 FPVGISAGSQ--TAGISISNAGSQTHFDKIEFIPITAFEAEDYDLERAQEAVALFTN 662
QY 667 TNPRGLKTDVXDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719
DB 663 TNPRRLKTDVTDYHIDQVSNLVACLSDSEFCLEKRELLEKVKYAKRLSDERNL 715

RESULT 12
US-09-826-660-25

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Qy	628	SSGNEVYIDRIEVPVVEVYIYEAEDYDEKAQEKVTALFTSTNPRGLKTDVKDTHIDQVSM	687
Db	650	ASGGEYVVDKFEIIPYNATFEABEDLDVAKAVNGLFTSKD-ALQTSVTDYQVQAANL	708
Qy	688	VESLSDEFFYLDKRELFIEIVKYAKQLHIERNM	719
Db	709	VECLSDELYNEKXGMLNDVAKKRLVQARNL	740
<p>RESULT 14</p> <p>US-10-428-961-6</p> <p>; Sequence 6, Application US/10428961</p> <p>; Publication No. US20030237111A1</p> <p>; GENERAL INFORMATION:</p> <p>; APPLICANT: Baum, James A.</p> <p>; APPLICANT: Cru, Chih-Rei</p> <p>; APPLICANT: Donovan, William P.</p> <p>; APPLICANT: Gilmer, Amy J.</p> <p>; APPLICANT: Rupar, Mark J.</p> <p>; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin</p> <p>; FILE REFERENCE: WCO201--1</p> <p>; CURRENT APPLICATION NUMBER: US/10/428,961</p> <p>; CURRENT FILING DATE: 2003-05-02</p> <p>; PRIOR APPLICATION NUMBER: 09/661,322</p> <p>; PRIOR FILING DATE: 2000-09-13</p> <p>; PRIOR APPLICATION NUMBER: 60/153,995</p> <p>; PRIOR FILING DATE: 1999-09-15</p> <p>; NUMBER OF SEQ ID NOS: 63</p> <p>; SOFTWARE: Patent in version 3.2</p> <p>; SEQ ID NO 6</p> <p>; LENGTH: 853</p> <p>; TYPE: PRT</p> <p>; ORGANISM: Bacillus thuringiensis</p> <p>US-10-428-961-6</p>			
<p>Query Match 44.7%; Score 1680.5; DB 14; Length 653;</p> <p>Best Local Similarity 51.5%; Pred. No. 9.2e-133;</p> <p>Matches 346; Conservative 106; Mismatches 173; Indels 47; Gaps 14;</p>			
Qy	13	SSNAKVDKISTDSLKN---ETDIELQININHEOCLKMEYENVEPPFVSASTIOTGICLACK	69
Db	2	NENEINAIUSIPAVSNHSAQMDLST-DARIESLCAEAGNNINPLVSASTVQTGINIAGR	60
Qy	70	ILGTGLVPPAGQVASYSTILGLBWPKGRKNQWEIFMEHVEEIIINQKISTYARNKALTDLK	129
Db	61	ILGLVPPAGQALSFYSFLVGLWPSGRDPNEIFLEYVEQLIRQQVTTENTALTARLE	120
Qy	130	GLGDALAVHDSLESWGVRNNVTRASRVKSVIALELMFVOKLSPFVSGREVPIILYIY	189
Db	121	GLGRGYRSQQALLETWLDNRNDARSIIILERYVALELDITTAIPLFIRNREEVFLLMVY	180
Qy	190	AQAANLHLLLRDASIFGKEWGLSSSEISTFTYNRQVERAGDYSCHCKWYSTGLANLRGT	249
Db	181	AQAANLHLLLRDASIFGSEWGNASSDVNQYQEQIRYEEVSNHCQVWYNTGLANLRGT	240
Qy	250	NASGWRVYNQFRDMTLMVLDLVALPSSYDTQNYPIKTTAQTREVTYDALTGVHPHPSF	309
Db	241	NASSWLRYNQFRDRLTLGLVLDLVALPSSYDTRYPINTSAQTLREIYTDPIGRTNAPSGF	300
Qy	310	TSITWNNNAPSATAEAAVVRPHLLDLFLEQVTIYSLLSRNSNTCYNNWGGHKLERT	369
Db	301	ASTNWNNNAPSATAEAAIFRPHLLDPPEQTIYSSASSRWSSTQHMYWVGHRLNFRP	360
Qy	370	IGGTLNISTQGST-NTSINPVLTFP-TSRDVTYTESLAGLNLFLLTPQVNGVPRVDFWKPF	427
Db	361	IGGTLNTSTQGLTNNTSINPVLTHYVSSRDVYRTESNAGTNILFTTPVNGVDPWARFN--F	418
Qy	428	VTHPIASDNFYYP-----GVVGIGTQLQDSENELPPEATGCPNYSYSRHLSHIG---	477
Db	419	ITLRIIFKKEAPLFTVNRIRBELGNYLIQKLNHQK-----QQNDQMNHIVIDISYR	470
Qy	478	LISASHVKALVYSWTHRSADRTNTIENPSGITOPLVKAENLSSGAAVVRGPGQFTGGDILR	537

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Db 471 LIIGTLAPVYSWTHRSADTNTIGNRITQIPAVKGRFLNG-SVIGSGPGETGDVVR 529
Qy 538 -RINTGTGTF---GDIRVNTN-BPFAQRVVRIRVASTTDLQFHTS-SINGKAINQGNFSAATWN 592
Db 530 LNRNNGNIQRCYIEVPQFTSTSTRYKRVRYASVTSIELNVNLGNSSIFTNTLPAATA 589
Qy 593 REDLDYKTRVGTGTTTFSELDVQSFT-----IGANFSSGNEWYIDRFEVPVEVT 646
Db 590 SLDNLQ-----SGDFGYEINNAFTSATGNIVGARNFASANAEBIIDRPEFIPVTAT 640
Qy 647 YEAEYDFEKAQE 658
Db 641 FEVEYDLREAQK 652

RESULT 15
US-10-782-141-16
; Sequence 16, Application US/10782141
; Publication No. US20040197917A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Kozziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and
; FILE REFERENCE: 045600/274143
; CURRENT APPLICATION NUMBER: US/10/782,141
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: 60/448,632
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 1157
; TYPE: PR1
; ORGANISM: Bacillus thuringiensis
US-10-782-141-16

Query Match 44.4%; Score 1669.5; DB 17; Length 1157;
Best Local Similarity 49.1%; Pred. No. 1.9e-131;
Matches 371; Conservative 98; Mismatches 230; Indels 57; Gaps 18

Qy 1 MKLKQDQKHQSFSSNAKVDKLSTDS---LKNETDTELQNHEDCLKMSEYE-----N 50
Db 1 MFPNQNEYEIDATPST-SYSSDSNPYPFANEPTDALQNMNYKDYLKMSGGGENPELFGN 59
Qy 51 VEPFVSASTIQTIGIAGKILGTGVFPAGQVASLYSFILGELWP-KGKNQWEI FMEHVE 109
Db 60 PETTFSSSTIQTIGIVGRILGALGVFPAQIASFFSVFVGLWPSKSVDIWGEINERVE 119
Qy 110 EFINOKISTYARKALTDKGLGDALAVYHDSLESWGNRNNTRASVVKVSQVIALELMF 169
Db 120 ELVDQKIEKYKDKALABKGLGNALDVYQOCSLEDLENRENDRARTSVVSNQFIALDLNF 179
Qy 170 VQKLPSFVSGSEVEPLLPIYAAQANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAG 229
Db 180 VSSIFSFVSGHEVULLIAYAAQANLHLLLRDASIFGEWGTPEISRFYNRQVQLTA 239
Qy 230 DYSDDCHVKWYSTGLNLEGTNWAEWRYNQFRDMTLMVLDLVALPFSYDTQWYPIKTTA 289
Db 240 EYSDYCVKWYKIGLDKLGKGTTSKSWLNHYQFRREMTLLDLVALFPNTDTHMYPJETTA 299
Qy 290 QLTREVTDAIGTVHPHSPST---TWYNNNAPSFSAEAAVVRNPHLLDPLEQVITY 345
Db 300 QLTDRVYTDPIA----FNIVTSTGFCNPWTHSGILFYEYENVNVRPPLHFDLSSVEIN 355
Qy 346 SLLSR-----WNGTQVMNMGHKLFR-----TIGTGLNISTOGSTNWSINPVTLPTFSR 396
Db 356 T--SRGGITLNDAYINWYSGHTLUKRYTADSTVYTYANYGRITSEKNS-----PALEDR 408

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QY	397	DVYRTESLAGLNFLTQPVNGVPRVDFHWKFVTHPIASDNFY-----YPGYVVGIGTQLOD	451
Db	409	DIFEINSTVANLANYYQKAYGVPQSWFH--VKRGTSSTTAYLYSKTHLTALQGC-TQVYE	465
QY	452	SENELPPEATQOPNYESYSHRLSHI-----GLISASHVKALVYSWTHRSADRTNIE	503
Db	466	SSDEIFLDRT-VPVAESYSHRLSHITSHSPKNG--SAYYGSFFVFWVWTHTSADLNNTIY	522
QY	504	PNSTIQIPLVKAFLSSGAUVVRGPGFTGGDILRRNTGTGDIRVNVINPPFAQRYRVRI	563
Db	523	SDKITQIFAVKGDMLYLGSSVWQPGFTGGDILKXTPSILGTFAVTVNGSLSQRYRVRI	582
QY	564	RYASTDLOFHTSINGKAINQGNFSATMNRGEDLDYKTFRTVGTFTTTPPSFLDVOSTFTIG	623
Db	583	RYASTTDEEF-TLYLGDITIEKNRNFKNMDNGASLTETFKFASFTTDFQFRETQDKILLS	641
QY	624	AWNRSNGNEVYIDRTIEFVPVEVTEAEYDFEKAQKVTALFTSTNPRGLKTDVKDYHIDQ	683
Db	642	MGDFSQGEVYIDRTIEFVPVEVTEAEYDFEKAQKVTALFTSTNPRGLKTDVKDYHIDQ	700
QY	684	VSNLYESLSDEFYLDKRELFYVYKAKOLHIERNM	719
Db	701	AANLYECLSDDLYPNEKRLLPDAVREAKRLSGARNL	736

Search completed: October 28, 2004, 18:41:07  
 Job time : 70.6795 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 28, 2004, 18:06:07 ; Search time 22.3343 Seconds  
(without alignments)  
2134.948 Million cell updates/sec

Title: US-10-019-823B-57

Perfect score: 3760

Sequence: 1 MKLKNQKHQSPSSNAKVDK.....KRELFEIVKYAKQLHIERNM 719

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA.\*  
1: /cgn2\_6/ptodata/1/iaa/5A.COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5B.COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A.COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B.COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PTUS.COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3752	99.8	719	3	US-08-286-870A-8
2	3472.5	92.4	710	4	US-09-661-322A-42
3	3394	90.3	648	3	US-08-286-870A-4
4	3373	89.7	719	2	US-09-003-217-2
5	3368	89.6	719	3	US-09-218-942-2
6	2800	74.5	535	3	US-08-286-870A-6
7	2445.5	65.0	1229	1	US-08-100-709-4
8	2445.5	65.0	1229	1	US-08-176-865-4
9	2445.5	65.0	1229	1	US-08-474-038-4
10	2445.5	65.0	1229	2	US-08-779-046-4
11	2445.5	65.0	1229	2	US-08-881-340-4
12	2340.5	62.2	488	1	US-08-448-170-10
13	2340.5	62.2	488	3	US-08-961-803-10
14	2264.5	60.2	1207	1	US-07-951-715A-7
15	2264.5	60.2	1207	2	US-08-459-448A-7
16	2264.5	60.2	1207	3	US-08-459-595A-7
17	2264.5	60.2	1207	3	US-08-459-504B-7
18	2264.5	60.2	1207	3	US-08-459-444-7
19	2264.5	60.2	1207	3	US-09-053-549-8
20	2264.5	60.2	1207	3	US-09-547-422-7
21	2264.5	60.2	1207	4	US-09-988-462-7
22	2263.5	60.2	1227	3	US-09-053-549-2
23	2195.5	58.4	1227	1	US-08-448-170-8
24	2195.5	58.4	1227	3	US-08-961-803-9
25	2186.5	58.2	1227	4	US-09-661-322A-63
26	2171.5	57.8	1186	3	US-09-178-252-23
27	2171.5	57.8	1186	4	US-09-826-660-23

## ALIGNMENTS

### RESULT 1

US-08-286-870A-8

; Sequence 8, Application US/08286870A

; Patent No. 6063605

; GENERAL INFORMATION:

; APPLICANT: ELY, S

; APPLICANT: TAILOR, RH

; APPLICANT: TIPPETT, JM

; APPLICANT: BLENK, RG

; TITLE OF INVENTION: BACTERIAL GENES

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CUSHMAN DABBY & CUSHMAN

; ADDRESSEE: Intellectual Property Group of

; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP

; STREET: 1100 New York Avenue, N.W.

; CITY: Washington

; STATE: DC

; COUNTRY: USA

; ZIP: 20005-3918

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/286,870A

; FILING DATE: 05-AUG-1994

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/520228

; FILING DATE: 09-MAY-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: GB 8910624.9

; FILING DATE: 09-MAY-1989

; ATTORNEY/AGENT INFORMATION:

; NAME: PAUL N. KOKULIS

; REGISTRATION NUMBER: 16,773

; REFERENCE/DOCKET NUMBER: 70608/220720

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 861-3000

; TELEFAX: (202) 822-0944

; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 719 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-286-870A-8

Sequence 38, Appl  
Sequence 25, Appl  
Sequence 25, Appl  
Sequence 4, Appl  
Sequence 6, Appl  
Sequence 30, Appl  
Sequence 2, Appl  
Sequence 2, Appl  
Sequence 2, Appl  
Sequence 5, Appl  
Sequence 5, Appl  
Sequence 5, Appl  
Sequence 5, Appl  
Sequence 5, Appl  
Sequence 5, Appl  
Sequence 72, Appl  
Sequence 72, Appl

1228 4 US-09-661-322A-38  
56.2 1228 4 US-09-661-322A-38  
51.4 643 3 US-09-178-252-25  
51.4 643 4 US-09-826-660-25  
380 5 PCT-US91-02560-4  
653 4 US-09-661-322A-6  
44.7 653 1 US-07-876-280-30  
44.4 1157 1 US-07-812-180A-2  
44.4 1157 1 US-08-315-468-2  
44.4 1157 3 US-07-941-650A-2  
44.4 1157 1 US-08-257-999-2  
40.0 1176 1 US-08-532-547-5  
38 1494 39.7 1157 2 US-08-379-656B-5  
39 1494 39.7 1157 2 US-08-455-838-5  
40 1494 39.7 1157 3 US-09-019-809-5  
41 1494 39.7 1157 4 US-09-471-177-5  
42 1494 39.7 1157 4 US-09-220-806-5  
43 1494 39.7 1157 4 US-09-220-806-5  
44 1487.5 39.6 1156 3 US-09-002-285-72  
45 1487.5 39.6 1156 4 US-09-589-477-72

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Query Match          99.8%; Score 3752; DB 3; Length 719;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 717; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNEDTIELQNHEDCLKMSYENVPFVSASTI 60
DB 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNEDTIELQNHEDCLKMSYENVPFVSASTI 60

QY 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEIFMEHVBEIINQKISTYA 120
DB 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEIFMEHVBEIINQKISTYA 120

QY 121 RNKALTDLKGDLGALAVYHDSLESWGNRNNTRAASVVKSOYIALELMFVKLPSFAVSG 180
DB 121 RNKALTDLKGDLGALAVYHDSLESWGNRNNTRAASVVKSOYIALELMFVKLPSFAVSG 180

QY 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSCHCVKWS 240
DB 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSCHCVKWS 240

QY 241 TGLNLRGTNAESWRYNQFRDMLVLDLVALPSPYDTOMYPIKTTAQLTREYVTDAL 300
DB 241 TGLNLRGTNAESWRYNQFRDMLVLDLVALPSPYDTOMYPIKTTAQLTREYVTDAL 300

QY 301 GTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMMW 360
DB 301 GTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMMW 360

QY 361 GGHKLEFRITGTLNISTQGSTNTSINPVTLPFTSRDVRVRESLAGLNLFTQPVNGVPR 420
DB 361 GGHKLEFRITGTLNISTQGSTNTSINPVTLPFTSRDVRVRESLAGLNLFTQPVNGVPR 420

QY 421 VDFHWKFVTHPIASDNFYYPGVGIGTQDQSENELPPEATQPNYESYSHRLSHIGLIS 480
DB 421 VDFHWKFVTHPIASDNFYYPGVGIGTQDQSENELPPEATQPNYESYSHRLSHIGLIS 480

QY 481 ASHVKALVYSWTHRSADRTNTEPNSTIQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 540
DB 481 ASHVKALVYSWTHRSADRTNTEPNSTIQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 540

QY 541 TGTFGDIRVNIAPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLKY 600
DB 541 TGTFGDIRVNIAPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLKY 600

QY 601 TPTVGTFTPPFSLDVQSTFTIGANWFSNGNEVYIDRIEFVPEVTEYAEYDFEKAQEV 660
DB 601 TPTVGTFTPPFSLDVQSTFTIGANWFSNGNEVYIDRIEFVPEVTEYAEYDFEKAQEV 660

QY 661 TALFTSTNPRGLKTDVQYHIDQVSNLVESLSDPYLDEKRELFEIVKYAKQLHIERNM 719
DB 661 TALFTSTNPRGLKTDVQYHIDQVSNLVESLSDPYLDEKRELFEIVKYAKQLHIERNM 719

RESULT 2
US-09-661-322A-42
; Sequence 42, Application US/09661322A
; Patent No. 6593293
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Chu, Chih-Rei
; APPLICANT: Donovan, William P.
; APPLICANT: Gilmer, Amy J.
; APPLICANT: Rugar, Mark J.
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin Compos
; FILE REFERENCE: MEC0201
; CURRENT APPLICATION NUMBER: US/09/661,322A
; CURRENT FILING DATE: 2000-09-13
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 42
; LENGTH: 710
; TYPE: PRT

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; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (200)..(200)
; OTHER INFORMATION: No. 6593293-Coding
US-09-661-322A-42

Query Match          92.4%; Score 3472.5; DB 4; Length 710;
Best Local Similarity 92.4%; Pred. No. 1.8e-302;
Matches 664; Conservative 15; Mismatches 31; Indels 9; Gaps 1;

QY 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNEDTIELQNHEDCLKMSYENVPFVSASTI 60
DB 1 MKSKNQNMHQSLSNNAVDKNFTGSLNNTNTTELQNFH-----EGIEPPFVSASTI 51

QY 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEIFMEHVBEIINQKISTYA 120
DB 52 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGSQWEIFMEHVBEIINQKISTYA 111

QY 121 RNKALTDLKGDLGALAVYHDSLESWGNRNNTRAASVVKSOYIALELMFVKLPSFAVSG 180
DB 112 RNKALADLKGDLGALAVYHESLESMTENNTTSTRSVKSOYITLELMFVQSLPSFAVSG 171

QY 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSCHCVKWS 240
DB 172 BEVPLLPPIYAQAANLHLLLRDASIFGKXWGLSDSEISTFYNQSGKSEYSDHCXKWN 231

QY 241 TGLNLRGTNAESWRYNQFRDMLVLDLVALPSPYDTOMYPIKTTAQLTREYVTDAL 300
DB 232 TGLNRLMGNAESWRYNQFRDMLVLDLVALPSPYDTOMYPIKTTAQLTREYVTDAL 291

QY 301 GTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMMW 360
DB 292 GTVHPHPSFTSTWYNNAPSFSTIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMMW 351

QY 361 GGHKLEFRITGTLNISTQGSTNTSINPVTLPFTSRDVRVRESLAGLNLFTQPVNGVPR 420
DB 352 GGHKLEFRITGTLNISTQGSTNTSINPVTLPFTSRDVRVRESLAGLNLFTQPVNGVPR 411

QY 421 VDFHWKFVTHPIASDNFYYPGVGIGTQDQSENELPPEATQPNYESYSHRLSHIGLIS 480
DB 412 VDFHWKFVTHPIASDNFYYPGVGIGTQDQSENELPPEATQPNYESYSHRLSHIGLIS 471

QY 481 ASHVKALVYSWTHRSADRTNTEPNSTIQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 540
DB 472 ASHVKALVYSWTHRSADRTNTEPNSTIQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 531

QY 541 TGTFGDIRVNIAPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLKY 600
DB 532 TGTFGDIRVNIAPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLKY 591

QY 601 TPTVGTFTPPFSLDVQSTFTIGANWFSNGNEVYIDRIEFVPEVTEYAEYDFEKAQEV 660
DB 592 TPTVGTFTPPFSLDVQSTFTIGANWFSNGNEVYIDRIEFVPEVTEYAEYDFEKAQEV 651

QY 661 TALFTSTNPRGLKTDVQYHIDQVSNLVESLSDPYLDEKRELFEIVKYAKQLHIERNM 719
DB 652 TALFTSTNPRGLKTDVQYHIDQVSNLVESLSDPYLDEKRELFEIVKYAKQLHIERNM 710

RESULT 3
US-08-286-870A-4
; Sequence 4, Application US/08286870A
; Patent No. 6063605
; GENERAL INFORMATION:
; APPLICANT: Ely, S
; APPLICANT: Tailor, RH
; APPLICANT: Tippett, JM
; APPLICANT: Blenk, RG
; TITLE OF INVENTION: BACTERIAL GENES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DABBY & CUSHMAN

```

ADDRESSEE: Intellectual Property Group of  
ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP  
STREET: 1100 New York Avenue, N.W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3918  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/286,870A  
FILING DATE: 05-AUG-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/520228  
FILING DATE: 09-MAY-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 8910624.9  
FILING DATE: 09-MAY-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: PAUL N. KOKULIS  
REGISTRATION NUMBER: 16,773  
REFERENCE/DOCKET NUMBER: 70608/220720  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 861-3000  
TELEFAX: (202) 822-0944  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 648 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-286-870A-4

Query Match 90.3%; Score 3394; DB 3; Length 648;  
Best Local Similarity 99.8%; Pred. No. 1.8e-295;  
Matches 647; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	MKLKQKHOSFSSNAKVDKISTSLKNETDIELQINHEDCCLKMSEYENVEPVSASTI	60
Db	1	MKLKQKHOSFSSNAKVDKISTSLKNETDIELQINHEDCCLKMSEYENVEPVSASTI	60
Qy	61	QTGIGIAGKILGTGVFPAGQVASYLSFILGELMPKGNQWEIFMEHVEEIIINQKISTYA	120
Db	61	QTGIGIAGKILGTGVFPAGQVASYLSFILGELMPKGNQWEIFMEHVEEIIINQKISTYA	120
Qy	121	RNKALTDLKGIDALAVYHDSLESWVGNNRNNTRARSVVKSQYIALELMFYQKLPFAVSG	180
Db	121	RNKALTDLKGIDALAVYHDSLESWVGNNRNNTRARSVVKSQYIALELMFYQKLPFAVSG	180
Qy	181	EEVPLLPYQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSCHCKWYS	240
Db	181	EEVPLLPYQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSCHCKWYS	240
Qy	241	TGLNLRGTNAESWVRYNQFRDQMTLMDLVALFPSYDTQMPYKITTQALTRREVTDAI	300
Db	241	TGLNLRGTNAESWVRYNQFRDQMTLMDLVALFPSYDTQMPYKITTQALTRREVTDAI	300
Qy	301	GTVPHPFSFTTWNNAEFSFAIEAAVVRNPHLLDFLEQVITYSLLSKWSQYNNMW	360
Db	301	GTVPHPFSFTTWNNAEFSFAIEAAVVRNPHLLDFLEQVITYSLLSKWSQYNNMW	360
Qy	361	GGHKLERTTGGTGLNISTQSTNTSINPVTLPFTSRDVRTESLAGLNLELTPQVNGVPR	420
Db	361	GGHKLERTTGGTGLNISTQSTNTSINPVTLPFTSRDVRTESLAGLNLELTPQVNGVPR	420
Qy	421	VDPHKVFTHPIASDNFYPGYVIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS	480
Db	421	VDPHKVFTHPIASDNFYPGYVIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS	480

Qy	481	ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAUVVRGPGFTGGDILRRTN	540
Db	481	ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAUVVRGPGFTGGDILRRTN	540
Qy	541	TCTEGDIRVNIINPPFAQRVVRIRYASTTDLQFHSTINGKAINQGNFSAATNRGDDLDYK	600
Db	541	TCTEGDIRVNIINPPFAQRVVRIRYASTTDLQFHSTINGKAINQGNFSAATNRGDDLDYK	600
Qy	601	TERTVGFTTFFSFLDVQSTFTTIGAWNFSSGNEVYIDRIEFVEVEVTYE	648
Db	601	TERTVGFTTFFSFLDVQSTFTTIGAWNFSSGNEVYIDRIEFVEVEVTYE	648

## RESULT 4

US-09-003-217-2  
Sequence 2, Application US/09003217  
Patent No. 5986177  
GENERAL INFORMATION:  
APPLICANT: Osman, Yehia A.  
APPLICANT: Madkour, Magdy A.  
APPLICANT: Bulla, Lee A.  
TITLE OF INVENTION: BACILLUS THURINGIENSIS ISOLATES WITH  
TITLE OF INVENTION: BROAD SPECTRUM ACTIVITY  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: W. Murray Spruill (Alston & Bird, LLP)  
STREET: 3605 Glenwood Ave. Suite 310  
CITY: Raleigh  
STATE: NC  
COUNTRY: US  
ZIP: 27622  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/003,217  
FILING DATE:  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Spruill, W. Murray  
REGISTRATION NUMBER: 32,943  
REFERENCE/DOCKET NUMBER: 5718-3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 919 420 2202  
TELEFAX: 919 881 3175  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 719 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-003-217-2

Query Match 89.7%; Score 3373; DB 2; Length 719;  
Best Local Similarity 89.7%; Pred. No. 1.6e-293;  
Matches 645; Conservative 33; Mismatches 41; Indels 0; Gaps 0;

Qy	1	MKLKQKHOSFSSNAKVDKISTSLKNETDIELQINHEDCCLKMSEYENVEPVSASTI	60
Db	1	MKLKQKHOSFSSNAKVDKISTSLKNETDIELQINHEDCCLKMSEYENVEPVSASTI	60
Qy	61	QTGIGIAGKILGTGVFPAGQVASYLSFILGELMPKGNQWEIFMEHVEEIIINQKISTYA	120
Db	61	QTGIGIAGKILGTGVFPAGQVASYLSFILGELMPKGNQWEIFMEHVEEIIINQKISTYA	120
Qy	121	RNKALTDLKGIDALAVYHDSLESWVGNNRNNTRARSVVKSQYIALELMFYQKLPFAVSG	180
Db	121	RNKALTDLKGIDALAVYHDSLESWVGNNRNNTRARSVVKSQYIALELMFYQKLPFAVSG	180
Qy	181	EEVPLLPYQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSCHCKWYS	240

Db 181 EEVPLLPYQAQANLHLLLRDASIFKKNGLSASEISTFFYNROVERTRDYSYHCVKWN 240  
 Qy 241 TGLNLRGTNABSWRYNQPRDMLVLDVALFPPSYDVTOMYPIKTTAQLTREVYDAI 300  
 Db 241 TGLNLRGTNABSWRYNQPRDMLVLDVALFPPSYDVTOMYPIKTTAQLTREVYDAI 300  
 Qy 301 GTVHPHPTSTWYNNAPSAEAAVAVRNPHLLDFLEQVTIYSLLSRNSNTQYNNMW 360  
 Db 301 GTVHPHPTSTWYNNAPSAEAAVAVRNPHLLDFLEQVTIYSLLSRNSNTQYNNMW 360  
 Qy 361 GGHLEFRITGGTINISITQSGSTNTSINPVTLPTSDRDFYRTESWAGNLFLTQPVNGVPR 420  
 Db 361 GGHLEFRITGGTINISITQSGSTNTSINPVTLPTSDRDFYRTESWAGNLFLTQPVNGVPR 420  
 Qy 421 VDFHMKFVTHPIASDNFYVGVGIGTQLODSENELPEATGQPNYESYSHRLSHIGLIS 480  
 Db 421 VDFHMKFVTHPIASDNFYVGVGIGTQLODSENELPEATGQPNYESYSHRLSHIGLIS 480  
 Qy 481 ASHVKALVYSWTHRSADRNTIENPSITQIPLVKAFNLSSGAAVVRGPGFTGGHILRRTK 540  
 Db 481 ASHVKALVYSWTHRSADRNTIENPSITQIPLVKAFNLSSGAAVVRGPGFTGGHILRRTK 540  
 Qy 541 TGTGDIRVNIWNPFAQRYRVRIRVASTDLOFHTSINGKAINOGNFSATNMGEDLDYK 600  
 Db 541 TGTGDIRVNIWNPFAQRYRVRIRVASTDLOFHTSINGKAINOGNFSATNMGEDLDYK 600  
 Qy 601 TPTVGTFTTFFSFLDVQSTFTIGAMNFSGNEVVIDRIEFVPEVVEYAEYDFEKAQEKV 660  
 Db 601 TPTVGTFTTFFSFLDVQSTFTIGAMNFSGNEVVIDRIEFVPEVVEYAEYDFEKAQEKV 660  
 Qy 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVSDELYLDEKRELFEIVKYAKQIHIERNM 719  
 Db 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVSDELYLDEKRELFEIVKYAKQIHIERNM 719

RESULT 5  
 US-09-218-942-2  
 ; Sequence 2, Application US/09218942  
 ; Patent No. 6232439  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Osman, Yehia  
 ; TITLE OF INVENTION: Bacillus Thuringiensis Isolates with Broad Spectrum  
 ; FILE REFERENCE: Cyt/I  
 ; CURRENT APPLICATION NUMBER: US/09/218,942  
 ; CURRENT FILING DATE: 1998-12-22  
 ; EARLIER APPLICATION NUMBER: 60/035,361  
 ; EARLIER FILING DATE: 1997-01-10  
 ; EARLIER APPLICATION NUMBER: 09/003,217  
 ; EARLIER FILING DATE: 1998-01-06  
 ; NUMBER OF SEQ ID NOS: 2  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 2  
 ; LENGTH: 719  
 ; TYPE: PRF  
 ; ORGANISM: Bacillus thuringiensis  
 US-09-218-942-2

Query Match 89.6%; Score 3368; DB 3; Length 719;  
 Best Local Similarity 89.7%; Pred. No. 4.5e-293;  
 Matches 645; Conservative 33; Mismatches 41; Indels 0; Gaps 0;

Qy 1 MKLKNQDKHQSPSSNAKYDKISTDLKNETDIELQNHEDCLXKSEYENVEPVSASTI 60  
 Db 1 MKLKNPDKHQTLSSNAKYDKIATDSLKNETDIELKNMANNEDYLRMSEHESIDPVSASTI 60  
 Qy 61 QTGIGIAGKILGTLPVFPAGQVASYLSFILGELPKGXQWEIEMFHEVVEIINOKISTYA 120  
 Db 61 QTGIGIAGKILGTLPVFPFGQIASYLSFILGELPKGXQWEIEMFHEVVEIINOKISTYA 120  
 Qy 121 RNKALTDLKLGDALAVHDSLESWGNNRNTNRSVVKVQYIALELMFVQKLPFAVSG 180  
 Db 121 RNKALTDLKLGDALAVHDSLESWGNNRNTNRSVVKVQYIALELMFVQKLPFAVSG 180

Qy 181 EEVPLLPYQAQANLHLLLRDASIFKKNGLSASEISTFFYNROVERAGDYSHCHVKWYS 240  
 Db 181 EEVPLLPYQAQANLHLLLRDASIFKKNGLSASEISTFFYNROVEREDYSYHCVKWN 240  
 Qy 241 TGLNLRGTNABSWRYNQPRDMLVLDVALFPPSYDVTOMYPIKTTAQLTREVYDAI 300  
 Db 241 TGLNLRGTNABSWRYNQPRDMLVLDVALFPPSYDVTOMYPIKTTAQLTREVYDAI 300  
 Qy 301 GTVHPHPTSTWYNNAPSAEAAVAVRNPHLLDFLEQVTIYSLLSRNSNTQYNNMW 360  
 Db 301 GTVHPHPTSTWYNNAPSAEAAVAVRNPHLLDFLEQVTIYSLLSRNSNTQYNNMW 360  
 Qy 361 GGHLEFRITGGTINISITQSGSTNTSINPVTLPTSDRDFYRTESWAGNLFLTQPVNGVPR 420  
 Db 361 GGHLEFRITGGTINISITQSGSTNTSINPVTLPTSDRDFYRTESWAGNLFLTQPVNGVPR 420  
 Qy 421 VDFHMKFVTHPIASDNFYVGVGIGTQLODSENELPEATGQPNYESYSHRLSHIGLIS 480  
 Db 421 VDFHMKFVTHPIASDNFYVGVGIGTQLODSENELPEATGQPNYESYSHRLSHIGLIS 480  
 Qy 481 ASHVKALVYSWTHRSADRNTIENPSITQIPLVKAFNLSSGAAVVRGPGFTGGHILRRTK 540  
 Db 481 ASHVKALVYSWTHRSADRNTIENPSITQIPLVKAFNLSSGAAVVRGPGFTGGHILRRTK 540  
 Qy 541 TGTGDIRVNIWNPFAQRYRVRIRVASTDLOFHTSINGKAINOGNFSATNMGEDLDYK 600  
 Db 541 TGTGDIRVNIWNPFAQRYRVRIRVASTDLOFHTSINGKAINOGNFSATNMGEDLDYK 600  
 Qy 601 TPTVGTFTTFFSFLDVQSTFTIGAMNFSGNEVVIDRIEFVPEVVEYAEYDFEKAQEKV 660  
 Db 601 TPTVGTFTTFFSFLDVQSTFTIGAMNFSGNEVVIDRIEFVPEVVEYAEYDFEKAQEKV 660  
 Qy 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVSDELYLDEKRELFEIVKYAKQIHIERNM 719  
 Db 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVSDELYLDEKRELFEIVKYAKQIHIERNM 719

RESULT 6  
 US-08-286-870A-6  
 ; Sequence 6, Application US/08286870A  
 ; Patent No. 6063605  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ELY, S  
 ; APPLICANT: TAILOR, RH  
 ; APPLICANT: TIPPETT, JM  
 ; APPLICANT: BLENN, RG  
 ; TITLE OF INVENTION: BACTERIAL GENES  
 ; NUMBER OF SEQUENCES: 10  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: CUSHMAN DARBY & CUSHMAN  
 ; ADDRESSEE: Intellectual Property Group of  
 ; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP  
 ; STREET: 1100 New York Avenue, N.W.  
 ; CITY: Washington  
 ; STATE: DC  
 ; COUNTRY: USA  
 ; ZIP: 20005-3918  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/286,870A  
 ; FILING DATE: 05-AUG-1994  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/520228  
 ; FILING DATE: 09-MAY-1990  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: GB 8910624.9  
 ; FILING DATE: 09-MAY-1989



```
; ATTORNEY/AGENT INFORMATION:
; NAME: PAUL N. KOKULIS
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 70608/220720
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 535 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-286-870A-6

Query Match 74.5%; Score 2800; DB 3; Length 535;
Best Local Similarity 99.8%; Pred. No. 2.5e-242;
Matches 534; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKLNQDKHQSFSNAKVDKISTDSLKNQETDIELQINHEDCLKMSEYENVEPVSASTI 60
DB 1 MKLNQDKHQSFSNAKVDKISTDSLKNQETDIELQINHEDCLKMSEYENVEPVSASTI 60
QY 61 QTGIGIAGKILGTIGVPFAGQVASYLFIIGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
DB 61 QTGIGIAGKILGTIGVPFAGQVASYLFIIGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
QY 121 RNKALTDLKLGDALAVYHDSLSWGNNRNTARSVVKSQYIALELMFVKLPSPAVSG 180
DB 121 RNKALTDLKLGDALAVYHDSLSWGNNRNTARSVVKSQYIALELMFVKLPSPAVSG 180
QY 121 RNKALTDLKLGDALAVYHDSLSWGNNRNTARSVVKSQYIALELMFVKLPSPAVSG 180
DB 121 RNKALTDLKLGDALAVYHDSLSWGNNRNTARSVVKSQYIALELMFVKLPSPAVSG 180
QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSCHVKWYS 240
DB 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSCHVKWYS 240
QY 241 TGLNLRGTAESVVRNQRDMLVLDLVALFPSYDTQMPYIKTTAQLTREVTDAI 300
DB 241 TGLNLRGTAESVVRNQRDMLVLDLVALFPSYDTQMPYIKTTAQLTREVTDAI 300
QY 301 GTVHPHPSFTSTWYNNNAPSFAEAIAAVRNPHLLDFLEQVTIYSLSRWSNTQYMNW 360
DB 301 GTVHPHPSFTSTWYNNNAPSFAEAIAAVRNPHLLDFLEQVTIYSLSRWSNTQYMNW 360
QY 361 GGHKLEFRTTGGTINISQSTNTSINPVLPTFSDRDVYRTESLAGNLFLETPQVNGVR 420
DB 361 GGHKLEFRTTGGTINISQSTNTSINPVLPTFSDRDVYRTESLAGNLFLETPQVNGVR 420
QY 421 VDFHKKFWTHPIASDNFYGYGIGTQLODSENELPEATGQPNYESYSHRLSHGLIS 480
DB 421 VDFHKKFWTHPIASDNFYGYGIGTQLODSENELPEATGQPNYESYSHRLSHGLIS 480
QY 481 ASHKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDI 535
DB 481 ASHKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDI 535

RESULT 7
US-08-100-709-4
; Sequence 4, Application US/08100709
; Patent No. 5322687
; GENERAL INFORMATION:
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yuping
; APPLICANT: Jany, Christine S.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS cryET4 AND cryET5
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
; ADDRESSEE: Nadel
; STREET: 1601 Market Street, 36th Floor
; CITY: Philadelphia

; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/100,709
; FILING DATE: 19930729
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Egolf, Christopher
; REGISTRATION NUMBER: 27633
; REFERENCE/DOCKET NUMBER: 7205-49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 213-757-1590
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1229 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-100-709-4

Query Match 65.0%; Score 2445.5; DB 1; Length 1229;
Best Local Similarity 65.6%; Pred. No. 6.2e-210;
Matches 470; Conservative 92; Mismatches 138; Indels 17; Gaps 6;

QY 13 SSNAKVDKISTDSLKN-ETDIELQ-NINHEDCLKMSEYENVEPVSASTIQTGIGIAGKI 70
DB 7 NENEIINALSTPTVSNPSTOMNLSDPARIEDSLCAEVNNDIPFVSASTVQTGINIAGRI 66
QY 71 LCTLGVFPAGQVASYLFIIGELWPKGNQWEIFMEHVEEIIINQKISTYARNKALTDLKG 130
DB 67 LGVLGVFPAGQVASYLFIIGELWPKGNQWEIFMEHVEEIIINQKISTYARNKALTDLKG 126
QY 131 LGDALAVYHDSLSWGNNRNTARSVVKSQYIALELMFVKLPSPAVSGEVPPLPIYA 190
DB 127 LGRGYSYQQALETWLDNRNDARSRSIILERYVALELDITTAIPLFRIINEEVPPLMYA 186
QY 191 QAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSCHVKWYSGLNLRGN 250
DB 187 QAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSCHVKWYSGLNLRGN 246
QY 251 AESWRYNQFRDMTLMVLDLVALFPSYDTQMPYIKTTAQLTREVTDAIGTVHPHPSFT 310
DB 247 AESWRYNQFRDMTLMVLDLVALFPSYDTQMPYIKTTAQLTREVTDAIGTVHPHPSFT 306
QY 311 STWYNNNAPSFAEAIAAVRNPHLLDFLEQVTIYSLSRWSNTQYMNWGWGHKLEFRTI 370
DB 307 STWYNNNAPSFAEAIAAVRNPHLLDFLEQVTIYSLSRWSNTQYMNWGWGHKLEFRTI 366
QY 371 GGTLMNISTQGST-NTSINPVLPTFSDRDVYRTESLAGNLFLETPQVNGVPRVDFHKKFWT 429
DB 367 GGTLMNISTQGST-NTSINPVLPTFSDRDVYRTESLAGNLFLETPQVNGVPRVDFHKKFWT 422
QY 430 HPIASDNFYPG-----YVIGTQLODSENELPEATGQPNYESYSHRLSHGLISAS 482
DB 423 --INFQNIYERGATTSPYQGVIGLDFSELPETTERPNYESYSHRLSHGLISGLTGN 480
QY 483 HVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDI LRRTNIG 542
DB 481 TRAPVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDI LRRTNIG 540
QY 543 TFGDIRVNINPFAQYRVIRIYASTTDLQFHTSINGKAINOCNTSATNWRGEDIKYTF 602
DB 541 TFGDIRLNINVELSQRYRVIRIYASTTDLQFHTSINGKAINOCNTSATNWRGEDIKYTF 600
QY 603 RTVGFTTPPEFLDVOSTFTIGAWNSSGNEVYDRIEFVPEVTVYEAEDREKAQKVTA 662
DB 601 RTAGFTTPPEFLDVOSTFTIGAWNSSGNEVYDRIEFVPEVTVYEAEDREKAQKVTA 659
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QY 663 LFTSTNPRGLKTDVYDHYDQVNSLVESLSDBFYLDKRELFPEIVKYAKQLHIERNM 719
DB 660 LFTSTNPRGLKTDVYDHYDQVNSLVESLSDBFYLDKRELFPEIVKYAKQLHIERNM 716

RESULT 8
US-08-176-865-4
; Sequence 4, Application US/08176865
; Patent No. 5616319
; GENERAL INFORMATION:
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yiping
; APPLICANT: Jany, Christine S.
; APPLICANT: Gonzalez Jr., Jose M.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS CYET4 AND CYET5
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
; ADDRESSEE: Nadel
; STREET: 1601 Market Street, 36th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/176.865
; FILING DATE: 30-DEC-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/100,709
; FILING DATE: 29-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Egoif, Christopher
; REGISTRATION NUMBER: 27633
; REFERENCE/DOCKET NUMBER: 7205-49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-757-1590
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1229 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-176-865-4

Query Match 65.0%; Score 2445.5; DB 1; Length 1229;
Best Local Similarity 65.6%; Pred. No. 6.2e-210;
Matches 470; Conservative 92; Mismatches 138; Indels 17; Gaps 6;

QY 13 SSNAKVDAISDLSKN-ETDIELQ-NINHECLKMSEVENVEPVASSTCTGTGIGAKI 70
DB 7 NENELINALSIPTVSNPSTQNLSPDARIEDSLCVAEVNIDPPVASTVQTGINIAGRI 66
QY 71 LGTLGVPPAGVVASLYSPILGELWPKGNQWEIEMHEVEEILNQIKISTYARNKALTDLKG 130
DB 67 LGVLGVPPAGVVASLYSPILGELWPKGNQWEIEMHEVEEILNQIKISTYARNKALTDLKG 126
QY 131 LGDALAVYHDSLESWGNGNNTARSVVKSOYIALELMFVKQLSPAVSGEEVPLPIYA 190
DB 127 LGRGYSYQQAELTDLNDRARSILERYVALELDITTAIFLPIRNEEVPPLMYYA 186
QY 191 QAANLHULLLRDASIFGKRWGLSSSEISTFTYNQVERAGDYSDHCVKWYSTGLNNLRGTN 250
DB 187 QAANLHULLLRDASIFGSEWGMASDVNQYQEQIRYITEEYSHCVQYNTGLNNLRGTN 246
QY 251 AESWRYNQFRDRTMVLVDLVALFPSTYDQYPIKTAQLTREVYTDAGTVHPSFT 310

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DB 247 AESWLRYNQFRDRTMVLVDLVALFPSTYDQYPIKTAQLTREVYTDAGTVHPSFT 306
QY 311 STTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWNSNTQVMNMGHKLFRFTI 370
DB 307 STWNFNNAFSAIEAAIFRPPHLLDFPEQLTIYSASSRSWSSTQHMNYVWGHRLNFRPI 366
QY 371 GGTINISTOGST-NTSINDVTLPTSRDYYRRESLAGLNFLTPQVNGVPRVDPHKKFVT 429
DB 367 GGTINISTOGST-NTSINDVTLPTSRDYYRRESLAGLNFLTPQVNGVPRVDPHKKFVT 422
QY 430 HPIASDNFYYPG-----YVGIGITQLODSENELEPEATGQPNYESYSHRLSHIGLISAS 482
DB 423 --INPQNIYERGATTYQPYQGVGIQFSELELPETTERPNYESYSHRLSHIGLIIEN 480
QY 483 HVKALVYSTHRSADRTNTEIENSITQILVAFNLSSGAAVVRGPGFTGGDILRTNTG 542
DB 481 TLRAPYVSTHRSADRTNTEIENRITQILVAFNLSSGAAVVRGPGFTGGDILRTNTG 540
QY 543 TFGDIRVNPFPFAQRYRIRYASTTDLOFHTSNGKAINQCNFSATMNRGDEDLYKTF 602
DB 541 TFGDIRVNPFPFAQRYRIRYASTTDLOFHTSNGKAINQCNFSATMNRGDEDLYKTF 600
QY 603 RTVGFTTSPFSLDVOSTFTIGAMNPSGNEVYDRIEFVPEVTVYEAEDFKAQEKVTA 662
DB 601 RTAGFSTPFNFNAOSTFTLGAQSPSN-QEVYIDRVFVPAEVTFEAEYDLERAQKAVNA 659
QY 663 LFTSTNPRGLKTDVYDHYDQVNSLVESLSDBFYLDKRELFPEIVKYAKQLHIERNM 719
DB 660 LFTSTNPRGLKTDVYDHYDQVNSLVESLSDBFYLDKRELFPEIVKYAKQLHIERNM 716

RESULT 9
US-08-474-038-4
; Sequence 4, Application US/08474038
; Patent No. 5679343
; GENERAL INFORMATION:
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yiping
; APPLICANT: Jany, Christine S.
; APPLICANT: Gonzalez Jr., Jose M.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS CYET4 AND CYET5
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
; ADDRESSEE: Nadel
; STREET: 1601 Market Street, 36th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474.038
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/176,865
; FILING DATE: 30-DEC-1993
; APPLICATION NUMBER: US 08/100,709
; FILING DATE: 29-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Egoif, Christopher
; REGISTRATION NUMBER: 27633
; REFERENCE/DOCKET NUMBER: 7205-49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-757-1590
; INFORMATION FOR SEQ ID NO: 4:

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SEQUENCE CHARACTERISTICS:  
 LENGTH: 1229 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-474-038-4

Query Match 65.0%; Score 2445.5; DB 1; Length 1229;  
 Best Local Similarity 65.6%; Pred. No. 6.2e-210;  
 Matches 470; Conservative 92; Mismatches 138; Indels 17; Gaps 6;  
 QY 13 SSNAKVDKISTDLSKN-ETDIELQ-NINHEDCMKSEYENVEPFVASTIQTGIGIAGKI 70  
 DB 7 NENEIINALSIPTVSNPSTQMLSPDARIEDSLCVAEWNIDPFVASTVQTGINIAGRI 66  
 QY 71 LGTLGVFPAGQVASYLSFTLGEKWPKNQWEIFMEHVEEIIINQKISTYARNKALDILKG 130  
 DB 67 LGVLGVFPAGQVASYLSFTLGEKWPKNQWEIFMEHVEEIIINQKISTYARNKALDILKG 126  
 QY 131 LGDALAVYHDSLSWGNRNNTARSVKQYIALELMFVQKLPSPFAVSSEVPLPIYA 190  
 DB 127 LGRGYSYQQALETWLDNRNDARSIIILERYVALELDITTAIPLFRIRNEEVPLLMVYA 186  
 QY 191 QAAHLHLLLRDASIFGKESWGLSSSEISTFYNNRQVERAGDYSDHCVKWYSTGLNNLRGTN 250  
 DB 187 QAAHLHLLLRDASIFGKESWGLSSSEISTFYNNRQVERAGDYSDHCVKWYSTGLNNLRGTN 246  
 QY 251 AESSWVYNQFRDMTLMVLVDLVALPFSYDTQMPYKTTAQLTREVTYDAIGTVHPHPSFT 310  
 DB 247 AESSWVYNQFRDMTLMVLVDLVALPFSYDTQMPYKTTAQLTREVTYDAIGTVHPHPSFT 306  
 QY 311 STTWYNNAPSSAIEAAVVRNPHLLDPLEQVITYSLLSRWSTNTQVMNMGHKLFRFTI 370  
 DB 307 STTWYNNAPSSAIEAAVVRNPHLLDPLEQVITYSLLSRWSTNTQVMNMGHKLFRFTI 366  
 QY 371 GGTINISTQGST-NTSINPVTLPSTRDVRATESLAGNLFLTOPVNGVPRVDFPHKFTV 429  
 DB 367 GGTINISTQGST-NTSINPVTLPSTRDVRATESLAGNLFLTOPVNGVPRVDFPHKFTV 422  
 QY 430 HPIASDNFYYPG-----YVGIGTQLQDSSENLPEATQPNYESYSHLSHIGLISAS 482  
 DB 423 --INPQNIYERGATTYSQYQGVQQLFDSSETLPETTERPNYESYSHLSHIGLIGN 480  
 QY 483 HVKALVYSWTHRSADRTNTPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTNTG 542  
 DB 481 TLRAPIYSWTHRSADRTNTPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTNTG 540  
 QY 543 TFGDIRVNNPFPQRYRVRIRYASTTDLPHTSINGKAINQGNFSATMARGSDLDYKTF 602  
 DB 541 TFGDIRVNNPFPQRYRVRIRYASTTDLPHTSINGKAINQGNFSATMARGSDLDYKTF 600  
 QY 603 RTVGFTTTPFDVQSTFTIGAMNPFSSGNEVYIDRIEFVPEVTVYEAIEYFEKAQKVT 652  
 DB 601 RTAGFTTTPFDVQSTFTIGAMNPFSSGNEVYIDRIEFVPEVTVYEAIEYFEKAQKVT 659  
 QY 663 LFTSTNPRGLKTDYKDHIDQVSNLVESLSEDFEYLDKRELFETVKYAKOLHIERNM 719  
 DB 660 LFTSTNPRGLKTDYKDHIDQVSNLVESLSEDFEYLDKRELFETVKYAKOLHIERNM 716

RESULT 10  
 US-08-779-046-4  
 Sequence 4, Application US/08779046  
 Patent No. 5854053  
 GENERAL INFORMATION:  
 APPLICANT: Donovan, William P.  
 APPLICANT: Tan, Yiping  
 APPLICANT: Jan, Christine S.  
 APPLICANT: Gonzalez Jr., Jose M.  
 TITLE OF INVENTION: BACILLUS THURINGIENSIS ctyET4 AND ctyET5  
 TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS  
 NUMBER OF SEQUENCES: 5  
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.  
 ADDRESSEE: Nadel  
 STREET: 1601 Market Street, 36th Floor  
 City: Philadelphia  
 STATE: Pennsylvania  
 COUNTRY: U.S.A.  
 ZIP: 19103  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/779,046  
 FILING DATE: 06-JAN-1997  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/100,709  
 FILING DATE: 29-JUL-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Egolf, Christopher  
 REGISTRATION NUMBER: 27633  
 REFERENCE/DOCKET NUMBER: 7205-49  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 215-757-1590  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1229 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-779-046-4

Query Match 65.0%; Score 2445.5; DB 2; Length 1229;  
 Best Local Similarity 65.6%; Pred. No. 6.2e-210;  
 Matches 470; Conservative 92; Mismatches 138; Indels 17; Gaps 6;  
 QY 13 SSNAKVDKISTDLSKN-ETDIELQ-NINHEDCMKSEYENVEPFVASTIQTGIGIAGKI 70  
 DB 7 NENEIINALSIPTVSNPSTQMLSPDARIEDSLCVAEWNIDPFVASTVQTGINIAGRI 66  
 QY 71 LGTLGVFPAGQVASYLSFTLGEKWPKNQWEIFMEHVEEIIINQKISTYARNKALDILKG 130  
 DB 67 LGVLGVFPAGQVASYLSFTLGEKWPKNQWEIFMEHVEEIIINQKISTYARNKALDILKG 126  
 QY 131 LGDALAVYHDSLSWGNRNNTARSVKQYIALELMFVQKLPSPFAVSSEVPLPIYA 190  
 DB 127 LGRGYSYQQALETWLDNRNDARSIIILERYVALELDITTAIPLFRIRNEEVPLLMVYA 186  
 QY 191 QAAHLHLLLRDASIFGKESWGLSSSEISTFYNNRQVERAGDYSDHCVKWYSTGLNNLRGTN 250  
 DB 187 QAAHLHLLLRDASIFGKESWGLSSSEISTFYNNRQVERAGDYSDHCVKWYSTGLNNLRGTN 246  
 QY 251 AESSWVYNQFRDMTLMVLVDLVALPFSYDTQMPYKTTAQLTREVTYDAIGTVHPHPSFT 310  
 DB 247 AESSWVYNQFRDMTLMVLVDLVALPFSYDTQMPYKTTAQLTREVTYDAIGTVHPHPSFT 306  
 QY 311 STTWYNNAPSSAIEAAVVRNPHLLDPLEQVITYSLLSRWSTNTQVMNMGHKLFRFTI 370  
 DB 307 STTWYNNAPSSAIEAAVVRNPHLLDPLEQVITYSLLSRWSTNTQVMNMGHKLFRFTI 366  
 QY 371 GGTINISTQGST-NTSINPVTLPSTRDVRATESLAGNLFLTOPVNGVPRVDFPHKFTV 429  
 DB 367 GGTINISTQGST-NTSINPVTLPSTRDVRATESLAGNLFLTOPVNGVPRVDFPHKFTV 422  
 QY 430 HPIASDNFYYPG-----YVGIGTQLQDSSENLPEATQPNYESYSHLSHIGLISAS 482  
 DB 423 --INPQNIYERGATTYSQYQGVQQLFDSSETLPETTERPNYESYSHLSHIGLIGN 480  
 QY 483 HVKALVYSWTHRSADRTNTPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTNTG 542  
 DB 481 TLRAPIYSWTHRSADRTNTPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTNTG 540

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QY 543 TFGDIRVNPFAQRYRIRYASTTDLQFTSINGKAINQNSPATSATWNGEDLDYKTP 602
DB 541 TFGDIRVNPFAQRYRIRYASTTDLQFTSINGKAINQNSPATSATWNGEDLDYKTP 600
QY 603 RTVGFTTPPSFLDVOSTFTIGAWNFSSGNEVVIDRIEFVPEVVEVYAEYDEKAEKVTA 662
DB 601 RTAGSTPNFLNAQSTFTLGAQSFN QEVVIDRVEFPAEYFVTEAEYDLEKAEKVTA 659
QY 663 LFTSTNPRGLKTDVXDYHIDQVSNLVESLDSFYLDKREKLEFVYKAKQLHIERNM 719
DB 660 LFTSTNPRGLKTDVXDYHIDQVSNLVESLDSFYLDKREKLEFVYKAKQLHIERNM 716

RESULT 11
US-08-881-340-4
; Sequence 4, Application US/08881340
; Patent No. 5942658
; GENERAL INFORMATION:
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yaping
; APPLICANT: Jany, Christine S.
; APPLICANT: Gonzalez Jr., Jose M.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS CRYET4 AND CRYET5
; NUMBER OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
; ADDRESSES: Nadel
; STREET: 1601 Market Street, 36th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/881.340
; FILING DATE: 24-JUN-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/100,709
; FILING DATE: 29-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Egolf, Christopher
; REGISTRATION NUMBER: 27633
; REFERENCE/DOCKET NUMBER: 7205-49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-757-1590
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1229 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-881-340-4

Query Match 65.0%; Score 2445.5; DB 2; Length 1229;
Best Local Similarity 65.6%; Pred. No. 6.2e-210;
Matches 470; Conservative 92; Mismatches 138; Indels 17; Gaps 6;

QY 13 SSNAKVDKISLQK-ETDLEQ-NINHECLKMSYENVEPVASSTCTGTGIGAKI 70
DB 7 NENEINLSIPTVSPNTQNLSPDARIEDSLCAEVNNDPVSASTVQTGTGNIAGRI 66
QY 71 LGTLGVPPAGVVASLYSIFLGELWPKGNQWEIEMVEHEEINQKISTYARNKALTDLKG 130
DB 67 LGVLGVPPAGVVASLYSIFLGELWPKGNQWEIEMVEHEEINQKISTYARNKALTDLKG 126
QY 131 LGDALAVYHDSLESVWGNRNTARSVVKSYIALEMFVKQLSPFAVSGEEVPLPIYA 190
DB 131 LGDALAVYHDSLESVWGNRNTARSVVKSYIALEMFVKQLSPFAVSGEEVPLPIYA 190

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DB 127 LGRGYRSYQALLETWLDNRNDARSRIILERYVALELDITTAIPLFRIRNEEVPLLMVA 186
QY 191 QAANLHLLLRDASIFGKEMGLSSSEISTFYNRQVERAGDYSCHVKWYSTGLNNLRGTN 250
DB 187 QAANLHLLLRDASIFGSEWGMASDVQYQOIRYTEEYSHNCVQWINTGLNNLRGTN 246
QY 251 AESWVYNQFRDMTLMVLDLVALFPSYDTQMPYIKTAQLTREVYTDGICVTHPSPST 310
DB 247 AESWVYNQFRDMTLMVLDLVALFPSYDTQMPYIKTAQLTREVYTDGICVTHPSPST 306
QY 311 STWYNNAPSPSAIEAAVVRNPHLLDFLEQVITIYLLSRWSNTQVMNMGHKLFEFRII 370
DB 307 STWYNNAPSPSAIEAAVVRNPHLLDFLEQVITIYLLSRWSNTQVMNMGHKLFEFRII 366
QY 371 GGTINISTQGST-NTSINPVTLPFTSRDYRTESLAGLNLFLTQPVNGVPRVDFHWKFTV 429
DB 367 GGTINISTQGST-NTSINPVTLPFTSRDYRTESLAGLNLFLTQPVNGVPRVDFHWKFTV 422
QY 430 HPIASDNFYYPG-----YVGIGTOLQDSENEPPEATGQPNYESYSHRLSHIGLISAS 482
DB 423 --INPQNIYERGATTYSQYQVGLQDFSETELPPTTERPNYESYSHRLSHIGLIGN 480
QY 483 HVKALYVSWTHRSADRTNIENSTQIPLVKAFNLSSGAAVVRGPGFTGGDILRTWTG 542
DB 481 TLRAPYVSWTHRSADRTNIENSTQIPLVKAFNLSSGAAVVRGPGFTGGDILRTWTG 540
QY 543 TFGDIRVNPFAQRYRIRYASTTDLQFTSINGKAINQNSPATSATWNGEDLDYKTF 602
DB 541 TFGDIRVNPFAQRYRIRYASTTDLQFTSINGKAINQNSPATSATWNGEDLDYKTF 600
QY 603 RTVGFTTPPSFLDVOSTFTIGAWNFSSGNEVVIDRIEFVPEVVEVYAEYDEKAEKVTA 662
DB 601 RTAGSTPNFLNAQSTFTLGAQSFN QEVVIDRVEFPAEYFVTEAEYDLEKAEKVTA 659
QY 663 LFTSTNPRGLKTDVXDYHIDQVSNLVESLDSFYLDKREKLEFVYKAKQLHIERNM 719
DB 660 LFTSTNPRGLKTDVXDYHIDQVSNLVESLDSFYLDKREKLEFVYKAKQLHIERNM 716

RESULT 12
US-08-448-170-10
; Sequence 10, Application US/08448170
; Patent No. 5723758
; GENERAL INFORMATION:
; APPLICANT: Payne, Jewel
; APPLICANT: Cummings, David A.
; APPLICANT: Cannon, Raymond J.C.
; APPLICANT: Narva, Kenneth B.
; APPLICANT: Stelman, Steve
; TITLE OF INVENTION: No. 5723758el Bacillus thuringiensis Isolate Denoted
; TITLE OF INVENTION: B.t. PS158C2, Active Against Lepidopteran Pests, and Genes
; TITLE OF INVENTION: Encoding Lepidopteran-Active Toxins
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/448.170
; FILING DATE: 01-JUNE-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/069,902
; FILING DATE: 01-JUNE-1993
; CLASSIFICATION: 424

```

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/759,247  
FILING DATE: 13-SEPT-1991  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Saliwanchik, David R.  
REGISTRATION NUMBER: 31,794  
REFERENCE/DOCKET NUMBER: M/S 102D.C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (904) 375-8100  
TELEFAX: (904) 372-5800  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 488 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-448-170-10

Query Match 62.2%; Score 2340.5; DB 1; Length 488;  
Best Local Similarity 89.5%; Pred. No. 3.6e-201;  
Matches 445; Conservative 13; Mismatches 30; Indels 9; Gaps 1;  
QY 1 MRLKQDKHQSFSNAKVDKISTDSLKNETDIELQINHEHEDCLKMSYEYENVEPVSASTI 60  
DB 1 MRSKNQNMHQSLSNNAVDKNTGSLNNTINTELQNFH-----EGIEPFSVSTI 51  
QY 61 QTGIGIAGKILGTGVFFAGQVASYLFFILGELWPKGNQWEIFMEHVBEIINQKISTYA 120  
DB 52 QTGIGIVGKILGNLGVFFAGQVASYLFFILGELWPKGQWEIFMEHVBEIINQKISTYA 111  
QY 121 RNKALTDLKGDLALAVYHDSLESWGVRNNTRARSVVKSOYIALELMFVKLPSPAVSG 180  
DB 112 RNKALADLKGDLALAVYHESLESWIEENRNNTRFESVVKQYITLLELMFVQSLPSPAVSG 171  
QY 181 EEVPLLPYQAANLHLLLRDASIFGKESLSSEISTFTFNQVVERAGDYSDHCYKWS 240  
DB 172 EEVPLLPYQAANLHLLLRDASIFGKXGLSDSEISTFTFNQSGKSEYSDHCYKWN 231  
QY 241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALFPSYDTOMYPIKTTAQLTRVYTDI 300  
DB 232 TGLARLMGNAESWVRYNQFRDMLVLDLVALFPSYDTOMYPIKTTAQLTRVYTDI 291  
QY 301 GTVHPHPSFTTWNNAAPSFSAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMNW 360  
DB 292 GTVHPHPSFTTWNNAAPSFSAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMNW 351  
QY 361 GGKLEPFTIGTGLNISTQGSTNTSINPVTLPFTSRDVRYSGLNGLFQTQVNGVPR 420  
DB 352 GGKLEPFTIGTGLNISTQGSTNTSINPVTLPFTSRDVRYSGLNGLFQTQVNGVPR 411  
QY 421 VDFHWKFTVTHPIASDNFYPGVVGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
DB 412 VDFHWKFTVTHPIASDNFYPGVVGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 471  
QY 481 ASHKVAVYSWTHRSAD 497  
DB 472 ASHKVAVYSWTHRSAD 488

RESULT 13  
US-08-961-803-10  
Sequence 10, Application US/08961803  
Patent No. 6150589  
GENERAL INFORMATION:  
APPLICANT: Payne, Jewel  
APPLICANT: Cummings, David A.  
APPLICANT: Cannon, Raymond J.C.  
APPLICANT: Narva, Kenneth E.  
APPLICANT: Stelman, Steve  
TITLE OF INVENTION: No. 6150589el Bacillus thuringiensis Isolate Denoted  
TITLE OF INVENTION: B.T. PS158C2, Active Against Lepidopteran Pests, and Genes

TITLE OF INVENTION: Encoding Lepidopteran-Active Toxins  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jay M. Sanders  
STREET: 2421 N.W. 41st Street, Suite A-1  
CITY: Gainesville  
STATE: Florida  
COUNTRY: USA  
ZIP: 32606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/961,803  
FILING DATE: 31-OCT-1997  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/069,902  
FILING DATE: 01-JUNE-1993  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/759,247  
FILING DATE: 13-SEPT-1991  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/448,170  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Sanders, Jay M.  
REGISTRATION NUMBER: 39,355  
REFERENCE/DOCKET NUMBER: M/S 102D.C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (352) 375-8100  
TELEFAX: (352) 372-5800  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 488 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-961-803-10

Query Match 62.2%; Score 2340.5; DB 3; Length 488;  
Best Local Similarity 89.5%; Pred. No. 3.6e-201;  
Matches 445; Conservative 13; Mismatches 30; Indels 9; Gaps 1;  
QY 1 MRLKQDKHQSFSNAKVDKISTDSLKNETDIELQINHEHEDCLKMSYEYENVEPVSASTI 60  
DB 1 MRSKNQNMHQSLSNNAVDKNTGSLNNTINTELQNFH-----EGIEPFSVSTI 51  
QY 61 QTGIGIAGKILGTGVFFAGQVASYLFFILGELWPKGNQWEIFMEHVBEIINQKISTYA 120  
DB 52 QTGIGIVGKILGNLGVFFAGQVASYLFFILGELWPKGQWEIFMEHVBEIINQKISTYA 111  
QY 121 RNKALTDLKGDLALAVYHDSLESWGVRNNTRARSVVKSOYIALELMFVKLPSPAVSG 180  
DB 112 RNKALADLKGDLALAVYHESLESWIEENRNNTRFESVVKQYITLLELMFVQSLPSPAVSG 171  
QY 181 EEVPLLPYQAANLHLLLRDASIFGKESLSSEISTFTFNQVVERAGDYSDHCYKWS 240  
DB 172 EEVPLLPYQAANLHLLLRDASIFGKXGLSDSEISTFTFNQSGKSEYSDHCYKWN 231  
QY 241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALFPSYDTOMYPIKTTAQLTRVYTDI 300  
DB 232 TGLARLMGNAESWVRYNQFRDMLVLDLVALFPSYDTOMYPIKTTAQLTRVYTDI 291  
QY 301 GTVHPHPSFTTWNNAAPSFSAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMNW 360  
DB 292 GTVHPHPSFTTWNNAAPSFSAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMNW 351

QY 361 GGHKLFRTGTLNISTOGSTNTSINPVTLPTSDRYRTSLAGLNLFLTPQVNGVPR 420  
 DB 352 GGHKLFRTGTLNISTOGSTNTSINPVTLPTSDRYRTSLAGLNLFLTPQVNGVPR 411  
 QY 421 VDFHWFVTHPIASDNFFYPGVGIGTQDSENELPPEATQPNYESYSHRLSHIGLIS 480  
 DB 412 VDFHWFVTHPIASDNFFYPGVGIGTQDSENELPPEATQPNYESYSHRLSHIGLIS 471  
 QY 481 ASHVXALVYSWTHRSAD 497  
 DB 472 ASHVXALVYSWTHRSAD 488

RESULT 14

US-07-951-715A-7  
 ; Sequence 7, Application US/07951715A  
 ; Patent No. 5625136  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Koziel, Michael G.  
 ; APPLICANT: Desai, Nalini M.  
 ; APPLICANT: Lewis, Kelly S.  
 ; APPLICANT: Kramer, Vance C.  
 ; APPLICANT: Warren, Gregory W.  
 ; APPLICANT: Evola, Stephen V.  
 ; APPLICANT: Crossland, Lyle D.  
 ; APPLICANT: Wright, Martha S.  
 ; APPLICANT: Merlin, Ellis J.  
 ; APPLICANT: Launis, Karen L.  
 ; APPLICANT: Rothstein, Steven J.  
 ; APPLICANT: Bowman, Cindy G.  
 ; APPLICANT: Dawson, John L.  
 ; APPLICANT: Dunder, Erik M.  
 ; APPLICANT: Pace, Gary M.  
 ; APPLICANT: Suttie, Janet L.  
 ; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
 ; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE  
 ; NUMBER OF SEQUENCES: 94  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: CIBA-GEIGY Corporation  
 ; STREET: 7 Skyline Drive  
 ; CITY: Hawthorne  
 ; STATE: New York  
 ; COUNTRY: USA  
 ; ZIP: 10532  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30B  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/07/951,715A  
 ; FILING DATE: 25-SEP-1992  
 ; CLASSIFICATION: 800  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/772,027  
 ; FILING DATE: 04-OCT-1991  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Spuill, W. Murray  
 ; REGISTRATION NUMBER: 32,943  
 ; REFERENCE/DOCKET NUMBER: S-18805/A/CGC 1577/CIP  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (919) 541-8615  
 ; TELEFAX: (919) 541-8689  
 ; INFORMATION FOR SEQ ID NO: 7:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1207 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-07-951-715A-7

Query Match 60.2%; Score 2264.5; DB 1; Length 1207;

Best Local Similarity 64.3%; Pred. No. 1e-193;  
 Matches 442; Conservative 78; Mismatches 154; Indels 13; Gaps 5;  
 QY 40 EDCMKSEYENVEPFFVSASTIQTGIGIAGKILGTGVPPAGQVASYLSFILGELWPKGN 99  
 DB 10 EDSLCIAEGNNIDPFFVSASTVQTGINIAGILGVLPFAGQLASFSYSLVGLWELWPRGD 69  
 QY 100 QWEIFEHVEEINOKISTYARNKALTDLKGLGDALAVYHDSLESWGNENNRARSYVK 159  
 DB 70 QWEIFEHVEEINOKISTYARNKALTDLKGLGDALAVYHDSLESWGNENNRARSYVK 129  
 QY 160 SQVIALELMFVQKLPSPFAVSGEEVPLPIPIYAQAANLHLLLRDASIFGKEWGLSSEIST 219  
 DB 130 TQVIALELDFLNAPLFAIRNQEVPLIMVYAQAANLHLLLRDASIFGSEFGILTQEIQR 189  
 QY 220 FYNQVERAGDYSCHCKWYSTGLNNLRGTNAESWYRQNFREDMTLMVLDLVALPPSYD 279  
 DB 190 YYERQVERTRDYSYCVWYNTGLNSLRGTNAESWYRQNFREDMTLMVLDLVALPPSYD 249  
 QY 280 TOMYPIKTAQLTREYVTDAGTVHPHPSFTSTWYNNNAPSPSAEAAVWNRPHLLDFL 339  
 DB 250 TRYPINTSAQLTREYVTDAGT--GVNWSMWNWNNNAPSPSAEAAVWNRPHLLDFL 307  
 QY 340 EQVTIYSLSRWNTQYMMNMGHKLFRFTIGTGLNISTOGSTNTSINPVTLPTSDRYVY 399  
 DB 308 EQLTIFSSASRWNTRHMTYWRGHTTQSRPIGGGLNTSTHGATNTSINPVTLPTSDRYVY 367  
 QY 400 RTESLAGLNF--LTOPVNGVPRVDFHWFVTHP-----IASDNFYPGVGVGTQLODS 452  
 DB 368 RTESYAGVLLWGIYLEPIHGVTVRENF--TNPQNISDRGTANKSQP-YESPGQLQKDS 423  
 QY 453 ENELPPEATQPNYESYSHRLSHIGLISASHVYKALVYSWTHRSADRTNTPNSITQIPL 512  
 DB 424 ETELPPETTERPNYESYSHRLSHIGLILQSRVNVVYSWTHRSADRTNTPNSITQIPL 483  
 QY 513 VKAFNLSSGAUVRGPGTGGDILRTNTGTGDIRVAINPFAQRYVRIRYASTTDLQ 572  
 DB 484 VKASELPQGTTVVRGPGTGGDILRTNTGGFGPIRVTVNGPLTQRYRIGFYASTVDFD 543  
 QY 573 FHTSINGKAINQGNFSATWNRGEDLDYKTFRTVGTFTTFFSFLDVQSTFTTIGAWNFSSGNE 632  
 DB 544 FVYRSGGTTVNNFRFLRTWNSGDELKYGNFVRAFTTPTFTTQIQDIIRTSIQGLSGNCE 603  
 QY 633 VIIDRIEFVPEVTEYAEYDFEKAQEKVTALTSTINPRGLKTDVXDYHIDQVSNLVESLS 692  
 DB 604 VIIDKIEIIPVTATFEAEYDLERAQEAVALFTNTPRRLKTDVTDYHIDQVSNLVACLS 663  
 QY 693 DEFYLDKEKLEFEIVKYAKQLHIERNM 719  
 DB 664 DEFCLDEKLEKVKYAKRLSDERNL 690

RESULT 15

US-08-459-448A-7  
 ; Sequence 7, Application US/08459448A  
 ; Patent No. 5859336  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Koziel, Michael G.  
 ; APPLICANT: Desai, Nalini M.  
 ; APPLICANT: Lewis, Kelly S.  
 ; APPLICANT: Kramer, Vance C.  
 ; APPLICANT: Warren, Gregory W.  
 ; APPLICANT: Evola, Stephen V.  
 ; APPLICANT: Crossland, Lyle D.  
 ; APPLICANT: Wright, Martha S.  
 ; APPLICANT: Merlin, Ellis J.  
 ; APPLICANT: Launis, Karen L.  
 ; APPLICANT: Rothstein, Steven J.  
 ; APPLICANT: Bowman, Cindy G.  
 ; APPLICANT: Dawson, John L.  
 ; APPLICANT: Dunder, Erik M.  
 ; APPLICANT: Pace, Gary M.  
 ; APPLICANT: Suttie, Janet L.

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; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 585933artis Corporation
; STREET: Patent & Trademark Dept., 520 White Plains
; STREET: Rd., POB 2005
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591-9005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,448A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/951,715
; FILING DATE: 25-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Pace, Gary M.
; REGISTRATION NUMBER: 40403
; REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8582
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1207 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-459-448A-7

```

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Query Match      60.2%; Score 2264.5; DB 2; Length 1207;
Best Local Similarity 64.3%; Pred. No. 1e-193;
Matches 442; Conservative 78; Mismatches 154; Indels 13; Gaps 5;

QY 40 EDCLKMEYENVEPVFSASTIQTGIGIAGKILGTLPVFPAGQVASYLSFILGELWPKGN 99
DB 10 EDSLCIAEGNNIDPFVSASIVQTGINAGRLGVLPVFPAGQLASFYSFLVGLWPRGRD 69
QY 100 QWEIFMBHVBEEINQKISTVARNKALTDLKGDLALAVYHDSLESWGNRNTRARSVK 159
DB 70 QWEIFLEHVEQLINQQTENARNALTALRQLGDSFRAYQOQSLDMLNEDDARTSVLY 129
QY 160 SQTALFLMFVKLPSPAVSGEEVPLPIVAQAANLHLLLRDASIFGKEWGLSSSEIST 219
DB 130 TQYTALEDFLNAMPLFAIRNQEVPLLMVQAANLHLLLRDASLFGSEFGITSQEIOR 189
QY 220 FYNQVERAGDYSCHVKVWYSTGLNNLRGTNAESWVRYNQFRDMTLMVLVDLVALPESYD 279
DB 190 YVERQVERTRDYSYCVENYNTGLNSLRGTNAASWVRYNQFRDLTLGLVDLVALPESYD 249
QY 280 TQMPYIKTKTAQLTREVYTDAGTGVHPHPSFTSTTWYNNAPSFAIEAAVVRNPHLLDEL 339
DB 250 TRTPYINTSAQLTREVYTDAGAT--GVNMAWMYNNAPSFAIEAAAIRSPHLLDFL 307
QY 340 EQVTIYSLRSWSNTQYNNMGGHKLFRITIGGTGLNISTQGSTNTSINPVTLPFTSRDYY 399
DB 308 EQLTIFSASSRWSNTRMTYWRGTIQSRPIGGGLNTSGHATNTSINPVTLPASRDYV 367
QY 400 RTESLAGNLFP--LTQPVNGVRVDVFWKFTVHP-----TASDNFYYPGVIGTQLQDS 452
DB 368 RTESYAGVLLWGIYLEPIHGVPTVRFPN---TNPQNSDRGTANYSQP-YESPGLQLKDS 423

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QY 453 ENELPPEATGPNYESYSHRLSHIGLISASHVKALVSWTHRSADRTNTIEPNSITOPL 512
DB 424 ETELFPETTERPNYESYSHRLSHIGLILQSRVNPVYSWTHRSADRTNTIGPNEITQIPM 483
QY 513 VKAFNLSSGAAVVRGPGFTGGDILERTNTGTGDIRVNNINPFPFAQRYKVRIRYASTDLQ 572
DB 484 VKASELPQGTIVVRGPGFTGGDILRRNTGTGGFPIRVTVNGPLTCRYAIGFRYASTVDFD 543
QY 573 FHTSINGKAINQGNFSAITMNRGDELDTYKTPRTVGTTPFPFLDYQSTFTIGANNFSSGNE 632
DB 544 FVVSREGGTTVANNFRPLRTMNSGDELKYGNFVRRAFTTPTFTQDIIIRTSIQGLSGNGE 603
QY 633 VYIDRIEFPVVEVTYEAAYDEFEKAEKVTALETSTNPRGLXTDVKDXHIDQVSNLVESLS 692
DB 604 VYIDKIEIIPVATFEAYDILERAQEAVALFTNTNPRRLXTDVTYHIDQVSNLVACLS 663
QY 693 DEFYLDKRELFPEIVKYAKQLHIERNM 719
DB 664 DEFCLDEKRELEKVKYAKRLSDENL 690

```

Search completed: October 28, 2004, 18:34:18  
Job time : 24.3343 secs





GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 28, 2004, 17:51:02 ; Search time 86.6903 Seconds  
(without alignments)  
2975.262 Million cell updates/sec

Title: US-10-019-823B-57

Perfect score: 3760  
Sequence: 1 MKLXNQDKHQSFSSNAKVDK.....KRELFEIVKYAKQLHIERM 719

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729239 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A Geneseq\_238ep04:.\*  
1: geneseqp1980s.\*  
2: geneseqp1980s.\*  
3: geneseqp2000s.\*  
4: geneseqp2001s.\*  
5: geneseqp2002s.\*  
6: geneseqp2003as.\*  
7: geneseqp2003bs.\*  
8: geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Length	DB ID	Description
1	3760	100.0	719	4 AAB66910	Aab66910 Insectici
2	3760	100.0	719	6 AAE36274	Aae36274 B. thurin
3	3756	99.9	719	4 AAB66908	Aab66908 Insectici
4	3756	99.9	719	6 AAE36272	Aae36272 B. thurin
5	3747	99.7	719	4 AAU02095	Aau02095 Bacillus
6	3745	99.6	719	4 AAB66911	Aab66911 Insectici
7	3745	99.6	719	6 AAE36275	Aae36275 B. thurin
8	3739	99.4	719	4 AAB66909	Aab66909 Insectici
9	3739	99.4	719	6 AAE36273	Aae36273 B. thurin
10	3735	99.3	719	2 AAR08041	Aar08041 81 kD end
11	3724.5	99.1	718	6 AAE36271	Aae36271 B. thurin
12	3718.5	98.9	718	6 AAE36270	Aae36270 Insectici
13	3547	94.3	719	7 ADM74717	Adm74717 B. thurin
14	3516	93.5	719	4 AAB66912	Aab66912 Insectici
15	3516	93.5	719	6 AAE36276	Aae36276 B. thurin
16	3472.5	92.4	710	4 AAU02041	Aau02041 B. thurin
17	3393	90.2	719	3 ABB07073	Abb07073 Bacillus
18	3373	89.7	719	2 AAU02089	Aau02089 Bacillus
19	3287	87.4	1217	4 AAU02092	Aau02092 Bacillus
20	2730	72.6	1208	4 AAU02093	Aau02093 Bacillus
21	2447	65.1	1230	8 ADK98484	Adk98484 B thuring
22	2447	65.1	1230	8 ADK98489	Adk98489 B thuring
23	2447	65.1	1230	8 ADK98481	Adk98481 B thuring
24	2447	65.1	1230	8 ADK98491	Adk98491 B thuring
25	2447	65.1	1230	8 ADK98487	Adk98487 B thuring

## ALIGNMENTS

## RESULT 1

AAB66910  
ID AAB66910 standard; protein; 719 AA.

XX AC AAB66910;  
XX AC  
XX 12-APR-2001 (first entry)  
XX DT  
XX Insecticidal protein cryIIa4.  
XX DE  
XX XX Insecticide; transgenic plant; insect-resistance.  
XX KW  
XX Insecticide; transgenic plant; insect-resistance.  
XX OS Paecilomyces sp.  
XX XX  
XX WO200100841-A1.  
XX PN  
XX PD 04-JAN-2001.  
XX PF 23-JUN-2000; 2000WO-GB002457.  
XX PR 29-JUN-1999; 99GB-00015215.  
XX PR 23-DEC-1999; 99GB-00030536.  
XX XX (ZENE ) ZENECA LTD.  
XX PA Griffin J, Carlile AJ, Cayley PU, Mackay EA, Warner SAJ;  
XX PI Vincent JL, Lee MD;  
XX XX  
XX DR WPI; 2001-123015/13.  
XX PT Novel insecticidal protein obtained from species of Paecilomyces for  
XX PT controlling insects, and for insect-resistant transgenic plant  
XX PT production.  
XX PS Claim 14; Page 60-62; 72pp; English.  
XX XX  
XX CC The present invention relates to novel insecticidal proteins obtained  
XX CC from Paecilomyces sp. (see AAB66910 and AAB66913). The  
XX CC insecticidal proteins can be used to produce transgenic plants, which are  
XX CC insect-resistant. Also, the insecticidal proteins are useful for  
XX CC controlling insects by providing them at a locus where insects feed

XX Sequence 719 AA;

Query Match 100.0%; Score 3760; DB 4; Length 719;

Best Local Similarity 100.0%; Pred.No. 1.2e-290;

Matches 719; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

26 2445.5 65.0 1229 2 AAR54074  
27 2445.5 65.0 1229 2 AAW35259  
28 2445.5 65.0 1229 2 AAW17699  
29 2445.5 65.0 1229 2 AAW87633  
30 2445.5 65.0 1229 2 AAY30923  
31 2445.5 65.0 1229 8 ADK98479  
32 2340.5 62.2 488 2 AAW44322  
33 2340.5 62.2 488 4 AAB19947  
34 2277.5 60.6 1228 2 AAR50955  
35 2272.5 60.4 1209 4 AAU02094  
36 2263.5 60.2 1227 2 AAY31990  
37 2195.5 58.4 1227 2 AAW44321  
38 2195.5 58.4 1227 4 AAB19950  
39 2186.5 58.2 1227 4 AAU02046  
40 2171.5 57.8 1186 2 AAY16796  
41 2155.5 57.3 1221 4 AAU00421  
42 2141.5 57.0 1221 4 AAU00420  
43 2115 56.2 1228 4 AAB84628  
44 2115 56.2 1228 4 AAU02039  
45 1932.5 51.4 643 2 AAY16797

Aar54074 CryET5. 2  
Aaw35259 Bacillus  
Aaw17699 CryET5. 3  
Aaw87633 CryET5 pr  
Aay30923 B. thurin  
Adk98479 B. thurin  
Aaw44322 Bacillus  
Aab19947 Bacillus  
Aar50955 Bacillus  
Aau02094 Bacillus  
Aay31990 Chimeric  
Aaw44321 Bacillus  
Aab19950 Bacillus  
Aau02046 B. thurin  
Aay16796 Amino aci  
Aau00421 B. thurin  
Aau00420 B. thurin  
Aab84628 Amino aci  
Aau02039 B. thurin  
Aay16797 Amino aci

QY 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKNSEYENVEPVSASTI 60  
 DB 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKNSEYENVEPVSASTI 60  
 QY 61 QTGIGIAGKILGTGLGVPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
 DB 61 QTGIGIAGKILGTGLGVPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
 QY 121 RNKALTDLKGDLAVYHDSLESWGNRNTRARSVVKSYIALELMFVKLPSPAVSG 180  
 DB 121 RNKALTDLKGDLAVYHDSLESWGNRNTRARSVVKSYIALELMFVKLPSPAVSG 180  
 QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKWLGSSEISTFYNRQVERAGDYSCHVCWYS 240  
 DB 181 EEPVLLPIYAQAANLHLLLRDASIFGKWLGSSEISTFYNRQVERAGDYSCHVCWYS 240  
 QY 241 TGLNNLRGTNAESWVRYNQFRDMLVLDLVALFPSSYDTQMPYIKTTAQTREVTDAI 300  
 DB 241 TGLNNLRGTNAESWVRYNQFRDMLVLDLVALFPSSYDTQMPYIKTTAQTREVTDAI 300  
 QY 301 GTVHPHPSTFTTWNNAAPSFAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYNNMW 360  
 DB 301 GTVHPHPSTFTTWNNAAPSFAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYNNMW 360  
 QY 361 GGHKLEFRTIGTGLNISQGSTNTSINPVTLPFTSRDVRTESLAGLNLFLTQPVNGVPR 420  
 DB 361 GGHKLEFRTIGTGLNISQGSTNTSINPVTLPFTSRDVRTESLAGLNLFLTQPVNGVPR 420  
 QY 421 VDFHWKFTVTHPIASDNFYPGVIGTQDSENELPEATGQPNYESYSHRLSHIGLIS 480  
 DB 421 VDFHWKFTVTHPIASDNFYPGVIGTQDSENELPEATGQPNYESYSHRLSHIGLIS 480  
 QY 481 ASHVKALVYSWTHRSADRTNIENSTQIPLVAFNLSSGAAVVRGPGTGGDILRTN 540  
 DB 481 ASHVKALVYSWTHRSADRTNIENSTQIPLVAFNLSSGAAVVRGPGTGGDILRTN 540  
 QY 541 TGTGDIRVNIPLPPAQRVRIYASTTDLQFHTSINGKAINQGNFSATWNGEDLDYK 600  
 DB 541 TGTGDIRVNIPLPPAQRVRIYASTTDLQFHTSINGKAINQGNFSATWNGEDLDYK 600  
 QY 601 TFRVTGFTTPSFSDVQSTFTIGAWNFSSGNEVYIDRIEFVVPVEVYEAEDFEKAQEKV 660  
 DB 601 TFRVTGFTTPSFSDVQSTFTIGAWNFSSGNEVYIDRIEFVVPVEVYEAEDFEKAQEKV 660  
 QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDSEFYLDKRELFPEIVKYAKQLHIERNM 719  
 DB 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDSEFYLDKRELFPEIVKYAKQLHIERNM 719

RESULT 2  
 AAEE36274  
 ID AAEE36274 standard; protein; 719 AA.  
 XX AAEE36274;  
 AC AAEE36274;  
 DT 26-JUN-2003 (first entry)  
 XX  
 DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa4.  
 XX Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.  
 KW Bacillus thuringiensis.  
 OS WO200298911-A2.  
 PN 12-DEC-2002.  
 PD 30-MAY-2002; 2002WO-GB002666.  
 PF 07-JUN-2001; 2001GB-00013900.  
 PR (SYGN ) SYNGENTA LTD.  
 XX

PI Vincent JL, Viner R;  
 XX WPI; 2003-175137/17.  
 DR  
 XX New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.  
 PT  
 XX Claim 12; Page 50-53; 67pp; English.  
 PS  
 XX The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects.  
 CC Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is  
 CC Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention  
 CC  
 XX Sequence 719 AA;  
 SQ  
 Query Match 100.0%; Score 3760; DB 6; Length 719;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-290;  
 Matches 719; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKNSEYENVEPVSASTI 60  
 DB 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKNSEYENVEPVSASTI 60  
 QY 61 QTGIGIAGKILGTGLGVPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
 DB 61 QTGIGIAGKILGTGLGVPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
 QY 121 RNKALTDLKGDLAVYHDSLESWGNRNTRARSVVKSYIALELMFVKLPSPAVSG 180  
 DB 121 RNKALTDLKGDLAVYHDSLESWGNRNTRARSVVKSYIALELMFVKLPSPAVSG 180  
 QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKWLGSSEISTFYNRQVERAGDYSCHVCWYS 240  
 DB 181 EEPVLLPIYAQAANLHLLLRDASIFGKWLGSSEISTFYNRQVERAGDYSCHVCWYS 240  
 QY 241 TGLNNLRGTNAESWVRYNQFRDMLVLDLVALFPSSYDTQMPYIKTTAQTREVTDAI 300  
 DB 241 TGLNNLRGTNAESWVRYNQFRDMLVLDLVALFPSSYDTQMPYIKTTAQTREVTDAI 300  
 QY 301 GTVHPHPSTFTTWNNAAPSFAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYNNMW 360  
 DB 301 GTVHPHPSTFTTWNNAAPSFAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYNNMW 360  
 QY 361 GGHKLEFRTIGTGLNISQGSTNTSINPVTLPFTSRDVRTESLAGLNLFLTQPVNGVPR 420  
 DB 361 GGHKLEFRTIGTGLNISQGSTNTSINPVTLPFTSRDVRTESLAGLNLFLTQPVNGVPR 420  
 QY 421 VDFHWKFTVTHPIASDNFYPGVIGTQDSENELPEATGQPNYESYSHRLSHIGLIS 480  
 DB 421 VDFHWKFTVTHPIASDNFYPGVIGTQDSENELPEATGQPNYESYSHRLSHIGLIS 480  
 QY 481 ASHVKALVYSWTHRSADRTNIENSTQIPLVAFNLSSGAAVVRGPGTGGDILRTN 540  
 DB 481 ASHVKALVYSWTHRSADRTNIENSTQIPLVAFNLSSGAAVVRGPGTGGDILRTN 540  
 QY 541 TGTGDIRVNIPLPPAQRVRIYASTTDLQFHTSINGKAINQGNFSATWNGEDLDYK 600  
 DB 541 TGTGDIRVNIPLPPAQRVRIYASTTDLQFHTSINGKAINQGNFSATWNGEDLDYK 600  
 QY 601 TFRVTGFTTPSFSDVQSTFTIGAWNFSSGNEVYIDRIEFVVPVEVYEAEDFEKAQEKV 660  
 DB 601 TFRVTGFTTPSFSDVQSTFTIGAWNFSSGNEVYIDRIEFVVPVEVYEAEDFEKAQEKV 660  
 QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDSEFYLDKRELFPEIVKYAKQLHIERNM 719  
 DB 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDSEFYLDKRELFPEIVKYAKQLHIERNM 719

RESULT 3  
ID AAB66908 standard; protein; 719 AA.  
AC AAB66908;  
XX  
XX 12-APR-2001 (first entry)  
XX Insecticidal protein cryIIa2.  
XX Insecticide; transgenic plant; insect-resistance.  
XX Paecilomyces sp.  
XX WO200100841-A1.  
XX 04-JAN-2001.  
XX 23-JUN-2000; 2000WO-GB002457.  
XX 29-JUN-1999; 99GB-00015215.  
XX 23-DEC-1999; 99GB-00030536.  
XX (ZENE ) ZENECA LTD.  
XX Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;  
XX Vincent JL, Lee MD;  
XX WPI; 2001-123015/13.  
XX  
XX Novel insecticidal protein obtained from species of Paecilomyces for  
XX controlling insects, and for insect-resistant transgenic plant  
XX production.  
XX Claim 14; Page 55-57; 72pp; English.  
XX  
XX The present invention relates to novel insecticidal proteins obtained  
XX from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The  
XX insecticidal proteins can be used to produce transgenic plants, which are  
XX insect-resistant. Also, the insecticidal proteins are useful for  
XX controlling insects by providing them at a locus where insects feed  
XX  
XX Sequence 719 AA;  
XX  
Query Match 99.9%; Score 3756; DB 4; Length 719;  
Best Local Similarity 99.9%; Pred. No. 2.5e-290;  
Matches 718; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 MGLKNDKQKHSFSSNAKVDKISTDSLNKNETDIELQININHEDCIKMGEYENVEPVSASTI 60  
Db 1 MGLKNDKQKHSFSSNAKVDKISTDSLNKNETDIELQININHEDCIKMGEYENVEPVSASTI 60  
Qy 61 QTGIGIAGKILGTLGVFPAGQVSLYSFIIGELWPKGNQWEIFMEHVBEIINOKISTYA 120  
Db 61 QTGIGIAGKILGTLGVFPAGQVSLYSFIIGELWPKGNQWEIFMEHVBEIINOKISTYA 120  
Qy 121 RNKALTDLKGIGDALAVYHDSLSWGNNRNTARSVVKSQYIALELMFVKLPSPAVSG 180  
Db 121 RNKALTDLKGIGDALAVYHDSLSWGNNRNTARSVVKSQYIALELMFVKLPSPAVSG 180  
Qy 181 EVELPLPIYQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGYSYDHCWKWYS 240  
Db 181 EVELPLPIYQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGYSYDHCWKWYS 240  
Qy 241 TGLNLLGTVAESWVRVYQFRDNTLMVLDLVALFPSYDTQMPYIKTTAQLTREYTDAL 300  
Db 241 TGLNLLGTVAESWVRVYQFRDNTLMVLDLVALFPSYDTQMPYIKTTAQLTREYTDAL 300  
Qy 301 GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSWSNTQYNNMW 360  
Db 301 GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSWSNTQYNNMW 360

Qy 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDYRTESLAGLNFLTQPVNGVPR 420  
Db 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDYRTESLAGLNFLTQPVNGVPR 420  
Qy 421 VDFHWKFTVTHPIASDNFYYPGVGIGTQLODSENELPEATGQPNYESYSRHLSHIGLIS 480  
Db 421 VDFHWKFTVTHPIASDNFYYPGVGIGTQLODSENELPEATGQPNYESYSRHLSHIGLIS 480  
Qy 481 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
Db 481 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
Qy 541 TGTGDIRVNINPPFAQRYRVRIRYASTTDIQFTSINGKAINQGNFSAATWNRGDDLYK 600  
Db 541 TGTGDIRVNINPPFAQRYRVRIRYASTTDIQFTSINGKAINQGNFSAATWNRGDDLYK 600  
Qy 601 TFRVTGFTTPFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDPEKAQEKV 660  
Db 601 TFRVTGFTTPFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDPEKAQEKV 660  
Qy 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDSFYLDEKELFEIVKYAKQLHIERNN 719  
Db 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDSFYLDEKELFEIVKYAKQLHIERNN 719  
RESULT 4  
AAB36272  
ID AAB36272 standard; protein; 719 AA.  
XX  
XX AAB36272;  
XX  
XX 26-JUN-2003 (first entry)  
XX B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa2.  
XX Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.  
XX Bacillus thuringiensis.  
XX WO200298911-A2.  
XX 12-DEC-2002.  
XX 30-MAY-2002; 2002WO-GB002666.  
XX 07-JUN-2001; 2001GB-00013900.  
XX (SYGN ) SYNGENTA LTD.  
XX Vincent JL, Viner R;  
XX WPI; 2003-175137/17.  
XX  
XX New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.  
XX Claim 12; Page 44-47; 67pp; English.  
XX The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects. CC Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is CC Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention  
XX Sequence 719 AA;  
Query Match 99.9%; Score 3756; DB 6; Length 719;  
Best Local Similarity 99.9%; Pred. No. 2.5e-290;  
Matches 718; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 M L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y E N V E P F V S A S T I 60
DB 1 M L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y E N V E P F V S A S T I 60
QY 61 Q T G I G I A G K I L G T L G V P F A G Q V A S I Y S F I L G E L M P K G N Q W E I F M E H V E E I I N Q K I S T Y A 120
DB 61 Q T G I G I A G K I L G T L G V P F A G Q V A S I Y S F I L G E L M P K G N Q W E I F M E H V E E I I N Q K I S T Y A 120
QY 121 R N K A L T D L K G L D A L A V H D S L E S W G N R N N T R A S V V K S Q Y I A L E M F V Q K L B S P A V S G 180
DB 121 R N K A L T D L K G L D A L A V H D S L E S W G N R N N T R A S V V K S Q Y I A L E M F V Q K L B S P A V S G 180
QY 181 E V P L L P I Y A Q A A N L H L L L D A S I F G K E W G L S S E I S T F Y N Q V R A G D Y S D H C V K W Y S 240
DB 181 E V P L L P I Y A Q A A N L H L L L D A S I F G K E W G L S S E I S T F Y N Q V R A G D Y S D H C V K W Y S 240
QY 241 T G L N N L R G T N A E S W Y R Y N Q F R D M T L M V L D L V A L P P S Y D T Q M Y P I K T T A Q L T R E V Y T D A I 300
DB 241 T G L N N L R G T N A E S W Y R Y N Q F R D M T L M V L D L V A L P P S Y D T Q M Y P I K T T A Q L T R E V Y T D A I 300
QY 301 G T V H P H P S F T S T T W Y N N N A P S F S A I E A A V R N P H L L D P L E O V T I Y S L L S R W S N T Q Y N M W 360
DB 301 G T V H P H P S F T S T T W Y N N N A P S F S A I E A A V R N P H L L D P L E O V T I Y S L L S R W S N T Q Y N M W 360
QY 361 G G H K L E F T I G G T L N I S T Q G S T N T S I N P V T L P F T S R D V Y R T E S L A G N L F L T Q P V N G V P R 420
DB 361 G G H K L E F T I G G T L N I S T Q G S T N T S I N P V T L P F T S R D V Y R T E S L A G N L F L T Q P V N G V P R 420
QY 421 V D F H W K F V T H P I A S D N F Y Y P G V I G T Q L D S E N L P P E A T G Q P N Y E S Y S H R L S H I G L I S 480
DB 421 V D F H W K F V T H P I A S D N F Y Y P G V I G T Q L D S E N L P P E A T G Q P N Y E S Y S H R L S H I G L I S 480
QY 481 A S H V K A L Y S W T H R S A D R T N I E P N S I T Q I P L V K A F N L S S G A A V R G P G T G G I L R T N 540
DB 481 A S H V K A L Y S W T H R S A D R T N I E P N S I T Q I P L V K A F N L S S G A A V R G P G T G G I L R T N 540
QY 541 T G T F G D I R V N I N P P P A Q R Y R V R I A S T T D L Q F H T S I N G K A I N Q N F S A T W N R G E D L D Y K 600
DB 541 T G T F G D I R V N I N P P P A Q R Y R V R I A S T T D L Q F H T S I N G K A I N Q N F S A T W N R G E D L D Y K 600

RESULT 5
AAU02095
ID AAU02095 standard; protein; 719 AA.
XX AC AAU02095;
XX DT 07-SEP-2001 (first entry)
XX DE Bacillus thuringiensis partial mutant CryIIa.
XX KW Crystal protein; CryIIa; CryIa; moth; butterfly; Colorado potato beetle;
XX mutant; mutein.
XX OS Bacillus thuringiensis.
XX FH Location/Qualifiers
XX FT Peptide
XX FT /label= Signal_peptide
XX FT 20..719
XX FT /label= Mature_CryIIa
XX PN EP1099760-A1.

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PD 16-MAY-2001.
XX 09-NOV-1999; 99EP-00203723.
XX 09-NOV-1999; 99EP-00203723.
XX (CPRO-) CPRO-DLO CENT PLANTENVEREDELINGS REPROD.
XX De Maagd RA, Bosch HJ;
XX MPI; 2001-337141/36.
XX DR N-PSDB; AAS04855.
XX New hybrid Bacillus thuringiensis hybrid toxins comprising structural
PT domains derived from at least 2 different crystal proteins, such as
PT CryIIa and CryIa, and having insecticidal activity, useful for combating
PT insects.
XX Example; Page 30-32; 43pp; English.
XX The sequence is B. thuringiensis (Bt) crystal protein CryIIa, the DNA
CC encoding which was mutated to allow cloning of domain III or domains I
CC and II, to make the hybrid protoxins of the invention. The hybrid toxins
CC of the invention, having structural domains I, II and III in this order
CC starting from the N-terminal derived from at least 2 different crystal
CC proteins, are useful for protecting plants against pest insects, e.g.
CC moths, butterflies and Colorado potato beetle or for combating insects
XX SQ Sequence 719 AA;
XX Query Match 99.7%; Score 3747; DB 4; Length 719;
XX Best Local Similarity 99.7%; Pred. No. 1.3e-289;
XX Matches 717; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 M L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y E N V E P F V S A S T I 60
DB 1 M L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y E N V E P F V S A S T I 60
QY 61 Q T G I G I A G K I L G T L G V P F A G Q V A S I Y S F I L G E L M P K G N Q W E I F M E H V E E I I N Q K I S T Y A 120
DB 61 Q T G I G I A G K I L G T L G V P F A G Q V A S I Y S F I L G E L M P K G N Q W E I F M E H V E E I I N Q K I S T Y A 120
QY 121 R N K A L T D L K G L D A L A V H D S L E S W G N R N N T R A S V V K S Q Y I A L E M F V Q K L B S P A V S G 180
DB 121 R N K A L T D L K G L D A L A V H D S L E S W G N R N N T R A S V V K S Q Y I A L E M F V Q K L B S P A V S G 180
QY 181 E V P L L P I Y A Q A A N L H L L L D A S I F G K E W G L S S E I S T F Y N Q V R A G D Y S D H C V K W Y S 240
DB 181 E V P L L P I Y A Q A A N L H L L L D A S I F G K E W G L S S E I S T F Y N Q V R A G D Y S D H C V K W Y S 240
QY 241 T G L N N L R G T N A E S W Y R Y N Q F R D M T L M V L D L V A L P P S Y D T Q M Y P I K T T A Q L T R E V Y T D A I 300
DB 241 T G L N N L R G T N A E S W Y R Y N Q F R D M T L M V L D L V A L P P S Y D T Q M Y P I K T T A Q L T R E V Y T D A I 300
QY 301 G T V H P H P S F T S T T W Y N N N A P S F S A I E A A V R N P H L L D P L E O V T I Y S L L S R W S N T Q Y N M W 360
DB 301 G T V H P H P S F T S T T W Y N N N A P S F S A I E A A V R N P H L L D P L E O V T I Y S L L S R W S N T Q Y N M W 360
QY 361 G G H K L E F T I G G T L N I S T Q G S T N T S I N P V T L P F T S R D V Y R T E S L A G N L F L T Q P V N G V P R 420
DB 361 G G H K L E F T I G G T L N I S T Q G S T N T S I N P V T L P F T S R D V Y R T E S L A G N L F L T Q P V N G V P R 420
QY 421 V D F H W K F V T H P I A S D N F Y Y P G V I G T Q L D S E N L P P E A T G Q P N Y E S Y S H R L S H I G L I S 480
DB 421 V D F H W K F V T H P I A S D N F Y Y P G V I G T Q L D S E N L P P E A T G Q P N Y E S Y S H R L S H I G L I S 480
QY 481 A S H V K A L Y S W T H R S A D R T N I E P N S I T Q I P L V K A F N L S S G A A V R G P G T G G I L R T N 540
DB 481 A S H V K A L Y S W T H R S A D R T N I E P N S I T Q I P L V K A F N L S S G A A V R G P G T G G I L R T N 540
QY 541 T G T F G D I R V N I N P P P A Q R Y R V R I A S T T D L Q F H T S I N G K A I N Q N F S A T W N R G E D L D Y K 600
DB 541 T G T F G D I R V N I N P P P A Q R Y R V R I A S T T D L Q F H T S I N G K A I N Q N F S A T W N R G E D L D Y K 600

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601 TFRVGTTPSFLDVOSTETIGAWNFSSNEVYIDRIEFVPEVTEYAEYDEKAEKV 660  
 601 TFRVGTTPSFLDVOSTETIGAWNFSSNEVYIDRIEFVPEVTEYAEYDEKAEKV 660  
 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFVYKAKQLHIERNM 719  
 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFVYKAKQLHIERNM 719

RESULT 6  
 AAB66911  
 ID AAB66911 standard; protein; 719 AA.  
 XX AC AAB66911;  
 XX DT 12-APR-2001 (first entry)  
 XX DE Insecticidal protein cryIIa5.  
 XX KW Insecticide; transgenic plant; insect-resistance.  
 XX OS Paecilomyces sp.  
 XX PN WO200100841-A1.  
 XX PD 04-JAN-2001.  
 XX PF 23-JUN-2000; 2000WO-GB002457.  
 XX PR 29-JUN-1999; 99GB-00015215.  
 XX PR 23-DEC-1999; 99GB-00030536.  
 XX PA (ZENE ) ZENECA LTD.  
 XX PI Griffin J, Carlile AJ, Cayley PJ, Mackay BA, Warner SAJ;  
 XX PI Vincent JL, Lee MD;  
 XX DR WPI; 2001-123015/13.  
 XX DT Novel insecticidal protein obtained from species of Paecilomyces for  
 XX PT controlling insects, and for insect-resistant transgenic plant  
 XX PT production.  
 XX PS Claim 14; Page 62-64; 72pp; English.  
 XX CC The present invention relates to novel insecticidal proteins obtained  
 XX CC from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The  
 XX CC insecticidal proteins can be used to produce transgenic plants, which are  
 XX CC insect-resistant. Also, the insecticidal proteins are useful for  
 XX CC controlling insects by providing them at a locus where insects feed  
 XX SQ Sequence 719 AA;

Query Match 99.6%; Score 3745; DB 4; Length 719;  
 Best Local Similarity 99.4%; Pred. No. 1.9e-289;  
 Matches 715; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MCLKNQKHQSFSSNAKVXKISTDSLKNETDIELQNHEDCLKMSYEYVFSVASTI 60  
 Db 1 MCLKNQKHQSFSSNAKVXKISTDSLKNETDIELQNHEDCLKMSYEYVFSVASTI 60  
 Qy 61 QTGIGIAGKILGTGVFPAGQVASLYSFLGELWPKGNQWEIFMEHVBEIINQKISTYA 120  
 Db 61 QTGIGIAGKILGTGVFPAGQVASLYSFLGELWPKGNQWEIFMEHVBEIINQKISTYA 120  
 Qy 121 RNKALTDLKGIDGALAYVHDSLSWGNRNNTARSVVKSQYIALELMFVKQLPSFAVSG 180  
 Db 121 RNKALTDLKGIDGALAYVHDSLSWGNRNNTARSVVKSQYIALELMFVKQLPSFAVSG 180  
 Qy 181 BEVPLLIYQAANLHLLLRDASIFGKENGSLSSSEISTFYNRQVGRAGDYSCHVKWYS 240  
 Db 181 BEVPLLIYQAANLHLLLRDASIFGKENGSLSSSEISTFYNRQVGRAGDYSCHVKWYS 240

Qy 241 TGLNNLRGTNAESVRYNQFRRDMLVLDLVALFPSSYDTQMPYIKTKTAQLTREYVTDAI 300  
 Db 241 TGLNNLRGTNAESVRYNQFRRDMLVLDLVALFPSSYDTQMPYIKTKTAQLTREYVTDAI 300  
 Qy 301 GTVHPHPSFTSTTWNNNAPSFAIEAAVVRNPHLLDFLEQVTTYSLLSRWSNTQYMMNW 360  
 Db 301 GTVHPHPSFTSTTWNNNAPSFAIEAAVVRNPHLLDFLEQVTTYSLLSRWSNTQYMMNW 360  
 Qy 361 GGHKLEPRTIGGTINISTOGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTOPVNGVPR 420  
 Db 361 GGHKLEPRTIGGTINISTOGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTOPVNGVPR 420  
 Qy 421 VDFHWKFVTHPIASDNFYYPGVGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 Db 421 VDFHWKFVTHPIASDNFYYPGVGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 Qy 481 ASHVKALVYSWTHRSADRTNTEPNSITQIFLVKAFNLSSGAAVVRGFGFTGGDILRRTN 540  
 Db 481 ASHVKALVYSWTHRSADRTNTEPNSITQIFLVKAFNLSSGAAVVRGFGFTGGDILRRTN 540  
 Qy 541 TGTFGDIRVNINPPPAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATNRRGEDLDYK 600  
 Db 541 TGTFGDIRVNINPPPAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATNRRGEDLDYK 600  
 Qy 601 TPTVTGFTTPSFSLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDEKAEKV 660  
 Db 601 TPTVTGFTTPSFSLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDEKAEKV 660  
 Qy 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFVYKAKQLHIERNM 719  
 Db 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFVYKAKQLHIERNM 719

RESULT 7  
 AAE36275  
 ID AAE36275 standard; protein; 719 AA.  
 XX AC AAE36275;  
 XX DT 26-JUN-2003 (first entry)  
 XX DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa5.  
 XX KW Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.  
 XX OS Bacillus thuringiensis.  
 XX PN WO200298911-A2.  
 XX PD 12-DEC-2002.  
 XX PF 30-MAY-2002; 2002WO-GB002666.  
 XX PR 07-JUN-2001; 2001GB-00013900.  
 XX PA (SYGN ) SYNGENTA LTD.  
 XX PI Vincent JL, Viner R;  
 XX DR WPI; 2003-175137/17.  
 XX PT New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.  
 XX PS Claim 12; Page 53-56; 67pp; English.  
 XX CC The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the CC invention are useful for producing plants or plant parts that are CC resistant to insects. The protein or synergistic combination is useful as CC an active ingredient of a pesticide or for controlling insects. CC Antibodies raised to the insecticidal proteins can be used to identify

CC other proteins with insecticidal activity. The present sequence is  
 CC *Bacillus thuringiensis* insecticidal crystal endotoxin (CRY) protein. This  
 CC sequence is used in the invention  
 XX  
 SQ Sequence 719 AA;

Query Match 99.6%; Score 3745; DB 6; Length 719;  
 Best Local Similarity 99.4%; Pred. No. 1.9e-289;  
 Matches 715; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MRLKNQDQHQSFSSNAKVDKISTSLKNETDIELQNHEDCLKNSEYENVEPVSASTI 60  
 DB 1 MRLKNQDQHQSFSSNAKVDKISTSLKNETDIELQNHEDCLKNSEYENVEPVSASTI 60

QY 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
 DB 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120

QY 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
 DB 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120

QY 121 RNKALTDLKLGDALAVYHDSLESWGNRNTRARSVVKSOYIALELMFYOKLPSPAVSG 180  
 DB 121 RNKALTDLKLGDALAVYHDSLESWGNRNTRARSVVKSOYIALELMFYOKLPSPAVSG 180

QY 121 RNKALTDLKLGDALAVYHDSLESWGNRNTRARSVVKSOYIALELMFYOKLPSPAVSG 180  
 DB 121 RNKALTDLKLGDALAVYHDSLESWGNRNTRARSVVKSOYIALELMFYOKLPSPAVSG 180

QY 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNRQVERAGDYSCHVKWYS 240  
 DB 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNRQVERAGDYSCHVKWYS 240

QY 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNRQVERAGDYSCHVKWYS 240  
 DB 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNRQVERAGDYSCHVKWYS 240

QY 241 TGLNNLRGTNAESWRYNQFRDMLVLDLVALPSPYDTQMPYIKTTAQITREYVTDAL 300  
 DB 241 TGLNNLRGTNAESWRYNQFRDMLVLDLVALPSPYDTQMPYIKTTAQITREYVTDAL 300

QY 301 GTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPHLLDLEQVTIYSLSRWSNTQYNNMW 360  
 DB 301 GTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPHLLDLEQVTIYSLSRWSNTQYNNMW 360

QY 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFTQPVNGVPR 420  
 DB 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFTQPVNGVPR 420

QY 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFTQPVNGVPR 420  
 DB 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFTQPVNGVPR 420

QY 421 VDFHMKFVTHPIASDNFYYPGVGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 DB 421 VDFHMKFVTHPIASDNFYYPGVGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480

QY 421 VDFHMKFVTHPIASDNFYYPGVGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 DB 421 VDFHMKFVTHPIASDNFYYPGVGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480

QY 481 ASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540  
 DB 481 ASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540

QY 541 TGTFGDIRVNPPEAQRVYRIRYASTDLOQHTSINGKAINQGNFSATWNRGDLDYK 600  
 DB 541 TGTFGDIRVNPPEAQRVYRIRYASTDLOQHTSINGKAINQGNFSATWNRGDLDYK 600

QY 541 TGTFGDIRVNPPEAQRVYRIRYASTDLOQHTSINGKAINQGNFSATWNRGDLDYK 600  
 DB 541 TGTFGDIRVNPPEAQRVYRIRYASTDLOQHTSINGKAINQGNFSATWNRGDLDYK 600

## RESULT 8

ID AAB66909  
 XX AAB66909 standard; protein; 719 AA.  
 AC AAB66909;  
 XX  
 DT 12-APR-2001 (first entry)  
 DE Insecticidal protein cryIIa3.  
 XX  
 KW Insecticide; transgenic plant; insect-resistance.  
 OS *Paecilomyces* sp.  
 XX

PN W0200100841-A1.  
 XX 04-JAN-2001.  
 XX 23-JUN-2000; 2000WO-GB002457.  
 XX 29-JUN-1999; 99GB-00015215.  
 PR 23-DEC-1999; 99GB-00030536.  
 XX (ZENE ) ZENECA LTD.  
 XX Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;  
 PI Vincent JL, Lee MD;  
 XX WPI; 2001-123015/13.  
 DR Novel insecticidal protein obtained from species of *Paecilomyces* for  
 PT controlling insects, and for insect-resistant transgenic plant  
 PT production.  
 XX Claim 14; Page 57-59; 72pp; English.  
 XX The present invention relates to novel insecticidal proteins obtained  
 CC from *Paecilomyces* sp. (see AAB66899 to AAB66901 and AAB66913). The  
 CC insecticidal proteins can be used to produce transgenic plants, which are  
 CC insect-resistant. Also, the insecticidal proteins are useful for  
 CC controlling insects by providing them at a locus where insects feed  
 XX  
 SQ Sequence 719 AA;

Query Match 99.4%; Score 3739; DB 4; Length 719;  
 Best Local Similarity 99.4%; Pred. No. 5.7e-289;  
 Matches 715; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MRLKNQDQHQSFSSNAKVDKISTSLKNETDIELQNHEDCLKNSEYENVEPVSASTI 60  
 DB 1 MRLKNQDQHQSFSSNAKVDKISTSLKNETDIELQNHEDCLKNSEYENVEPVSASTI 60

QY 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
 DB 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120

QY 121 RNKALTDLKLGDALAVYHDSLESWGNRNTRARSVVKSOYIALELMFYOKLPSPAVSG 180  
 DB 121 RNKALTDLKLGDALAVYHDSLESWGNRNTRARSVVKSOYIALELMFYOKLPSPAVSG 180

QY 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNRQVERAGDYSCHVKWYS 240  
 DB 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNRQVERAGDYSCHVKWYS 240

QY 241 TGLNNLRGTNAESWRYNQFRDMLVLDLVALPSPYDTQMPYIKTTAQITREYVTDAL 300  
 DB 241 TGLNNLRGTNAESWRYNQFRDMLVLDLVALPSPYDTQMPYIKTTAQITREYVTDAL 300

QY 301 GTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPHLLDLEQVTIYSLSRWSNTQYNNMW 360  
 DB 301 GTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPHLLDLEQVTIYSLSRWSNTQYNNMW 360

QY 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFTQPVNGVPR 420  
 DB 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFTQPVNGVPR 420

QY 421 VDFHMKFVTHPIASDNFYYPGVGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 DB 421 VDFHMKFVTHPIASDNFYYPGVGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480

QY 481 ASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540  
 DB 481 ASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540

QY 541 TGTFGDIRVNPPEAQRVYRIRYASTDLOQHTSINGKAINQGNFSATWNRGDLDYK 600  
 DB 541 TGTFGDIRVNPPEAQRVYRIRYASTDLOQHTSINGKAINQGNFSATWNRGDLDYK 600

QY 601 TFRVTGTTTFFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEYEAEDFEKAQKV 660  
 DB 601 TFRVTGTTTFFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEYEAEDFEKAQKV 660  
 QY 661 TALFTSTNPRGLKTDVKDHYDQVSNLVESLSDEFYLDKRELFVYKAKQLHIERNM 719  
 DB 661 TALFTSTNPRGLKTDVKDHYDQVSNLVESLSDEFYLDKRELFVYKAKQLHIERNM 719

## RESULT 9

AAE36273  
 ID AAE36273 standard; protein; 719 AA.

XX AC AAE36273;

XX DT 26-JUN-2003 (first entry)

XX DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa3.  
 XX KW Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.  
 XX OS Bacillus thuringiensis.

XX FN WO200298911-A2.

XX PD 12-DEC-2002.

XX PF 30-MAY-2002; 2002WO-GB002666.

XX PR 07-JUN-2001; 2001GB-00013900.

XX PA (SYGN ) SYNGENTA LTD.

XX PI Vincent JL, Viner R;

XX XX WPI; 2003-175137/17.

XX DT New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.  
 XX PS Claim 12; Page 47-50; 67pp; English.  
 XX CC The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects.  
 XX CC Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention

XX SQ Sequence 719 AA;

Query Match 99.4%; Score 3739; DB 6; Length 719;  
 Best Local Similarity 99.4%; Pred. No. 5.7e-289;  
 Matches 715; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MLLXNQDKHQSFSNAKVDKISTDSLKNETDIELQINIHEDCLKMSYENVEPFVSASTI 60  
 DB 1 MLLXNQDKHQSFSNAKVDKISTDSLKNETDIELQINIHEDCLKMSYENVEPFVSASTI 60  
 QY 61 QTGIGIAGKILGTGVFPAGQVASYLSYFILGELWPKGNQWEIFMEHVEIINQISTYA 120  
 DB 61 QTGIGIAGKILGTGVFPAGQVASYLSYFILGELWPKGNQWEIFMEHVEIINQISTYA 120  
 QY 121 RNKALTDLKGLGDALAVYHDSLEWGNRNNTARSVVKSQYIALELMFVKLPSFAVSG 180  
 DB 121 RNKALTDLKGLGDALAVYHDSLEWGNRNNTARSVVKSQYIALELMFVKLPSFAVSG 180

QY 181 BEVPLLPYQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWS 240

DB 181 BEVPLLPYQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWS 240  
 QY 241 TGLNNLRGTNAESWRYNQFRDMLVLDLVALFPSTYDTOMYPIKTTAQUTREYVTDAL 300  
 DB 241 TGLNNLRGTNAESWRYNQFRDMLVLDLVALFPSTYDTOMYPIKTTAQUTREYVTDAL 300  
 QY 301 GTVHPHPSTSTTWYNNNAPSFAIEAAAVRNPHLLDFLEQVTIYSLLSRSNTQYMMW 360  
 DB 301 GTVHPHPSTSTTWYNNNAPSFAIEAAAVRNPHLLDFLEQVTIYSLLSRSNTQYMMW 360  
 QY 361 GGHKLEFRTIGTLNISTQGSTNTSINPVTLPFTSRDVTRESLAGLNLFTOPVNGVPR 420  
 DB 361 GGHKLEFRTIGTLNISTQGSTNTSINPVTLPFTSRDVTRESLAGLNLFTOPVNGVPR 420  
 QY 421 VDFHMKFVTHPIASDNFYYPGVGIGTQLODSENELPPEATGQPNYESYSHLSHIGLIS 480  
 DB 421 VDFHMKFVTHPIASDNFYYPGVGIGTQLODSENELPPEATGQPNYESYSHLSHIGLIS 480  
 QY 481 ASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 540  
 DB 481 ASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 540  
 QY 541 TGTFGDIEVWINPPPAQRYRVRIYASTTDIQFHTSINGKAINQGNFSATNRRGDLDYK 600  
 DB 541 TGTFGDIEVWINPPPAQRYRVRIYASTTDIQFHTSINGKAINQGNFSATNRRGDLDYK 600  
 QY 601 TPTVTGFTTFFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEYEAEDFEKAQKV 660  
 DB 601 TPTVTGFTTFFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEYEAEDFEKAQKV 660  
 QY 661 TALFTSTNPRGLKTDVKDHYDQVSNLVESLSDEFYLDKRELFVYKAKQLHIERNM 719  
 DB 661 TALFTSTNPRGLKTDVKDHYDQVSNLVESLSDEFYLDKRELFVYKAKQLHIERNM 719

## RESULT 10

AAE08041  
 ID AAE08041 standard; protein; 719 AA.

XX AC AAE08041;

XX DT 24-OCT-2003 (revised)

XX DT 25-MAR-2003 (revised)

XX DT 27-FEB-1991 (first entry)

XX DE 81 kD endotoxin deduced from DNA carried on pJH12.  
 XX KW Crystal; insecticide; toxin; delta endotoxin.

XX OS Bacillus thuringiensis; JHCC 4353 and 4835.

XX PN WO9013651-A.

XX PD 15-NOV-1990.

XX PF 09-MAY-1989; 89GB-00010624.

XX PR 09-MAY-1989; 89GB-00010624.

XX XX (ICIL ) IMPERIAL CHEM IND PLC.

XX PI Blenk RG, Ely S, Tailor RH, Tippet JW;

XX DR WPI; 1990-361486/48.

XX DR N-PSDB; AAQ06636.

XX PT Bacillus thuringiensis strains - used for producing an endotoxin for protecting plants against insects, partic. Lepidoptera and Coleoptera.  
 XX PS Claim 5; Fig 5-10; 66pp; English.  
 XX CC The sequence carried on pJH12 which was isolated from B. thuringiensis strains JHCC4835 and JHCC 4353 (NCIB 40091 and 40090 resp.). The DNA can

CC be used to produce transformants E.coli strain MC12022/pJH12 (NCIB 40278,  
CC or bacteriophage EMBL4 vector (NCIB 40279) or E.coli strain BL21/pJH11  
CC (NCIB 40275). The delta-endo- toxin produced by the transformants can be  
CC used in formulations for combatting Lepidoptera and Coleoptera pests.  
CC (Updated on 25-MAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to  
CC standardise OS field)  
XX Sequence 719 AA;

Query Match 99.3%; Score 3735; DB 2; Length 719;  
Best Local Similarity 99.4%; Pred. No. 1.2e-288;  
Matches 715; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 1 MKLNQDQKHQSFSSNAKVDKISTDSLNKNETDIELQNHEDCLMKSEYENVEPVSASTI 60  
Db 1 MKLNQDQKHQSFSSNAKVDKISTDSLNKNETDIELQNHEDCLMKSEYENVEPVSASTI 60  
QY 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELMPKGNQWEIEMHVEEIIINQKISTYA 120  
Db 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELMPKGNQWEIEMHVEEIIINQKISTYA 120  
QY 121 RNKALTDLKGGLDALAVYHDSLESVGNRNTRARSVVKSQVIALELMFVOKLPSFAVSG 180  
Db 121 RNKALTDLKGGLDALAVYHDSLESVGNRNTRARSVVKSQVIALELMFVOKLPSFAVSG 180  
QY 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHVKWYS 240  
Db 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHVKWYS 240  
QY 241 TGLNNLRGTNAESWRYNQFRDMTLMVLDLVALPSPYDTQMPYIKTTAQTREVVYDAI 300  
Db 241 TGLNNLRGTNAESWRYNQFRDMTLMVLDLVALPSPYDTQMPYIKTTAQTREVVYDAI 300  
QY 301 GTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDPLEOVITYSLLSRWSNTQYNNMW 360  
Db 301 GTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDPLEOVITYSLLSRWSNTQYNNMW 360  
QY 361 GGHKLEFRTIGTGLNISQGSTNTSINPVTLPFTSRDYRTESLAGNLFITQPNVGR 420  
Db 361 GGHKLEFRTIGTGLNISQGSTNTSINPVTLPFTSRDYRTESLAGNLFITQPNVGR 420  
QY 421 VDFHWKFTVTHPIASDNFYYPGVGIGTQDSENELPEATGQPNYSYSHRSHIGLIS 480  
Db 421 VDFHWKFTVTHPIASDNFYYPGVGIGTQDSENELPEATGQPNYSYSHRSHIGLIS 480  
QY 481 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 540  
Db 481 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 540  
QY 541 TGTGDIRVNNPPAQRVRIYASTTDLOFTSINGKAINQGNFSATNRRGEDLDYK 600  
Db 541 TGTGDIRVNNPPAQRVRIYASTTDLOFTSINGKAINQGNFSATNRRGEDLDYK 600  
QY 601 TFRVTGFTPTPSFLDVQSTFTIGAWNFSSGNEVIDRIEFVFPVETVEAEYDEKAEKV 660  
Db 601 TFRVTGFTPTPSFLDVQSTFTIGAWNFSSGNEVIDRIEFVFPVETVEAEYDEKAEKV 660  
QY 661 TALEFTSNPRGLKTDVKDHYHDQVSNLVESLSDBFYLDKELPEIVKYAKQLHIERNM 719  
Db 661 TALEFTSNPRGLKTDVKDHYHDQVSNLVESLSDBFYLDKELPEIVKYAKQLHIERNM 719

RESULT 11  
AAE36271  
ID AAE36271 standard; protein; 718 AA.  
XX  
AC AAE36271;  
XX  
DT 26-JUN-2003 (first entry)  
XX  
DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa1.  
XX Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.  
KW

XX Bacillus thuringiensis.  
XX WO200298911-A2.  
XX 12-DEC-2002.  
XX  
XX 30-MAY-2002; 2002WO-GB002666.  
XX  
XX 07-JUN-2001; 2001GB-00013900.  
XX (SYGN ) SYNGENTA LTD.  
XX Vincent JL, Viner R;  
XX WPI; 2003-175137/17.  
XX  
XX New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.  
XX Claim 12; Page 42-44; 67pp; English.  
XX The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects.  
XX Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is CC Bacillus thuringiensis insecticidal crystal endotoxin (Cry) protein. This CC sequence is used in the invention  
XX  
XX Sequence 718 AA;

Query Match 99.1%; Score 3724.5; DB 6; Length 718;  
Best Local Similarity 99.4%; Pred. No. 8.2e-288;  
Matches 715; Conservative 0; Mismatches 3; Indels 1; Gaps 1;  
QY 1 MKLNQDQKHQSFSSNAKVDKISTDSLNKNETDIELQNHEDCLMKSEYENVEPVSASTI 60  
Db 1 MKLNQDQKHQSFSSNAKVDKISTDSLNKNETDIELQNHEDCLMKSEYENVEPVSASTI 60  
QY 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELMPKGNQWEIEMHVEEIIINQKISTYA 120  
Db 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELMPKGNQWEIEMHVEEIIINQKISTYA 120  
QY 121 RNKALTDLKGGLDALAVYHDSLESVGNRNTRARSVVKSQVIALELMFVOKLPSFAVSG 180  
Db 121 RNKALTDLKGGLDALAVYHDSLESVGNRNTRARSVVKSQVIALELMFVOKLPSFAVSG 180  
QY 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHVKWYS 240  
Db 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHVKWYS 240  
QY 241 TGLNNLRGTNAESWRYNQFRDMTLMVLDLVALPSPYDTQMPYIKTTAQTREVVYDAI 300  
Db 241 TGLNNLRGTNAESWRYNQFRDMTLMVLDLVALPSPYDTQMPYIKTTAQTREVVYDAI 300  
QY 301 GTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDPLEOVITYSLLSRWSNTQYNNMW 360  
Db 301 GTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDPLEOVITYSLLSRWSNTQYNNMW 360  
QY 361 GGHKLEFRTIGTGLNISQGSTNTSINPVTLPFTSRDYRTESLAGNLFITQPNVGR 420  
Db 361 GGHKLEFRTIGTGLNISQGSTNTSINPVTLPFTSRDYRTESLAGNLFITQPNVGR 420  
QY 421 VDFHWKFTVTHPIASDNFYYPGVGIGTQDSENELPEATGQPNYSYSHRSHIGLIS 480  
Db 421 VDFHWKFTVTHPIASDNFYYPGVGIGTQDSENELPEATGQPNYSYSHRSHIGLIS 480  
QY 481 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 540  
Db 481 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 540



QY 541 TGTGDIRVNINPPFAQRYRIRYASTTDLOQHTSINGKAINQGNFSAATMNRGDLDYK 600  
 DB 540 TGTGDIRVNINPPFAQRYRIRYASTTDLOQHTSINGKAINQGNFSAATMNRGDLDYK 599  
 QY 601 TFRVTGFTTFFSFLDQSTFTIGAMNFSSGNEVYIDRIEFVPEVYEAEDPEKAQEKV 660  
 DB 600 TFRVTGFTTFFSFLDQSTFTIGAMNFSSGNEVYIDRIEFVPEVYEAEDPEKAQEKV 659  
 QY 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVSLSDEFYLDKRELFELVYKAKQLHIERNM 719  
 DB 660 TALFTSTNPRGLKTDVKDHYHIDQVSNLVSLSDEFYLDKRELFELVYKAKQLHIERNM 718

RESULT 12  
 AAB66907  
 ID AAB66907 standard; protein; 718 AA.  
 AC AAB66907;  
 DT 12-APR-2001 (first entry)  
 DE Insecticidal protein cryIIa1.  
 DE Insecticide; transgenic plant; insect-resistance.  
 KW Paecilomyces sp.  
 OS Paecilomyces sp.  
 PN WO200100841-A1.  
 PD 04-JAN-2001.  
 PP 23-JUN-2000; 2000WO-GB002457.  
 PR 29-JUN-1999; 99GB-00015215.  
 PR 23-DEC-1999; 99GB-00030536.  
 XX (ZENE ) ZENECA LTD.  
 XX Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;  
 PI Vincent JL, Lee MD;  
 XX WPI; 2001-123015/13.  
 XX Novel insecticidal protein obtained from species of Paecilomyces for  
 PT controlling insects, and for insect-resistant transgenic plant  
 PT production.  
 XX Claim 14; Page 53-55; 72pp; English.  
 XX The present invention relates to novel insecticidal proteins obtained  
 CC from Paecilomyces sp. (see AAB66907 to AAB66901 and AAB66913). The  
 CC insecticidal proteins can be used to produce transgenic plants, which are  
 CC insect-resistant. Also, the insecticidal proteins are useful for  
 CC controlling insects by providing them at a locus where insects feed  
 CC  
 SQ Sequence 718 AA;

Query Match 98.8%; Score 3718.5; DB 4; Length 718;  
 Best Local Similarity 99.3%; Pred. No. 2.5e-287;  
 Matches 714; Conservative 0; Mismatches 4; Indels 1; Gaps 1;  
 QY 1 MRLKNQDKHQSFSSNAKVKDSTLSKNETDIELQNIHEDCLKMSYENVEFPVSASTI 60  
 DB 1 MRLKNQDKHQSFSSNAKVKDSTLSKNETDIELQNIHEDCLKMSYENVEFPVSASTI 60  
 QY 61 QTGIGIAGKILGTGVFPAGVQASLYSIFILGELWPKGNQWEIPMEHVEHINQKISTYA 120  
 DB 61 QTGIGIAGKILGTGVFPAGVQASLYSIFILGELWPKGNQWEIPMEHVEHINQKISTYA 120  
 QY 121 RNKALTDLKGIGDALAVYHDSLSMGVGNRNNTRARSVVKQYTALELMFVKLPSPFAVSG 180  
 DB 121 RNKALTDLKGIGDALAVYHDSLSMGVGNRNNTRARSVVKQYTALELMFVKLPSPFAVSG 180

QY 181 BEVPLLPYQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWS 240  
 DB 181 BEVPLLPYQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWS 240  
 QY 241 TGLANLRGTNAESWVRVYVQFRDMLVLDVALVPSYDTOMYPIKTTAQITREYTDI 300  
 DB 241 TGLANLRGTNAESWVRVYVQFRDMLVLDVALVPSYDTOMYPIKTTAQITREYTDI 300  
 QY 301 GTVHPHPSFTTWTNNNAPSFAIEAAVVRNPHLLDPLEQVTIYSLSRNSNTQYNNMW 360  
 DB 301 GTVHPHPSFTTWTNNNAPSFAIEAAVVRNPHLLDPLEQVTIYSLSRNSNTQYNNMW 360  
 QY 361 GGHKLEFFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTERSLAGLNLFTQPNV 420  
 DB 361 GGHKLEFFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTERSLAGLNLFTQPNV 419  
 QY 421 VDFHWKFTVHTPIASDNFYVGVIGTQLODSENEPEATGQPNYESYSHRLSHIGLIS 480  
 DB 420 VDFHWKFTVHTPIASDNFYVGVIGTQLODSENEPEATGQPNYESYSHRLSHIGLIS 479  
 QY 481 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 540  
 DB 480 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 539  
 QY 541 TGTGDIRVNINPPFAQRYRIRYASTTDLOQHTSINGKAINQGNFSAATMNRGDLDYK 600  
 DB 540 TGTGDIRVNINPPFAQRYRIRYASTTDLOQHTSINGKAINQGNFSAATMNRGDLDYK 599  
 QY 601 TFRVTGFTTFFSFLDQSTFTIGAMNFSSGNEVYIDRIEFVPEVYEAEDPEKAQEKV 660  
 DB 600 TFRVTGFTTFFSFLDQSTFTIGAMNFSSGNEVYIDRIEFVPEVYEAEDPEKAQEKV 659  
 QY 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVSLSDEFYLDKRELFELVYKAKQLHIERNM 719  
 DB 660 TALFTSTNPRGLKTDVKDHYHIDQVSNLVSLSDEFYLDKRELFELVYKAKQLHIERNM 718

RESULT 13  
 ADM74717  
 ID ADM74717 standard; protein; 719 AA.  
 AC ADM74717;  
 DT 03-JUN-2004 (first entry)  
 DE B. thuringiensis cryIIel SEQ ID NO:2.  
 KW cryI; toxicity; lepidoptera; cryIIa; cryIIb; coleoptera; diptera;  
 KW cryIIel.  
 OS Bacillus thuringiensis.  
 XX CN1401772-A.  
 PD 12-MAR-2003.  
 PF 20-AUG-2001; 2001CN-00124163.  
 PR 20-AUG-2001; 2001CN-00124163.  
 PA (PLAN-) PLANT PROTECTION INST CHINESE ACAD AGRIC.  
 XX Song F, Zhang J, Huang D;  
 XX WPI; 2003-442339/42.  
 XX N-PSDB; ADM74716.  
 XX Bacillus thuringiensis cryI gene, expression vector, nucleotide sequence  
 PT with high-toxicity to lepidoptera pests, encoded protein, primer  
 PT sequences and the shuttle vector pSX422b, useful as a pesticide.  
 XX Example 3; SEQ ID NO 2; 29pp; Chinese.

XX CC The invention relates to a novel *Bacillus thuringiensis* cryI gene, gene  
 CC combination, expression vector, nucleotide sequence of the B  
 CC *thuringiensis* cryI gene with high-toxicity to lepidoptera pests and the  
 CC amino acid sequence of the protein encoded by it, cooperative use of the  
 CC cryI gene with the expression product of cryIaB or cryIaC, primer  
 CC sequences for expressing the genes, and the constructed shuttle vector  
 CC pSX422b. The gene in combination with the cryIaB or cryIaC genes  
 CC displays high toxicity to the lepidoptera, coleoptera and diptera pests.  
 CC The present sequence represents the cryIaI protein.  
 XX CC Sequence 719 AA;  
 XX CC  
 XX CC Query Match 94.3%; Score 3547; DB 7; Length 719;  
 XX CC Best Local Similarity 93.5%; Pred. No. 1.2e-273;  
 XX CC Matches 672; Conservative 26; Mismatches 21; Indels 0; Gaps 0;  
 XX CC  
 XX QY 1 M K L K N Q D K H Q S P S S N A K V D K I S T S L K N E T D I E L Q N I N H E D C L K M S E Y N V E P F V S A S T I 60  
 XX Db 1 M K L K N P D R H Q S L S S N A K V D K I A T S L K N E T D I E L K N I N H E D F L M S E H E S I D P F V S A S T I 60  
 XX QY 61 Q T G I G I A K I L G T L G V P P A G V A S I Y S F I L G E L W P K G K N Q W E I F M E H V E E I I N Q K I S T Y A 120  
 XX Db 61 Q T G I G I A K I L G T L G V P P A G V A S I Y S F I L G E L W P K G S Q W E I F M E H V E E I I D Q K I S T Y A 120  
 XX QY 121 R N K A L T D L K G L G D A L A V H D S L E S W G N R N T R A S V V K S O V I A L E M F V Q K L P S P A V S G 180  
 XX Db 121 R N I A L A D I L K G L G D A L A V H E S L E S W K R N N A R A T S V V K S O I A L E L L F V Q K L P S P A V S G 180  
 XX QY 181 E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S E I S T F Y N R Q V R A G D Y S D H C V K W Y S 240  
 XX Db 181 E V P L L P I Y A Q A A N L H L L L R D A S V F G K E W G L S N S Q I S T F Y N R Q V E R T S D Y S D H C V K W Y S 240  
 XX QY 241 T G L N L R G T N A E S W R Y N Q F R D M T L M V L D I A L V A L P P S Y D T Q M Y P I K T A Q L T R E V Y T D A I 300  
 XX Db 241 T G L N N L R G T N A E S W R Y N Q F R D M T L M V L D I A L P P S Y D T L V Y P I K T S Q L T R E V Y T D A I 300  
 XX QY 301 G T V H P H P S F T S T T W N N N A P S F S A I E A A V V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y N N W 360  
 XX Db 301 G T V H E N A S F A S T T W N N N A P S F S A I E S A V V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y N N W 360  
 XX QY 361 G G H K L E F T I G T L N I S T Q G S T N T S I N P V T L P F T S R D V Y R T E S L A G L N L F L T Q P V N G V P R 420  
 XX Db 361 G G H R L E F T I G G V L N T S Q G S T N T S I N P V T L P F T S R D V Y R T E S L A G L N L F L T Q P V N G V P R 420  
 XX QY 421 V D F H W K F T P I A S D N F Y Y L G V A G V G T Q L O D S E N E L P P E A T G Q N Y S Y S H R L S H I G L I S 480  
 XX Db 421 V D F H W K F A T L P I A S D N F Y Y L G Y A G V G T Q L O D S E N E L P P E T T G Q N Y S Y S H R L S H I G L I S 480  
 XX QY 481 A S H V K A L Y S W T H R S A D R T N T I E N S T Q I P L V A F N L S S G A A V V R G P G T G G D I L R T N 540  
 XX Db 481 A S H V K A L Y S W T H R S A D R T N T I E P N S T Q I P L V A F N L S S G A A V V R G P G T G G D I L R T N 540  
 XX QY 541 T G T P G D I R V N I P P P A Q R Y R I R Y A S T T D L Q F T S I N G K A I N Q G N S A T M N R G E D L D Y K 600  
 XX Db 541 T G T P G D I R V N I P P P A Q R Y R I R Y A S T T D L Q F T S I N G K A I N Q G N S A T M N R G E D L D Y K 600  
 XX QY 601 T F R T V G F T P P S F L D V Q S T F T I G A W N F S S G N E V I D R I E F V P V E V T Y E A Y D F E K A Q E K V 660  
 XX Db 601 T F R T V G F T P P S F S D V Q S T F T I G A W N F S S G N E V I D R I E F V P V E V T Y E A Y D F E K A Q E K V 660  
 XX QY 661 T A L F T S T N P R G L K T D V K D Y H I D Q V N L V E S I S D E F Y L D E K R E L F E I V K Y A K Q L H I E R N M 719  
 XX Db 661 T A L F T S T N P R G L K T D V K D Y H I D Q V N L V E S I S D E F Y L D E K R E L F E I V K Y A K Q L H I E R N M 719

RESULT 14

AAB66912

ID AAB66912 standard; protein; 719 AA.

XX AAB66912;

AC AAB66912;

XX DT 12-APR-2001 (first entry)

XX Insecticidal protein cryIaI.  
 XX Insecticide; transgenic plant; insect-resistance.  
 XX Paecilomyces sp.  
 XX WO200100841-A1.  
 XX 04-JAN-2001.  
 XX 23-JUN-2000; 2000WO-GB002457.  
 XX 29-JUN-1999; 99GB-00015215.  
 XX 23-DEC-1999; 99GB-00030536.  
 XX (ZENE ) ZENECA LTD.  
 XX Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;  
 XX Vincent JL, Lee MD;  
 XX WPI; 2001-123015/13.  
 XX Novel insecticidal protein obtained from species of Paecilomyces for  
 XX controlling insects, and for insect-resistant transgenic plant  
 XX production.  
 XX Claim 14; Page 64-66; 72pp; English.  
 XX The present invention relates to novel insecticidal proteins obtained  
 XX from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The  
 XX insecticidal proteins can be used to produce transgenic plants, which are  
 XX insect-resistant. Also, the insecticidal proteins are useful for  
 XX controlling insects by providing them at a locus where insects feed  
 XX Sequence 719 AA;  
 XX Query Match 93.5%; Score 3516; DB 4; Length 719;  
 XX Best Local Similarity 92.8%; Pred. No. 3.5e-271;  
 XX Matches 667; Conservative 31; Mismatches 21; Indels 0; Gaps 0;  
 XX  
 XX QY 1 M K L K N Q D K H Q S P S S N A K V D K I S T S L K N E T D I E L Q N I N H E D C L K M S E Y N V E P F V S A S T I 60  
 XX Db 1 M K L K N P D R H Q S L S S N A K V D K I A T S L K N E T D I E L K N I N H E D F L M S E H E S I D P F V S A S T I 60  
 XX QY 61 Q T G I G I A K I L G T L G V P P A G V A S I Y S F I L G E L W P K G K N Q W E I F M E H V E E I I N Q K I S T Y A 120  
 XX Db 61 Q T G I G I A K I L G T L G V P P A G V A S I Y S F I L G E L W P K G S Q W E I F M E H V E E I I N Q K I S T Y A 120  
 XX QY 121 R N K A L T D L K G L G D A L A V H D S L E S W G N R N T R A S V V K S O V I A L E M F V Q K L P S P A V S G 180  
 XX Db 121 R N K A L S D L R G L G D A L A V H E S L E S W N R N T R A S V V K N Q V I A L E M F V Q K L P S P A V S G 180  
 XX QY 181 E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S E I S T F Y N R Q V R A G D Y S D H C V K W Y S 240  
 XX Db 181 E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S A S E I S T F Y N R Q V E R T D Y S D H C I K W Y N 240  
 XX QY 241 T G L N L R G T N A E S W R Y N Q F R D M T L M V L D I A L V A L P P S Y D T Q M Y P I K T A Q L T R E V Y T D A I 300  
 XX Db 241 T G L N N L R G T N A E S W R Y N Q F R D M T L M V L D I A L P P S Y D T L V Y P I K T S Q L T R E V Y T D A I 300  
 XX QY 301 G T V H P H P S F T S T T W N N N A P S F S A I E A A V V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y N N W 360  
 XX Db 301 G T V H E N Q A F A S T T W N N N A P S F S A I E A A V I R S P H L L D F L E K V T I Y S L S R W S N T Q Y N N W 360  
 XX QY 361 G G H K L E F R T I G T L N I S T Q G S T N T S I N P V T L P F T S R D V Y R T E S L A G L N L F L T Q P V N G V P R 420  
 XX Db 361 G G H R L E S R P I G G A L N T S T Q G S T N T S I N P V T L Q F T S R D V Y R T E S L A G L N L F L T Q P V N G V P R 420  
 XX QY 421 V D F H W K F T P I A S D N F Y Y L G V A G V G T Q L O D S E N E L P P E A T G Q N Y S Y S H R L S H I G L I S 480  
 XX Db 421 V D F H W K F T L P I A S D N F Y Y L G V A G V G T Q L O D S E N E L P P E T T G Q N Y S Y S H R L S H I G L I S 480

QY 481 ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRTN 540  
 Db 481 ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRTN 540  
 QY 541 TGTGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLDYK 600  
 Db 541 TGTGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLDYK 600  
 QY 601 TFRVVGTTTFFSFDVQSTTTIGAWNFSSGNEVVIDRIEFVPEVTVYEAEDYDEKAQEKV 660  
 Db 601 TFRVVGTTTFFSFDVQSTTTIGAWNFSSGNEVVIDRIEFVPEVTVYEAEDYDEKAQEKV 660  
 QY 661 TALFTSTNPRGLKTDVVDKDYHIDQVSNLVESLSDEFYLDKRELFPEIVKYAKQIHIERNM 719  
 Db 661 TALFTSTNPRGLKTDVVDKDYHIDQVSNLVESLSDEFYLDKRELFPEIVKYAKQIHIERNM 719

RESULT 15  
 AAE36276  
 ID AAE36276 standard; protein; 719 AA.  
 XX  
 AC  
 AC  
 XX  
 XX  
 DT 26-JUN-2003 (first entry)  
 XX  
 XX  
 DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIb1.  
 XX  
 XX Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.  
 XX  
 KW Bacillus thuringiensis.  
 OS  
 XX  
 XX WO200298911-A2.  
 XX  
 PD 12-DEC-2002.  
 XX  
 XX 30-MAY-2002; 2002WO-GB002666.  
 XX  
 XX 07-JUN-2001; 2001GB-00013900.  
 XX  
 XX (SYGN ) SYNGENTA LTD.  
 XX  
 XX Vincent JL, Viner R;  
 XX  
 XX WPI; 2003-175137/17.  
 XX  
 XX New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.  
 XX  
 XX Claim 12; Page 56-58; 67pp; English.

The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects. Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention

XX Sequence 719 AA;

Query Match 93.5%; Score 3516; DB 6; Length 719;  
 Best Local Similarity 92.8%; Pred. No. 3.5e-271;  
 Matches 667; Conservative 31; Mismatches 21; Indels 0; Gaps 0;

QY 1 MKLKNQDKHQSFNNAKVDKISTSLKNETDIELQININHEDCIKMSYENVEPVSASTI 60  
 Db 1 MKLKNPDKHQSLSNAKVDKIATDSLKNETDIELKNMNDYLRMSHESIDPPVSASTI 60  
 QY 61 QTGIGIACKILGTGVPPAGQVASYLSPILGELMPKGNQWEIPEHVEEIIINQIISTYA 120  
 Db 61 QTGIGIACKILGTGVPPAGQIASIYSPILGELMPKGSQWEIPEHVEEIIINQIILTYA 120

QY 121 RNKALTDJLGLDALAVVHDSLESWGNRNINTRARSVVKSVQYIALELMFVQKLPFAVSG 180  
 Db 121 RNKALSDJLGLDALAVVHDSLESWGNRNINTRARSVVKSVQYIALELMFVQKLPFAVSG 180  
 QY 181 BEVPILPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNROVERAGDYSCHCKVAYS 240  
 Db 181 BEVPILPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNROVERAGDYSCHCKVAYS 240  
 QY 241 TGLNLRGTNAESWRYNQFRDRMTLMVLDLVALFSPSYDTQMPYIKTTAQLTREYVTDAT 300  
 Db 241 TGLNLRGTNAESWRYNQFRDRMTLMVLDLVALFSPSYDTQMPYIKTTAQLTREYVTDAT 300  
 QY 301 GTVHPHPSTSTWNNNAPSASIAEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMMNW 360  
 Db 301 GTVHPNQAFASTWNNNAPSASIAEAAVIRSFHLLDFLEKVTIYSLSRWSNTQYMMNW 360  
 QY 361 GGHKLEFRITGGTLNISTQGSTNTSINPVTLPTTGRDVRVYRTESLAGLNLFLTQPVNGVPR 420  
 Db 361 GGHRLSEPRIGGALNTSQGSTNTSINPVTLQFTSRDVRVYRTESLAGLNLFLTQPVNGVPR 420  
 QY 421 VDFHWKFTVTHPIASDNFYYPGVYIGTQLQDSSENELPPEATQGPYVESYSHRLSHIGLIS 480  
 Db 421 VDFHWKFTPLPIASDNFYVLGYAGVGTQLQDSSENELPPEATTQGPYVESYSHRLSHIGLIS 480  
 QY 481 ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRTN 540  
 Db 481 ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRTN 540  
 QY 541 TGTGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLDYK 600  
 Db 541 TGTGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLDYK 600  
 QY 601 TFRVVGTTTFFSFDVQSTTTIGAWNFSSGNEVVIDRIEFVPEVTVYEAEDYDEKAQEKV 660  
 Db 601 TFRVVGTTTFFSFDVQSTTTIGAWNFSSGNEVVIDRIEFVPEVTVYEAEDYDEKAQEKV 660  
 QY 661 TALFTSTNPRGLKTDVVDKDYHIDQVSNLVESLSDEFYLDKRELFPEIVKYAKQIHIERNM 719  
 Db 661 TALFTSTNPRGLKTDVVDKDYHIDQVSNLVESLSDEFYLDKRELFPEIVKYAKQIHIERNM 719

Search completed: October 28, 2004, 18:20:02  
 Job time : 89.6903 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 28, 2004, 18:05:43 ; Search time 19.191 Seconds  
(without alignments)  
3604.811 Million cell updates/sec

Title: US-10-019-823B-58  
Perfect score: 3761  
Sequence: 1 MKLKNQDKHQSFPSSNAKVDK.....KRELFIYKYNELHIERNM 719

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_79:.\*  
1: Pir1.\*  
2: Pir2.\*  
3: Pir3.\*  
4: Pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3724	99.0	719	2 139814	insecticidal prote
2	3724	99.0	719	2 139815	insecticidal prote
3	3715	98.8	719	2 S25383	parasporal crystal
4	3484	92.6	719	2 140590	crystallin protein -
5	2248.5	59.8	1228	2 S00873	parasporal crystal
6	1872	49.8	380	2 B42459	hypothetical prote
7	1466	39.0	1157	1 S49247	parasporal crystal
8	1488.5	38.8	1166	2 S32645	parasporal crystal
9	1450	38.6	1155	2 A26513	parasporal crystal
10	1449	38.5	1174	2 S32649	parasporal crystal
11	1443	38.4	1155	2 J00002	parasporal crystal
12	1443	38.4	1156	2 A29125	parasporal crystal
13	1434	38.1	1155	2 139838	parasporal crystal
14	1430.5	38.0	934	2 A22798	parasporal crystal
15	1429.5	38.0	1176	2 J00241	parasporal crystal
16	1426	37.9	1155	2 S02134	parasporal crystal
17	1425.5	37.9	1181	2 A41052	parasporal crystal
18	1423.5	37.8	1176	2 J02219	parasporal crystal
19	1419.5	37.7	1176	2 A22617	parasporal crystal
20	1415.5	37.6	1176	2 S02215	parasporal crystal
21	1338	35.6	1174	2 A42459	parasporal crystal
22	1335	35.2	1138	2 A48944	parasporal crystal
23	1315	35.0	1156	2 A29838	parasporal crystal
24	1304.5	34.7	823	2 S04181	parasporal crystal
25	1295.5	34.4	1189	2 S00944	parasporal crystal
26	1281	34.1	1154	2 S99536	parasporal crystal
27	1248	33.2	1171	2 I40572	parasporal crystal
28	1248	33.2	1171	2 A37829	parasporal crystal
29	1235	32.8	1176	2 A48970	parasporal crystal

30	1208	32.1	1160	2 S32647	parasporal crystal
31	1193.5	31.7	1165	2 S11446	parasporal crystal
32	1188.5	31.6	655	2 JC7140	protocxin - Bacillu
33	1172	31.2	1172	2 S32689	parasporal crystal
34	1154	30.7	1160	2 I40589	parasporal crystal
35	1139.5	30.3	1178	1 USBSXH	parasporal crystal
36	1139	30.3	1177	2 A49785	parasporal crystal
37	1137	30.2	652	2 A27323	parasporal crystal
38	1113	29.6	659	2 S10228	parasporal crystal
39	1080.5	28.7	652	2 139811	parasporal crystal
40	966	25.7	649	1 JHC261	parasporal crystal
41	917	24.4	618	2 S11445	parasporal crystal
42	881	23.4	1156	2 S19306	parasporal crystal
43	800	21.3	1136	1 USBS81	parasporal crystal
44	693.5	18.4	934	2 B39838	parasporal crystal
45	645	17.1	1180	2 139870	parasporal crystal

ALIGNMENTS

RESULT 1

I39814  
Insecticidal protein cryVI - Bacillus thuringiensis  
C/Species: Bacillus thuringiensis  
C/Date: 19-Jul-1996 #sequence\_revision 19-Jul-1996 #text\_change 26-Aug-1999  
C/Accession: I39814  
R/Shin, B.S.; Park, S.H.; Choi, S.K.; Koo, B.T.; Lee, S.T.; Kim, J.I.  
Appl. Environ. Microbiol. 61, 2402-2407, 1995  
A/Title: Distribution of cryV-type insecticidal protein genes in Bacillus thuringiensis  
tomocidus.  
A/Reference number: I39814; MUID:95314293; PMID:7793960  
A/Accession: I39814  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-719 <RES>  
A/Cross-references: GB:L36338; NID:g540281; PIDN:AA36999.1; PID:g540282  
C/Genetics:  
A/Gene: cryVI  
C/Superfamily: parasporal crystal protein

Query Match 99.0%; Score 3724; DB 2; Length 719;  
Best Local Similarity 99.4%; Pred-No 2 4e-254;  
Matches 716; Conservative 1; Mismatches 1; Indels 2; Gaps 2;

QY	1	MKLKNQDKHQSFPSSNAKVDKISTDLKNETDIELQININHEDCMKSEYENVPFVSASTI	60
DB	1	MKLKNQDKHQSFPSSNAKVDKISTDLKNETDIELQININHEDCMKSEYENVPFVSASTI	60
QY	61	QTGIGTAGKILGTGLGVPPAGQVASYFTLGLMFKGNQWEILFMEHVEE-INOKISTY	119
DB	61	QTGIGTAGKILGTGLGVPPAGQVASYFTLGLMFKGNQWEILFMEHVEE-INOKISTY	119
QY	120	ARNKALTDLKLGDALAVVHDSLESWVGNNRNRARSVVRVRSQYIALELMFVKLPSPFVS	179
DB	120	ARNKALTDLKLGDALAVVHDSLESWVGNNRNRARSVVRVRSQYIALELMFVKLPSPFVS	179
QY	180	GEVPLLPPIYAQAANLHLLLDASIFGKENGSLSSSEISTFYNRQVERAGDSDHCVKWY	239
DB	180	GEVPLLPPIYAQAANLHLLLDASIFGKENGSLSSSEISTFYNRQVERAGDSDHCVKWY	239
QY	240	STGLNLRGTNAESWRYNQFRDMTLVLDLVALPSPSYDTQMPYIKTTAQLTREYVYTD	299
DB	240	STGLNLRGTNAESWRYNQFRDMTLVLDLVALPSPSYDTQMPYIKTTAQLTREYVYTD	299
QY	300	IGTVPHPSFTSTTWYNNNAPSFSAEAAVVRNPHLLDFLEQVITYSLLSRNSNTQYMM	359
DB	300	IGTVPHPSFTSTTWYNNNAPSFSAEAAVVRNPHLLDFLEQVITYSLLSRNSNTQYMM	359
QY	360	WGCHKLEFRITGTLNISTQGSTNTSINPVTLPFTSRDVRVRESLGLNLFITQPNGVP	419
DB	360	WGCHKLEFRITGTLNISTQGSTNTSINPVTLPFTSRDVRVRESLGLNLFITQPNGVP	419

QY 420 RYDFHKKFVTHPIASDNFYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLI 479  
 Db 420 RYDFHKKFVTHPIASDNFYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLI 479  
 QY 480 SASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT 539  
 Db 480 SASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT 539  
 QY 540 NTGTFGDIRVNNPPPAQRYRVRIRYASTTDLOFHTSINGKAINQCNFSATNWRGDDLDY 599  
 Db 540 NTGTFGDIRVNNPPPAQRYRVRIRYASTTDLOFHTSINGKAINQCNFSATNWRGDDLDY 599  
 QY 600 KTFRTVGTTPPSFLDVQSTFTIGAWNFSSGNEVVIDRIEFVPEVVEVYEAAYDFEKAQEK 659  
 Db 600 KTFRTVGTTPPSFLDVQSTFTIGAWNFSSGNEVVIDRIEFVPEVVEVYEAAYDFEKAQEK 659  
 QY 660 VTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFVVKYANELHIERNM 719  
 Db 660 VTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFVVKYANELHIERNM 719

## RESULT 2

I39815  
 Insecticidal protein cryv - Bacillus thuringiensis  
 C:Species: Bacillus thuringiensis  
 C:Date: 19-Jul-1996 #sequence\_revision 19-Jul-1996 #text\_change 09-Jul-2004  
 C:Accession: I39815  
 R:Gleave, A.P.; Williams, R.; Hedges, R.J.  
 Appl. Environ. Microbiol. 59, 1683-1687, 1993  
 A:Title: Screening by polymerase chain reaction of Bacillus thuringiensis serotypes for  
 iensis subsp. kurstaki.  
 A:Reference number: I39815; MUID:93298009; PMID:8517758  
 A:Accession: I39815  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-719 <RES>  
 A:Cross-references: UNIPROT:Q45752; GB:M98544; NID:g142767; PIDN:AAA22354.1; PID:g142768  
 C:Gene: cryv  
 C:Superfamily: parasporal crystal protein

Query Match 99.0%; Score 3724; DB 2; Length 719;  
 Best Local Similarity 99.3%; Pred. No. 2.4e-254;  
 Matches 715; Conservative 2; Mismatches 1; Indels 2; Gaps 2;

QY 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDCMKSEYENVEPVSASTI 60  
 Db 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDCMKSEYENVEPVSASTI 60  
 QY 61 QTGIGIAGKILGTGVPAGOVASLYSFLGELMPKGNQWEILFMEHVEE-INQKISTY 119  
 Db 61 QTGIGIAGKILGTGVPAGOVASLYSFLGELMPKGNQWEILFMEHVEE-INQKISTY 119  
 QY 120 ARNKALTDKGLGDALAVYHDSLESWVGNRNNTARSVRVSQYIALELMFVKQLPSFAVS 179  
 Db 120 ARNKALTDKGLGDALAVYHDSLESWVGNRNNTARSVRVSQYIALELMFVKQLPSFAVS 179  
 QY 180 GEEVPLLPYQAANLHLLLRDASI FKGWGLSSSEISTFYNRQVERAGDYSDHCVKWY 239  
 Db 180 GEEVPLLPYQAANLHLLLRDASI FKGWGLSSSEISTFYNRQVERAGDYSDHCVKWY 239  
 QY 240 STGLNNLRGTNAESWVRVYNQFRDMLVLDLVALFPSYDTQMPYPIKTTAQLTREVYVTA 299  
 Db 240 STGLNNLRGTNAESWVRVYNQFRDMLVLDLVALFPSYDTQMPYPIKTTAQLTREVYVTA 299  
 QY 300 IGTVHPHPSFTSTTYNNNAPSFSAIEAAVVRNPHLLDFLEQVITYSLLSRWNTQYNNM 359  
 Db 300 IGTVHPHPSFTSTTYNNNAPSFSAIEAAVVRNPHLLDFLEQVITYSLLSRWNTQYNNM 359  
 QY 360 WGGHKLERTTIGGTINISTQGSTNTSINPVLPTSDRVYTESLAGNLFLTPQVNGVP 419  
 Db 360 WGGHKLERTTIGGTINISTQGSTNTSINPVLPTSDRVYTESLAGNLFLTPQVNGVP 419

QY 420 RYDFHKKFVTHPIASDNFYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLI 479  
 Db 420 RYDFHKKFVTHPIASDNFYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLI 479  
 QY 480 SASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT 539  
 Db 480 SASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT 539  
 QY 540 NTGTFGDIRVNNPPPAQRYRVRIRYASTTDLOFHTSINGKAINQCNFSATNWRGDDLDY 599  
 Db 540 NTGTFGDIRVNNPPPAQRYRVRIRYASTTDLOFHTSINGKAINQCNFSATNWRGDDLDY 599  
 QY 600 KTFRTVGTTPPSFLDVQSTFTIGAWNFSSGNEVVIDRIEFVPEVVEVYEAAYDFEKAQEK 659  
 Db 600 KTFRTVGTTPPSFLDVQSTFTIGAWNFSSGNEVVIDRIEFVPEVVEVYEAAYDFEKAQEK 659  
 QY 660 VTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFVVKYANELHIERNM 719  
 Db 660 VTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFVVKYANELHIERNM 719

## RESULT 3

S25383  
 Parasporal crystal protein cryIIaI - Bacillus thuringiensis  
 N:Alternate names: delta-endotoxin; parasporal crystal protein cryv  
 C:Species: Bacillus thuringiensis  
 C:Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 09-Jul-2004  
 C:Accession: S25383  
 R:Tailor, R.; Tippet, J.; Gibb, G.; Pells, S.; Pike, D.; Jordan, L.; Ely, S.  
 Mol. Microbiol. 8, 1211-1217, 1992  
 A:Title: Identification and characterization of a novel Bacillus thuringiensis delta-end  
 A:Reference number: S25383; MUID:92269582; PMID:1588820  
 A:Accession: S25383  
 A:Molecule type: DNA  
 A:Residues: 1-719 <TAI>  
 A:Cross-references: UNIPROT:Q45752; EMBL:X62821; NID:g40289; PIDN:CAA44633.1; PID:g40290  
 C:Gene: cryv  
 C:Superfamily: parasporal crystal protein  
 C:Keywords: delta-endotoxin

Query Match 98.8%; Score 3715; DB 2; Length 719;  
 Best Local Similarity 99.2%; Pred. No. 1.1e-253;  
 Matches 714; Conservative 2; Mismatches 2; Indels 2; Gaps 2;

QY 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDCMKSEYENVEPVSASTI 60  
 Db 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDCMKSEYENVEPVSASTI 60  
 QY 61 QTGIGIAGKILGTGVPAGOVASLYSFLGELMPKGNQWEILFMEHVEE-INQKISTY 119  
 Db 61 QTGIGIAGKILGTGVPAGOVASLYSFLGELMPKGNQWEILFMEHVEE-INQKISTY 119  
 QY 120 ARNKALTDKGLGDALAVYHDSLESWVGNRNNTARSVRVSQYIALELMFVKQLPSFAVS 179  
 Db 120 ARNKALTDKGLGDALAVYHDSLESWVGNRNNTARSVRVSQYIALELMFVKQLPSFAVS 179  
 QY 180 GEEVPLLPYQAANLHLLLRDASI FKGWGLSSSEISTFYNRQVERAGDYSDHCVKWY 239  
 Db 180 GEEVPLLPYQAANLHLLLRDASI FKGWGLSSSEISTFYNRQVERAGDYSDHCVKWY 239  
 QY 240 STGLNNLRGTNAESWVRVYNQFRDMLVLDLVALFPSYDTQMPYPIKTTAQLTREVYVTA 299  
 Db 240 STGLNNLRGTNAESWVRVYNQFRDMLVLDLVALFPSYDTQMPYPIKTTAQLTREVYVTA 299  
 QY 300 IGTVHPHPSFTSTTYNNNAPSFSAIEAAVVRNPHLLDFLEQVITYSLLSRWNTQYNNM 359  
 Db 300 IGTVHPHPSFTSTTYNNNAPSFSAIEAAVVRNPHLLDFLEQVITYSLLSRWNTQYNNM 359  
 QY 360 WGGHKLERTTIGGTINISTQGSTNTSINPVLPTSDRVYTESLAGNLFLTPQVNGVP 419  
 Db 360 WGGHKLERTTIGGTINISTQGSTNTSINPVLPTSDRVYTESLAGNLFLTPQVNGVP 419

QY 420 RVDHFKFVTHPIASDNFFYGYAGIGTQLODSNELPPEATGQPNYESYSHRLSHIGLI 479  
DB 420 RVDHFKFVTHPIASDNFFYGYAGIGTQLODSNELPPEATGQPNYESYSHRLSHIGLI 479  
QY 480 SASHVKALVYSWTHRSADRTNTIIPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRT 539  
DB 480 SASHVKALVYSWTHRSADRTNTIIPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRT 539  
QY 540 NTGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKALNQGNSATMNRGDDLY 599  
DB 540 NTGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKALNQGNSATMNRGDDLY 599  
QY 600 KTRFTVGFTTFFSFLDVQSTFTTCAMNFSNGEVYIDRIEFVPEVYEAEDFEKAQEK 659  
DB 600 KTRFTVGFTTFFSFLDVQSTFTTCAMNFSNGEVYIDRIEFVPEVYEAEDFEKAQEK 659  
QY 660 VTALFTSTNPRGLKTDVKDHYDQVSNLVESLSDEFYLDKRELFELVKYAKQIHIERNM 719  
DB 660 VTALFTSTNPRGLKTDVKDHYDQVSNLVESLSDEFYLDKRELFELVKYAKQIHIERNM 719

RESULT 4  
I40590  
cryv465 protein - Bacillus thuringiensis  
C/Species: Bacillus thuringiensis  
C/Date: 12-Aug-1996 #sequence\_revision 12-Aug-1996 #text\_change 09-Jul-2004  
C/Accession: I40590  
R/Shin, B.S.; Park, S.H.; Choi, S.K.; Koo, B.T.; Lee, S.T.; Kim, J.I.  
Appl. Environ. Microbiol. 61, 2402-2407, 1995  
A/Title: Distribution of cryV-type insecticidal protein genes in Bacillus thuringiensis  
tomocidus.  
A/Reference number: I39814; MUID:95314293; PMID:7793960  
A/Accession: I40590  
A/Status: preliminary; translated from GE/EMBL/DDBJ  
A/Molecule type: DNA  
A/Residues: 1-719 <RES>  
A/Cross-references: UNIPROT:Q45709; EMBL:U07642; NID:9467234; PIDN:AAA82114.1; PID:94672  
C/Genetics:  
A/Gene: cryV465  
C/Superfamily: parasporal crystal protein

Query Match 92.6%; Score 3484; DB 2; Length 719;  
Best Local Similarity 92.2%; Pred. No. 2e-237;  
Matches 664; Conservative 33; Mismatches 21; Indels 2; Gaps 2;

QY 1 MRLKNQKHQFSNAKVDKISTDSLNKNETDIELKNHEDCLKXSEYNEVPFVSASTI 60  
DB 1 MRLKNPKHQSLSSNAKVDKIATDSLNKNETDIELKNMNNEDYLRMSHESIDPFVSASTI 60  
QY 61 QTGIGIAGKILGTGVPPAGOVASLYSFLIGELMPKGNQWEILFMEHVEE-INOKISTY 119  
DB 61 QTGIGIAGKILGTGVPPAGQIASLYSFLIGELMPKGNQWEIL-FMEHVEEILNQKILTY 119  
QY 120 ARNKALDPLKGLDALAVYHDSLESWGNRNNTARSVRSQYIALELMFVQKLPSPAVS 179  
DB 120 ARNKALSDLRGLDALAVYHDSLESWGNRNNTARSVRSQYIALELMFVQKLPSPAVS 179  
QY 180 GEEVPLLIPIYAQAANLHLLLRDASIFGKEWGLSGSSEISTFYNNQVERAGDYSCHVKWY 239  
DB 180 GEEVPLLIPIYAQAANLHLLLRDASIFGKEWGLSGSSEISTFYNNQVERTRDYSCHVKWY 239  
QY 240 STGLNNLRGTNAESVVRNQFRDRLTMVLVDLVALFPSYDTQMPYPIKTTAQLTRVYTD 299  
DB 240 NTGLNNLRGTNAESVVRNQFRDRLTMVLVDLVALFPSYDTQMPYPIKTTAQLTRVYTD 299  
QY 300 IGTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDFLEQVITYSLLSWSNTQYNNM 359  
DB 300 IGTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDFLEQVITYSLLSWSNTQYNNM 359  
QY 360 WGGHKLFRPTIGTGLNISTQGSTNTSINPVTLPFTSRDVRVYTESIAGLNLFELTOPVNGVP 419  
DB 360 WGGHKLFRPTIGTGLNISTQGSTNTSINPVTLPFTSRDVRVYTESIAGLNLFELTOPVNGVP 419

QY 420 RVDHFKFVTHPIASDNFFYGYAGIGTQLODSNELPPEATGQPNYESYSHRLSHIGLI 479  
DB 420 RVDHFKFVTHPIASDNFFYGYAGIGTQLODSNELPPEATGQPNYESYSHRLSHIGLI 479  
QY 480 SASHVKALVYSWTHRSADRTNTIIPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRT 539  
DB 480 SASHVKALVYSWTHRSADRTNTIIPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRT 539  
QY 540 NTGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKALNQGNSATMNRGDDLY 599  
DB 540 NTGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKALNQGNSATMNRGDDLY 599  
QY 600 KTRFTVGFTTFFSFLDVQSTFTTCAMNFSNGEVYIDRIEFVPEVYEAEDFEKAQEK 659  
DB 600 KTRFTVGFTTFFSFLDVQSTFTTCAMNFSNGEVYIDRIEFVPEVYEAEDFEKAQEK 659  
QY 660 VTALFTSTNPRGLKTDVKDHYDQVSNLVESLSDEFYLDKRELFELVKYAKQIHIERNM 719  
DB 660 VTALFTSTNPRGLKTDVKDHYDQVSNLVESLSDEFYLDKRELFELVKYAKQIHIERNM 719

RESULT 5  
S00873  
parasporal crystal protein cryBa1 - Bacillus thuringiensis subsp. thuringiensis  
N/Alternate names: parasporal crystal protein cryA4  
C/Species: Bacillus thuringiensis subsp. thuringiensis  
C/Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 09-Jul-2004  
C/Accession: S00873  
R/Brizard, B.L.; Whiteley, H.R.  
Nucleic Acids Res. 16, 2723-2724, 1988  
A/Title: Nucleotide sequence of an additional crystal protein gene cloned from Bacillus t  
A/Reference number: S00873; MUID:88203216; PMID:3362680  
A/Accession: S00873  
A/Molecule type: DNA  
A/Residues: 1-1228 <BRI>  
A/Cross-references: UNIPROT:P05517; EMBL:X06711; NID:940264; PIDN:CAA29898.1; PID:958094;  
C/Genetics:  
A/Gene: cryA4  
A/Start codon: TTG  
A/Superfamily: parasporal crystal protein  
C/Keywords: delta-endotoxin

Query Match 59.8%; Score 2248.5; DB 2; Length 1228;  
Best Local Similarity 62.5%; Pred. No. 5.7e-150;  
Matches 448; Conservative 78; Mismatches 164; Indels 27; Gaps 8;

QY 23 TDSLKNETDIELQNINH-----EDCLKMSEYNEVPFVSASTIQTGIGIAGRI 70  
DB 2 TSNRRKNEEIIINAVSNHSAQMDLLPDARIEDSLCIAEGNIDPFVSASTIQTGIGIAGRI 61  
QY 71 LGTLGVPPAGOVASLYSFLIGELMPKGNQWEILFMEHVEE-INOKISTYARKALTDJUK 129  
DB 62 LGVLGVPPAGOVASLYSFLIGELMPKGNQWEILFMEHVEE-INOKISTYARKALTDJUK 120  
QY 130 GLGDALAVYHDSLESWGNRNNTARSVRSQYIALELMFVQKLPSPAVSGEVPPLPIY 189  
DB 121 GLGDSFRAYQCSLEDVLENRDARTKSVLYTQYIALELDFLNAPLFAIRNEVPPLMY 180  
QY 190 AQANLHLLLRDASIFGKEWGLSGSSEISTFYNNQVERAGDYSCHVKWYSTGLNNLRGT 249  
DB 181 AQANLHLLLRDASIFGSEFGLTSGEIQRYVERQVTRDYSDYCVENYNTGLNLRGT 240  
QY 250 NAEVRYNQFRDRLTMVLVDLVALFPSYDTQMPYPIKTTAQLTRVYTDGIVTHHPSP 309  
DB 241 NAEVRYNQFRDRLTMVLVDLVALFPSYDTQMPYPIKTTAQLTRVYTDGIVTHHPSP 298  
QY 310 TSTWYNNAPSFSAIEAAVVRNPHLLDFLEQVITYSLLSWSNTQYNNMGGHKLFRPT 369  
DB 299 ASWYNNAPSFSAIEAAVVRNPHLLDFLEQVITYSLLSWSNTQYNNMGGHKLFRPT 358  
QY 370 IGTGLNISTQGSTNTSINPVTLPFTSRDVRVYTESIAGLNLFELTOPVNGVPDHWK 427  
DB 359 IGTGLNISTQGSTNTSINPVTLPFTSRDVRVYTESIAGLNLFELTOPVNGVPDHWK 416





Db 708 QYGHDKKMLLEAVRAAKRLSRERNL 732

RESULT 8

S32645

parasporeal crystal protein crylGai - Bacillus thuringiensis

C:Species: Bacillus thuringiensis

C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004

C:Accession: S32645

R:Lambert, B.

A:Title: Nucleotide sequence of the insecticidal protein gene of Bacillus thuringiensis

A:Reference number: S32645

A:Accession: S32645

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1166 <L>

A:Cross-references: UNIPROT:Q45746; EMBL:Z22510; NID:g295861; PIDN:CAA80233.1; PID:g2958

A:Superfamily: parasporeal crystal protein

C:Keywords: delta-endotoxin

Query Match 38.8%; Score 1458.5; DB 2; Length 1166;

Best Local Similarity 46.28; Pred. No. 2.5e-94;

Matches 326; Conservative 97; Mismatches 206; Indels 77; Gaps 19;

QY 41 DCLXMSYE---NVEPVASASTIQTGIGIAGKILGTGVFPAGQVAVSLVSFILGELWPK 96

Db 13 NCLNPESEIFNARNSEGLVSVSSGL---TRFLLEAAVPEAGFALGLFDIIWGAL--- 66

QY 97 GKQWELFWEHVEE-INQKISTYARNKALTDKLGCDALAVYHDSLESVGNRNTRAR 155

Db 67 GVDQMS-LFLRQIBOLRQIBETELERNRATILTLGLSSSNLYVEALRENDPNPASQ 125

QY 156 SVKRSQVIALELMPVKLPSPFVSGEVPPLPIYAQAANLHLLLRDASIFGKWLSS 215

Db 126 ERVTRERLDDAIVTGLPLAIENLEVNLSVYQAANLHLLLRDASVYFGERWGLTQA 185

QY 216 EISTYRQVERAGYSDHCVKVSTGLNNLRGNAESWRYNQPRDMLVLDLVALF 275

Db 186 NIEDLYRLTSNIQFSDHCAWYNQGLNEIGGISR---RYLDFORDLTISVLDIVALF 241

QY 276 PSYDTQWPIKTTAQLTRVYTDAL--GTVHPHPSFTSTWYNNNAPSFAISAIAVVRNP 333

Db 242 PNYDIRYPIPTQQLTRVYTSFVAGNI-----NFGLSIANVLRA 284

QY 334 HLLDFLEQVITYLLSRWSNTQYNNMGHKLFRFTTG-GLTN-----ISTQGSTNT 384

Db 285 HLMDFIDRIVITYNSR--STPY---WAGHEVISRRTCQGGNEIRPPLGYVAANABPV 339

QY 385 SINFTLPTSDRYRTES-----LAGNLFLTPVNGVPRVDFHMKVTHPTASDNFY 438

Db 340 TIRPTGFTDEORQYRARSVRVSRSSGQDFSLVDVG-----FLT-IPSAVSIY 388

QY 439 YPGVAGIGTQLQDSNELPPEATGQPNYESYSHRSLSHIGLISAS-----HYKALVYSWTH 493

Db 389 RNGP-GEFT---DTIDEPIEGTDP--FTGYSHLCHVGFPLASSPFTISQVAPAFISWTH 442

QY 494 RSADRTNIENSTIQLPVKAFNLSSGAAVVRGPGTGGDILRRTNTGTGDIIRVNI 553

Db 443 RSATLTNTIAPDVITQIPLVAFNLHSGATIVKPGFTGGDILRRTNVGSGMRVNITA 502

QY 554 PFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLDTKTRFTVGTFTPSF 613

Db 503 PLSQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLDTKTRFTVGTFTPSF 562

QY 614 LDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVTEAEYDFPKAQEKVLTALFTSTNPKL 673

Db 563 SDANSTFTIGAFGSPNNNEVYIDRIEFVPEVTEAEYDFPKAQEKVLTALFTSTNPKL 622

QY 674 TDVKDYHIDQVSNLVSLSDEFYLDKRELFEIVKYANELHIERNM 719

Db 623 TDVTDYHIDQVSNLVSLSDEFYLDKRELFEIVKYANELHIERNM 668

RESULT 9

A26513

parasporeal crystal protein - Bacillus thuringiensis (strain aizawai)

C:Species: Bacillus thuringiensis

C:Date: 11-Mar-1988 #sequence\_revision 11-Mar-1988 #text\_change 09-Jul-2004

C:Accession: A26513

R:Oeda, K.; Oshie, K.; Shimizu, M.; Nakamura, K.; Yamamoto, H.; Nakayama, I.; Ohkawa, H.

A:Title: Nucleotide sequence of the insecticidal protein gene of Bacillus thuringiensis

A:Reference number: A26513; PMID:3297927

A:Accession: A26513

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1155 <OE>

A:Cross-references: UNIPROT:P06578; GB:M16463; NID:g143098; PIDN:AAA22551.1; PID:g143099

A:Superfamily: parasporeal crystal protein

C:Keywords: delta-endotoxin

Query Match 38.6%; Score 1450; DB 2; Length 1155;

Best Local Similarity 44.1%; Pred. No. 9.8e-94;

Matches 313; Conservative 110; Mismatches 232; Indels 54; Gaps 12;

QY 36 NINHEDCLKMSEYENVE-PFVSASTIQTG-----IGIAGKILGTGVFPAGQVAVSLVS 87

Db 4 NFNINECTPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEP-VPGAGFVLGLVD 62

QY 88 FILGELWPKGNQWELFWEHVEEINQKISTYARNKALTDKLGCDALAVYHDSLESVWG 147

Db 63 IIWGIF--GPSQMDAFLVQIEQLINQRIEFPARQAIISRLGSLNLYQIYVAESFWEBA 119

QY 148 NNNNTFARSVVSQVIALELMPVKLPSPFVSGEVPPLPIYAQAANLHLLLRDASIFG 207

Db 120 DFTNALHEMRIQNDMNSALTTPAIFAVQNYQVPLSVYQAANLHLLVRDVSFVG 179

QY 208 KEWGLSSSEISTFYRQVERAGYSDHCVKVSTGLNNLRGNAESWRYNQPRDMLTUM 267

Db 180 QRWGFDAATINSRYNDLRLIGNYTDHVRVNTGLERVWGPDSRDWIRYQFRELTLT 239

QY 268 VLDLVALPSTYDTQWPIKTTAQLTRVYTDALGTVHPHPSFTSTWYNNNAPSFAISA 327

Db 240 VLDIVSLFPNDSRTYPIRTVSQLTREIYNFV-----LENFGSFRALAQ 285

QY 328 AV---VRNPHLLDFLEQVITYLLSR---WENTQYMMN---WGGHKLFRFTTGTLNIS 377

Db 286 GIEGSIIRSHLMDILNSITIIYTDHAGEVYWSGHQIMASPVGSGPEFTFPLYGTMGNA 345

QY 378 TQGSTNWSINPVLPTSDRYRTESLAGNLFLTPVNGVPRVDFHMKVTHPTASDNF 437

Db 346 PQORIYAQLGQGYRTLSLTLYRRPFNIGIN---NQLSVLDGTEFAYG-----TSSNL 396

QY 438 YPGVAGIGTQLQDSNELPPEATGQPNYESYSHRSLSHIGLI-----SASHVKALVYS 490

Db 397 PSAVYRKSQT--VDSLDEIPQNNVPPRQGFSHRSLSHVSMFSGFSNVSIIIRAPMFS 454

QY 491 WTHRSADRTNIENSTIQLPVKAFNLSSGAAVVRGPGTGGDILRRTNTGTGDIIRVNI 550

Db 455 WIHRSAEFNIIPTSSQITQIPLTKSTNLGSGTSVVKPGTGGDILRRTSPQISTLRVN 514

QY 551 INPFPQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLDTKTRFTVGTFTP 610

Db 515 ITAPLSQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLDTKTRFTVGTFTP 574

QY 611 FSPDLVQSTFTIGAMNFSNGNEVYIDRIEFVPEVTEAEYDFPKAQEKVLTALFTSTNPK 670

Db 575 FNFSGNSVFTLSAHVFNSENGNEVYIDRIEFVPAEVTFAEYDLERAKQAVNELFTSSNQI 634

QY 671 GLKTDVKYHIDQVSNLVSLSDEFYLDKRELFEIVKYANELHIERNM 719

Db 635 GLKTDVTDYHIDQVSNLVSLSDEFYLDKRELFEIVKYANELHIERNM 683

parasporal crystal protein cry1Fa3 - *Bacillus thuringiensis*

C:Species: *Bacillus thuringiensis*  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
C:Accession: S32649

REVISION: 032043  
R; Lambert, B.

submitted to the EMBL Data

A;Reference number: S32645

A;Accession: S32649

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-1174 <LAM>

A;Cross-References: UNIPROT:Q45749; EMBL:U00006.1;C-Superfamily: v. parasporal crystal protein

C;superfamily: parasporal crystal protein  
C;Keywords: delta-endotoxin

Key words: delta-endotoxin

Query Match	38.5%;	Score 1449;	DB 2;	Length 1174;
Best Local Similarity	44.5%;	Pred. No. 1.2e-93;		
Matches 323;	Conservative 100;	Mismatches 207;	Indels 96;	Gaps 17;

QY 36 NINHE---DCLKMSEYENVEPFVSASTIQTGIGIA-GKILGTLGVPFAGOVASLYSEIL 90

Country	Year	Value	Unit
Algeria	1980	1.00	1000
Algeria	1981	1.00	1000
Algeria	1982	1.00	1000
Algeria	1983	1.00	1000
Algeria	1984	1.00	1000
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Algeria	2065	1.00	1000
Algeria	2066	1.00	1000
Algeria	2067	1.00	1000

**C**

QY 91 GELWPKGNQWEILFMEHVEEINQKISTYARNKALTDLKLGDALAVYHDSLESWVGNRN 150

Db 64 GFITP--SEWSLFLQIEQLIEQRIETLERNRAITTLRGLADSYEVYLEALREWEENPN 120

.....

[illegible]

Db 121 NAQLREDVRIRFANTDDALITAINNFTLTSTFEIPLSVVQAAHLHSLLRDAVSFGQGW 180

QY 211 GLSSEISTFYNRQVERAGDYS DHCVKWYSTGLNNLRGTNAESWVRYNQFRDDMTLMVLD 270

[illegible]

2000

QY 271 LVALFPSYDTQMPYPIKTTAQLTREVTDAIGTVHPHPSFTSTTWYNNAPS-FSAIEAAV 329

Db 241 IVALFPNYDARAYPIQTSSQLTREIYTSSV--IEDSP-----VSANIPNGFNRAEFG- 290

[illegible]

100

100

Db 332 NFPIYGIENPGGAIWIADEDPRPFYRT-----LSDPV-----FVRGGFGN 371

435 DNFYYPGYAGIGTQLQ-----DSENELPPEATGQPNYESYSHRLSHI--- 476

[illegible]

100

477 --GLISASHV-KALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSGAAVVRGPGFTGG 533

Db 431 WPGEIAGSDSWRAPMFSWTHRSADRTNIINPNIITQIPAVKAHLHSGSTVVRGPGFTGG 490

**Table 1**

[illegible]

Db 491 DLLRRNTGTFADIRVNITGPLSQRYRVIRYASTDLQFFTRINGTSVNQGNFQRTMNR 550

RESULT 11

120 DPTNPALEEMRIQFNDMSALTTAIPFAVQNYQVPLLSVYQAAHLNHLVLRDVSFVG 179  
 208 KEWGLSSSEISTFYNQVERAGDYSCHCKVWYSTGLNNLRTNAESWVRYNQFRDMLTLM 267  
 180 QRWGFDAAATINSRYNDLTRIGNYTDHVRWYNTGLERWVGPDSDRDMIRYNQFRELTLT 239  
 268 VLDLVALPSPYDQYPIKTAQTLREVYDAIGTVHPHPSFTSTWYNNAPSF-----S 323  
 240 VLDIVSLFPNDYRTPIRTVSQLTRREIYNPV-----LENFDSFGSGSAQ 285  
 324 AIEAAVVRNPHLLDFLEQVITYLSLR-----WSNTQYMM-----WGHKLEPRTIGTGLNI 376  
 286 GIEGS-IRSPHMLDILNSITITDAHGEYVWSGHQIMASPVGSGPZFTFPLYGTMGNA 344  
 377 STQGSTNTSINPVLPTFTSDVRYTESLAGNLFLTPQVNGVPRVDFHVKVTHPIASDN 436  
 286 GIEGS-IRSPHMLDILNSITITDAHGEYVWSGHQIMASPVGSGPZFTFPLYGTMGNA 344  
 377 STQGSTNTSINPVLPTFTSDVRYTESLAGNLFLTPQVNGVPRVDFHVKVTHPIASDN 436  
 345 APOQRIVAQLOGGVYRTLSSTLYRPFNIGIN-----NQOLSVDGTGEFAYG-----TSSN 395  
 437 FYYPGAGICTQDSENELEPPATGQPNYESYSHRLSHIGLI-----SASHVKALVY 489  
 396 LPSAVYRKSGT--VDSLDEIPQNNVPPRQGFSHRLSHVSMFRSGFSNVSIIIRAPMF 453  
 490 SWTHRSADRNTTIEPNSITQIPLVKAFNLSSGAAVRGPGFTGGDILRTNTGTGDIRV 549  
 454 SWTHRSADRNTTIEPNSITQIPLVKAFNLSSGAAVRGPGFTGGDILRTNTGTGDIRV 513  
 550 NINPPFAQRYVRIRYASTTDLQPHITSINGKAINQGNFSAATMNRGCDLDYKTRTGVGFTT 609  
 514 NITAPLSQRVRIRYASTTDLQPHITSINGKAINQGNFSAATMNRGCDLDYKTRTGVGFTT 573  
 610 PFQFLDVOSTFTTIGAMNFFSGNEVYIDRIEFVPEVYEAIEFEKAQEKVTLFTSTNP 669  
 574 PFNPSGSSVFTLSAHVFNESGNEVYIDRIEFVPAEVTFAEYDLERAQKAVNELFTSSNQ 633  
 670 RGLKTDVKDHYHIDQVSNLVESLDFEYLDKRELFETVKYANELHIERNM 719  
 634 IGLKTDVTDYHIDQVSNLVESLDFEYLDKRELFETVKYANELHIERNM 683

RESULT 12  
 A29125  
 Parasporal crystal protein Bt2 - Bacillus thuringiensis subsp. kurstaki (strain HD-1)  
 C:Species: Bacillus thuringiensis subsp. kurstaki  
 C>Date: 15-Dec-1988 #sequence\_revision 15-Dec-1988 #text\_change 09-Jul-2004  
 C:Accession: A29125  
 R:/Fischhoff, D.A.; Bowdish, K.S.; Perlak, F.J.; Marrone, P.G.; McCormick, S.M.; Niedermeyer, D.A.; Bio/Technology 5, 807-813, 1987  
 A>Title: Insect tolerant transgenic tomato plants.  
 A/Reference number: A29125  
 A/Accession: A29125  
 A/Status: not compared with conceptual translation  
 A/Molecule type: DNA  
 A/Residues: 1-1156 <PIS>  
 A/Cross-references: UNIPROT:Q9F296; UNIPROT:Q93R21  
 C:Superfamily: parasporal crystal protein  
 C/Keywords: delta-endotoxin

Query Match 38.4%; Score 1443; DB 2; Length 1156;  
 Best Local Similarity 44.2%; Pred. No. 3.1e-93;  
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 36 NINHEDECLMSEYENVE-PFVSASTIQG-----IGIAGKILGTGLGVFPAGQVASLYS 87  
 4 NPNINECIYCNLSNPEVEVLGGRIETGYPIDISLSLQFLSEF-VPGAGFVLGLVD 62  
 88 FILGELMPKGNQWEILFMEHVEEINOKISTYARKALTDLKGDLALAYVHDSLESWVG 147  
 63 IIWGIF---GPSQWDAFLVQIEQLNORIEEFARQAISRLEGLSNLYQIYAESFREWEA 119  
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 120 DPTNPALEEMRIQFNDMSALTTAIPFAVQNYQVPLLSVYQAAHLNHLVLRDVSFVG 179

208 KEWGLSSSEISTFYNQVERAGDYSCHCKVWYSTGLNNLRTNAESWVRYNQFRDMLTLM 267  
 180 QRWGFDAAATINSRYNDLTRIGNYTDHVRWYNTGLERWVGPDSDRDMIRYNQFRELTLT 239  
 268 VLDLVALPSPYDQYPIKTAQTLREVYDAIGTVHPHPSFTSTWYNNAPSF-----S 323  
 240 VLDIVSLFPNDYRTPIRTVSQLTRREIYNPV-----LENFDSFGSGSAQ 285  
 324 AIEAAVVRNPHLLDFLEQVITYLSLR-----WSNTQYMM-----WGHKLEPRTIGTGLNI 376  
 286 GIEGS-IRSPHMLDILNSITITDAHGEYVWSGHQIMASPVGSGPZFTFPLYGTMGNA 344  
 377 STQGSTNTSINPVLPTFTSDVRYTESLAGNLFLTPQVNGVPRVDFHVKVTHPIASDN 436  
 345 APOQRIVAQLOGGVYRTLSSTLYRPFNIGIN-----NQOLSVDGTGEFAYG-----TSSN 395  
 437 FYYPGAGICTQDSENELEPPATGQPNYESYSHRLSHIGLI-----SASHVKALVY 489  
 396 LPSAVYRKSGT--VDSLDEIPQNNVPPRQGFSHRLSHVSMFRSGFSNVSIIIRAPMF 453  
 490 SWTHRSADRNTTIEPNSITQIPLVKAFNLSSGAAVRGPGFTGGDILRTNTGTGDIRV 549  
 454 SWTHRSADRNTTIEPNSITQIPLVKAFNLSSGAAVRGPGFTGGDILRTNTGTGDIRV 513  
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 514 NITAPLSQRVRIRYASTTDLQPHITSINGKAINQGNFSAATMNRGCDLDYKTRTGVGFTT 573  
 610 PFQFLDVOSTFTTIGAMNFFSGNEVYIDRIEFVPEVYEAIEFEKAQEKVTLFTSTNP 669  
 574 PFNPSGSSVFTLSAHVFNESGNEVYIDRIEFVPAEVTFAEYDLERAQKAVNELFTSSNQ 633  
 670 RGLKTDVKDHYHIDQVSNLVESLDFEYLDKRELFETVKYANELHIERNM 719  
 634 IGLKTDVTDYHIDQVSNLVESLDFEYLDKRELFETVKYANELHIERNM 683

RESULT 13  
 I39838  
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 C:Species: Bacillus thuringiensis  
 C>Date: 19-Jul-1996 #sequence\_revision 19-Jul-1996 #text\_change 09-Jul-2004  
 C:Accession: I39838  
 R:/Hefford, M.A.; Brouseau, R.; Prefontaine, G.; Hanna, Z.; Condie, J.A.; Lau, P.C.K.  
 J. Biochem. Mol. 6, 307-322, 1987  
 A>Title: Sequence of a lepidopteran toxin gene of Bacillus thuringiensis subsp. kurstaki  
 A/Reference number: I39838  
 A/Accession: I39838  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: DNA  
 A/Residues: 1-1155 <RES>  
 A/Cross-references: UNIPROT:P06578; GB:M37263; NID:G142865; PIDN:AAA22420.1; PID:G142886  
 C:Superfamily: parasporal crystal protein  
 C/Keywords: delta-endotoxin

Query Match 38.1%; Score 1434; DB 2; Length 1155;  
 Best Local Similarity 44.1%; Pred. No. 1.3e-92;  
 Matches 313; Conservative 109; Mismatches 232; Indels 56; Gaps 13;  
 36 NINHEDECLMSEYENVE-PFVSASTIQG-----IGIAGKILGTGLGVFPAGQVASLYS 87  
 4 NPNINECIYCNLSNPEVEVLGGRIETGYPIDISLSLQFLSEF-VPGAGFVLGLVD 62  
 88 FILGELMPKGNQWEILFMEHVEEINOKISTYARKALTDLKGDLALAYVHDSLESWVG 147  
 63 IIWGIF---GPSQWDAFLVQIEQLNORIEEFARQAISRLEGLSNLYQIYAESFREWEA 119  
 148 NNNTRARSVRSQVIALELMFVQKLPSPFASGEVPELPIYQAANLHLLLRDASIFG 207  
 120 DPTNPALEEMRIQFNDMSALTTAIPFAVQNYQVPLLSVYQAAHLNHLVLRDVSFVG 179  
 208 KEWGLSSSEISTFYNQVERAGDYSCHCKVWYSTGLNNLRTNAESWVRYNQFRDMLTLM 267

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 QY 328 AV---VRNPHLLDFLEQVITYLLSRWSNTQVNMWGHKLEFRITGGT---LNTSTQGS 381  
 Db 286 RIBQNIQPHLMDILNRIITYTDVHRG-----FNWMSGHQITASPVGSGPFAFPFLFN 340  
 QY 382 TMTSINPVLPTFSRDVRYTESL-----AGLNLPLTQPVNGVPRVDFHWKVTTHPI 432  
 Db 341 AGNAAPFLVSLTGLIFRILSPLYRRIILSGPN---NQELFVLDTGTEFASLTNLT 397  
 QY 433 ASDNFYYPGAGIGTOLQDSENELPPEATGQPNYESYSHRLSHIGLISAS-----HVKAL 487  
 Db 398 PSTIYRQRTV-----DSLVDIPPQDNSVPPRAGFSHRLSHVMTLSQAAGAVYTLRAP 450  
 QY 488 VYSWTHRSADRTNTEPNSITOIPLVKAENLSSGAAVRGPGTGGDILRRNTTCTFGDI 547  
 Db 451 TSWQHRSAEFNNIIPSSQITQIPLKSTNLGSGTSVWAGPGTGGDILRRTPQISTL 510  
 QY 548 RVNINPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLDYKTPRTVGF 607  
 Db 511 RVNITAPLSQRYRVRIRYASTTNLQFHTSIDGRPINQGNFSATMSSGSLQSGSFRTVGF 570  
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 QY 668 NFRGLKTDVYHIDQVSNLVSLSDEFYLDKRELFEIVKYANELHIERNM 719  
 Db 631 NQGLKTDVYHIDQVSNLVSLSDEFYLDKRELFEIVKYANELHIERNM 682  
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 parasporal crystal protein - Bacillus thuringiensis (strain aizawai IPL7)  
 N;Alternate names: 135K insecticidal protein  
 C;Species: Bacillus thuringiensis  
 C;Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 09-Jul-2004  
 C;Accession: JT0241  
 R;Shimizu, M.; Oshie, K.; Nakamura, K.; Takada, Y.; Oeda, K.; Ohkawa, H.  
 Agric. Biol. Chem. 52, 1565-1573, 1988  
 A;Title: Cloning and expression in Escherichia coli of the 135-kDa insecticidal protein  
 A;Reference number: JT0241  
 A;Accession: JT0241  
 A;Molecule type: DNA  
 A;Residues: 1-1176 <SHI>  
 A;Cross-references: UNIPROT:P02965  
 A;Note: b. thuringiensis aizawai IPL7 produces similar 130K and 135K insecticidal protein  
 C;Comment: The authors translated the codon ACA for residue 264 as Ser.  
 C;Superfamily: parasporal crystal protein  
 C;Keywords: delta-endotoxin

Query Match 38.0%; Score 1430.5; DB 2; Length 934;  
 Best Local Similarity 43.3%; Pred. No. 1.7e-92;  
 Matches 308; Conservative 116; Mismatches 227; Indels 61; Gaps 12;  
 QY 36 NINHEDCIKMSEYENVE-PFVSASTIQTG-----IGIAGKILGTGVFPAGOVASLYS 87  
 Db 4 NPNINECIPIYNCLSNPEVEVLGGERIEGTYPIDISLSITQFLSEF-VPGAGFVLGLVD 62  
 QY 88 FILGELWPKGNQWEILFMEHVEINOKISTYARKALTDLKLGLDAMALVYHDSLESVWG 147  
 Db 63 IIWGIF---GPSQWDAFLVQIEQLINQRIEFARNQAIISLEGSLNLYQIYAESFWEA 119  
 QY 148 NNNTRARSVVRVSOYIALELMFVKLPFAVSGVEVPLPIYQAANLHLLLRDASIFG 207  
 Db 120 DPTNPALREENRIQFNDMNSALTTAIPFAVQNVQVLLSVYQAANLHLSVLRDVSFVG 179  
 QY 208 KEWGLSSSETSTFVNRQVERAGDYSCHVCKWYSTGLNNLRGTNAESWVRVYNQFRDWTLM 267  
 Db 180 QWGFDAATINRSYNDLTRLIGNYDTHAVRWNTGLERWGPDSRDWRVYNQFRRLTLT 239

QY 268 VLDLVALFSDYDTQMYPIKTTAQLTRVYTDAGTVHPHPSFTSTTWYNNAPFSABIA 327  
 Db 240 VLDLVALFSDYDTRRYPPIRTVSQLTRIEYTNFV-----LENFDSGRGMAQ 285  
 QY 328 AV---VRNPHLLDFLEQVITYLLSRWSNTQVNMWGHKLEFRITGGT---LNTSTQGS 381  
 Db 286 RIBQNIQPHLMDILNRIITYTDVHRG-----FNWMSGHQITASPVGSGPFAFPFLFN 340  
 QY 382 TMTSINPVLPTFSRDVRYTESL-----AGLNLPLTQPVNGVPRVDFHWKVTTHPI 432  
 Db 341 AGNAAPFLVSLTGLIFRILSPLYRRIILSGPN---NQELFVLDTGTEFASLTNLT 397  
 QY 433 ASDNFYYPGAGIGTOLQDSENELPPEATGQPNYESYSHRLSHIGLISAS-----HVKAL 487  
 Db 398 PSTIYRQRTV-----DSLVDIPPQDNSVPPRAGFSHRLSHVMTLSQAAGAVYTLRAP 450  
 QY 488 VYSWTHRSADRTNTEPNSITOIPLVKAENLSSGAAVRGPGTGGDILRRNTTCTFGDI 547  
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 Db 571 TTPFNFSNGSVFTLSAHVFNSEVYIDRIEFVPAEVTFEAEYDLERAQKAVNELFTSS 630  
 QY 668 NFRGLKTDVYHIDQVSNLVSLSDEFYLDKRELFEIVKYANELHIERNM 719  
 Db 631 NQGLKTDVYHIDQVSNLVSLSDEFYLDKRELFEIVKYANELHIERNM 682  
 RESULT 15  
 JT0241  
 parasporal crystal protein - Bacillus thuringiensis (strain aizawai IPL7)  
 N;Alternate names: 135K insecticidal protein  
 C;Species: Bacillus thuringiensis  
 C;Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 09-Jul-2004  
 C;Accession: JT0241  
 R;Shimizu, M.; Oshie, K.; Nakamura, K.; Takada, Y.; Oeda, K.; Ohkawa, H.  
 Agric. Biol. Chem. 52, 1565-1573, 1988  
 A;Title: Cloning and expression in Escherichia coli of the 135-kDa insecticidal protein  
 A;Reference number: JT0241  
 A;Accession: JT0241  
 A;Molecule type: DNA  
 A;Residues: 1-1176 <SHI>  
 A;Cross-references: UNIPROT:P02965  
 A;Note: b. thuringiensis aizawai IPL7 produces similar 130K and 135K insecticidal protein  
 C;Comment: The authors translated the codon ACA for residue 264 as Ser.  
 C;Superfamily: parasporal crystal protein  
 C;Keywords: delta-endotoxin

Query Match 38.0%; Score 1429.5; DB 2; Length 1176;  
 Best Local Similarity 43.3%; Pred. No. 2.8e-92;  
 Matches 308; Conservative 115; Mismatches 222; Indels 61; Gaps 12;  
 QY 36 NINHEDCIKMSEYENVE-PFVSASTIQTG-----IGIAGKILGTGVFPAGOVASLYS 87  
 Db 4 NPNINECIPIYNCLSNPEVEVLGGERIEGTYPIDISLSITQFLSEF-VPGAGFVLGLVD 62  
 QY 88 FILGELWPKGNQWEILFMEHVEINOKISTYARKALTDLKLGLDAMALVYHDSLESVWG 147  
 Db 63 IIWGIF---GPSQWDAFLVQIEQLINQRIEFARNQAIISLEGSLNLYQIYAESFWEA 119  
 QY 148 NNNTRARSVVRVSOYIALELMFVKLPFAVSGVEVPLPIYQAANLHLLLRDASIFG 207  
 Db 120 DPTNPALREENRIQFNDMNSALTTAIPFAVQNVQVLLSVYQAANLHLSVLRDVSFVG 179  
 QY 208 KEWGLSSSETSTFVNRQVERAGDYSCHVCKWYSTGLNNLRGTNAESWVRVYNQFRDWTLM 267  
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Qy 268 VLDLVALPSPYDTOMYPIKTAQLTREYVTDALGTVHPHPSFTSTTWYNNAPSPSAIEA 327
Db 240 VLDLVALPSPYDSTRYPIRVTSQLTREIYNPV-----LENFDCSFRGMAQ 285
Qy 328 AV---VBNPHLLDFLEQVITYLSLRSWNTQYMMMGHKLERTIGGT---LNIQTQS 381
Db 286 RIEQNIQPHLMDILNLSITYTDVHRG-----FNYMSGHQITASPVGSGPEFAFLFGN 340
Qy 382 TNSINPVTLPFTSRDVRTESE-----AGLNLFLTQPVNGVPRVDFHKKFVTHPI 432
Db 341 AGNAPPVLSLTGLGIFRILSSPLYRRIILGSGPN---NQELFVLGTEFSGASITNL 397
Qy 433 ASDNFYYPGYAGIGTQLQDSENLPEATQCPNYESYSHLSHIGLISAS-----HVKAL 487
Db 398 PSTIYRQGTIV-----DSLDTVPQDNGSVPRAGFSELSHVMTLSQAAGAVYTLRAP 450
Qy 488 VYSWTHESADRTWTFIENSITOTPLVKAFLNLSGAAVVRGPGTGGDILRRTNTGTGDI 547
Db 451 TFSWQHSABFNFIIPSSQITQIPLTKSTNLGSGTSVVRGPGTGGDILRRTSPGQISTL 510
Qy 548 RVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQNFSAITMNRGEDLDYKTRTVGF 607
Db 511 RVNITAPLSQRYRVRIRYASTTNLQFHTSIDGRFINQNFSAITMSSGSLQSGSFRIVGF 570
Qy 608 TTPSFLDVQSTFTIGAMNFSSGNEVYIDRIEFPVPEVTVYEAZYDFEKAQKVTALFTST 667
Db 571 TTPFNFGSGSVFTLSAHVFNNGNEVYIDRIEFPVPAEVTPEAEYDLERAQKAVNELFTSS 630
Qy 668 NPGCKTDVXDYHIDQVSNLVESLSDEFYLDKRELPEIVKYANELHIERNM 719
Db 631 NQIGLKTVDVTHIDQVSNLVESLSDEFCLDEKQELSEKVKHAKRLSDERNL 682

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Search completed: October 28, 2004, 18:31:57  
Job time : 21.191 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 28, 2004, 18:06:07 ; Search time 22.3343 Seconds  
(without alignments)  
2134.948 Million cell updates/sec

Title: US-10-019-823B-58  
Perfect score: 3761  
Sequence: 1 MKLKNQDKHQSFSNAKVDK.....KRELFEIVYANLHIERM 719

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3720	98.9	719	3	US-08-286-870A-8
2	3442.5	91.5	710	4	US-09-661-322A-42
3	3370	89.6	648	3	US-08-286-870A-4
4	3341	88.8	719	2	US-08-003-217-2
5	3336	88.7	719	3	US-08-218-942-2
6	2776	73.8	535	3	US-08-286-870A-6
7	2417.5	64.3	1229	1	US-08-100-709-4
8	2417.5	64.3	1229	1	US-08-176-865-4
9	2417.5	64.3	1229	1	US-08-474-038-4
10	2417.5	64.3	1229	2	US-08-779-046-4
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22	2235.5	59.4	1227	3	US-09-053-549-2
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37	1481.5	39.4	1176	1	US-08-257-999-2
38	1466	39.0	1157	2	US-08-532-547-5
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40	1466	39.0	1157	3	US-08-455-838-5
41	1466	39.0	1157	3	US-09-019-809-5
42	1466	39.0	1157	4	US-09-471-177-5
43	1466	39.0	1157	4	US-09-220-806-5
44	1461	38.8	1168	1	US-08-291-368-4
45	1461	38.8	1168	2	US-08-962-190-4

ALIGNMENTS

RESULT 1  
US-08-286-870A-8  
; Sequence 8, Application US/08286870A  
; Patent No. 6063605  
; GENERAL INFORMATION:  
; APPLICANT: ELY, S.....  
; APPLICANT: TAILOR, RH  
; APPLICANT: TIPPETT, JM  
; APPLICANT: BLENK, RG  
; TITLE OF INVENTION: BACTERIAL GENES  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN  
; ADDRESSEE: Intellectual Property Group of  
; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP  
; STREET: 1100 New York Avenue, N.W.  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3918  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/286,870A  
; FILING DATE: 05-AUG-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/520228  
; FILING DATE: 09-MAY-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 8910624.9  
; FILING DATE: 09-MAY-1989  
; ATTORNEY/AGENT INFORMATION:  
; NAME: PAUL N. KOKULIS  
; REGISTRATION NUMBER: 16,773  
; REFERENCE/DOCKET NUMBER: 70609/220720  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 861-3000  
; TELEFAX: (202) 822-0944  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 719 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-286-870A-8

Query Match 98.9%; Score 3720; DB 3; Length 719;  
 Best Local Similarity 99.2%; Pred. No. 0;  
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QY 1 MKLKNQDKHQSSNAKVDKISTDSLKNETDIELQNHEDCLKMSYENVEPFFVSASTI 60  
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 DB 540 NTGTFGDIRVNINPPFAQRYRIRYASTTDLQHTSINGKAINQGNFSATMNRGEDLDY 599  
 QY 600 KTFRTVGTTPPSFLDVOSTFTTIGAWNFSSGNEVYIDRIEFVPEVVTYEAEDPEKAQEK 659  
 DB 600 KTFRTVGTTPPSFLDVOSTFTTIGAWNFSSGNEVYIDRIEFVPEVVTYEAEDPEKAQEK 659  
 QY 660 VTALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719  
 DB 660 VTALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719

RESULT 2  
 US-09-661-322A-42  
 ; Sequence 42, Application US/09661322A  
 ; Patent No. 6593293  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baum, James A.  
 ; APPLICANT: Chu, Chih-Rei  
 ; APPLICANT: Donovan, William P.  
 ; APPLICANT: Gilmer, Amy J.  
 ; APPLICANT: Ruper, Mark J.  
 ; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin Compos  
 ; FILE REFERENCE: MECO201  
 ; CURRENT APPLICATION NUMBER: US/09/661.322A  
 ; CURRENT FILING DATE: 2000-09-13  
 ; NUMBER OF SEQ ID NOS: 63  
 ; SOFTWARE: Patent version 3.0  
 ; SEQ ID NO 42  
 ; LENGTH: 710  
 ; TYPE: PRT

ORGANISM: Bacillus thuringiensis  
 FEATURE:  
 NAME/KEY: misc feature  
 LOCATION: (200)...(200)  
 OTHER INFORMATION: No. 6593293-Coding  
 US-09-661-322A-42

Query Match 91.5%; Score 3442.5; DB 4; Length 710;  
 Best Local Similarity 91.9%; Pred. No. 33e-304;  
 Matches 662; Conservative 16; Mismatches 31; Indels 11; Gaps 3;

QY 1 MKLKNQDKHQSSNAKVDKISTDSLKNETDIELQNHEDCLKMSYENVEPFFVSASTI 60  
 DB 1 MKLKNQDKHQSSNAKVDKISTDSLKNETDIELQNHEDCLKMSYENVEPFFVSASTI 51  
 QY 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEILFMEHVEE-INOKISTY 119  
 DB 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEILFMEHVEE-INOKISTY 119  
 QY 120 ANKALTDLKGGLDALAVYHDSLESWGNRNTRARSVRSQYIALELMFVKLPSPAVS 179  
 DB 120 ANKALTDLKGGLDALAVYHDSLESWGNRNTRARSVRSQYIALELMFVKLPSPAVS 179  
 QY 180 GEEVPLLPPIYAQAANLHLLLRDASI FGKEWGLSSSEISTFYNQVERAGDYSDHCVKWY 239  
 DB 180 GEEVPLLPPIYAQAANLHLLLRDASI FGKEWGLSSSEISTFYNQVERAGDYSDHCVKWY 239  
 QY 240 STGLNNLRGTNAESWVRYNQFRDMLVLDLVALFPSYDTQMPYIKTTAQLTREVTDA 299  
 DB 240 STGLNNLRGTNAESWVRYNQFRDMLVLDLVALFPSYDTQMPYIKTTAQLTREVTDA 299  
 QY 300 ICTVHPHPSFTSTWNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYNNM 359  
 DB 300 ICTVHPHPSFTSTWNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYNNM 359  
 QY 360 WGHKLEFRTIGTLNISTQGSTNTSINPVLPTFSRDVYRTESLAGLNLFLTQPVNGVP 419  
 DB 360 WGHKLEFRTIGTLNISTQGSTNTSINPVLPTFSRDVYRTESLAGLNLFLTQPVNGVP 419  
 QY 420 RVDFFHKVFTPIASDNFYPCYAGIGTQLODSENELPPEATQPNYESYSHRLSHIGLI 479  
 DB 420 RVDFFHKVFTPIASDNFYPCYAGIGTQLODSENELPPEATQPNYESYSHRLSHIGLI 479  
 QY 480 SASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT 539  
 DB 480 SASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT 539  
 QY 540 NTGTFGDIRVNINPPFAQRYRIRYASTTDLQHTSINGKAINQGNFSATMNRGEDLDY 599  
 DB 540 NTGTFGDIRVNINPPFAQRYRIRYASTTDLQHTSINGKAINQGNFSATMNRGEDLDY 599  
 QY 600 KTFRTVGTTPPSFLDVOSTFTTIGAWNFSSGNEVYIDRIEFVPEVVTYEAEDPEKAQEK 659  
 DB 600 KTFRTVGTTPPSFLDVOSTFTTIGAWNFSSGNEVYIDRIEFVPEVVTYEAEDPEKAQEK 659  
 QY 660 VTALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719  
 DB 660 VTALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719

RESULT 3  
 US-08-286-870A-4  
 ; Sequence 4, Application US/08286870A  
 ; Patent No. 6063605  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ELY, S  
 ; APPLICANT: TAILOR, RH  
 ; APPLICANT: TIPPETT, JM  
 ; APPLICANT: BLENN, RG  
 ; TITLE OF INVENTION: BACTERIAL GENES  
 ; NUMBER OF SEQUENCES: 10  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: CUSHMAN DABY & CUSHMAN



ADDRESSEE: Intellectual Property Group of  
ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP  
STREET: 1100 New York Avenue, N.W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3918  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/286,870A  
FILING DATE: 05-AUG-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/520228  
FILING DATE: 09-MAY-1990  
APPLICATION NUMBER: GB 8910624.9  
FILING DATE: 09-MAY-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: PAUL N. KOKULIS  
REGISTRATION NUMBER: 16,773  
REFERENCE/DOCKET NUMBER: 70608/220720  
TELEPHONE: (202) 861-3000  
TELEFAX: (202) 822-0944  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 648 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-286-870A-4

Query Match 89.6%; Score 3370; DB 3; Length 648;  
Best Local Similarity 99.5%; Pred. No. 1.1e-297;  
Matches 646; Conservative 1; Mismatches 0; Indels 2; Gaps 2;  
QY 1 M K L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y E N V E F V S A S T I 60  
DB 1 M K L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y E N V E F V S A S T I 60  
QY 61 Q T G I G I A G K I L G T L G V F F A G Q V A S L Y S F I L G E L W P K G K N Q W E I L F M E H V E E - I N Q K I S T Y 119  
DB 61 Q T G I G I A G K I L G T L G V F F A G Q V A S L Y S F I L G E L W P K G K N Q W E I - F M E H V E E I N Q K I S T Y 119  
QY 120 A R N K A L T D L K G L G D A L A V Y H D S L E S W G V G N R N N T R A R S V V R S Q Y I A L E L M F V Q K L P S F A V S 179  
DB 120 A R N K A L T D L K G L G D A L A V Y H D S L E S W G V G N R N N T R A R S V V R S Q Y I A L E L M F V Q K L P S F A V S 179  
QY 180 G E E V P L L P I Y A Q A N L H L L R D A S I F G K E W G L S S S E I S T F Y N R Q V E R A G D Y S D H C V K W Y 239  
DB 180 G E E V P L L P I Y A Q A N L H L L R D A S I F G K E W G L S S S E I S T F Y N R Q V E R A G D Y S D H C V K W Y 239  
QY 240 S T G L N L R G T N A E S W R Y N Q F R D M T L M V L D L V A L P S Y D T Q M Y P I K T T A Q L T R E V Y T D A 299  
DB 240 S T G L N L R G T N A E S W R Y N Q F R D M T L M V L D L V A L P S Y D T Q M Y P I K T T A Q L T R E V Y T D A 299  
QY 300 I G T V H P H S F T S T T W Y N N A P S F S A I E A A V V R P H L L D F L E Q V T I Y S L L S R W S N T Q M N M 359  
DB 300 I G T V H P H S F T S T T W Y N N A P S F S A I E A A V V R P H L L D F L E Q V T I Y S L L S R W S N T Q M N M 359  
QY 360 W G H K L F R T I G G T L N I S T Q S T N T S I N P V T L P T S R D V Y R T E S L A G L N L F L T Q P V N G V P 419  
DB 360 W G H K L F R T I G G T L N I S T Q S T N T S I N P V T L P T S R D V Y R T E S L A G L N L F L T Q P V N G V P 419  
QY 420 R V D F H W F V T H P I A S D N F Y P G Y A G I G T Q L O D S E N L P P A T G O P N Y E S Y S H R L S H I G L I 479  
DB 420 R V D F H W F V T H P I A S D N F Y P G Y A G I G T Q L O D S E N L P P A T G O P N Y E S Y S H R L S H I G L I 479

QY 480 S A S H V K A L V Y S W T H R S A D R T N T I P N S T Q I P L V K A F N L S S G A A V V R G P G T G D I L R R T 539  
DB 480 S A S H V K A L V Y S W T H R S A D R T N T I P N S T Q I P L V K A F N L S S G A A V V R G P G T G D I L R R T 539  
QY 540 N T G F G D I R V N I N P P F A Q R Y E R I R Y A S T T D L Q F H T S I N G K A I N Q G N F S A T M R G E D L D Y 599  
DB 540 N T G F G D I R V N I N P P F A Q R Y E R I R Y A S T T D L Q F H T S I N G K A I N Q G N F S A T M R G E D L D Y 599  
QY 600 K T F R T V G T T F S F L D V Q S T T I G A W N F S S G N E V Y I D R I E F V P V E V T Y E 648  
DB 600 K T F R T V G T T F S F L D V Q S T T I G A W N F S S G N E V Y I D R I E F V P V E V T Y E 648

## RESULT 4

US-09-003-217-2  
Sequence 2, Application US/09003217  
Patent No. 5986177  
GENERAL INFORMATION:  
APPLICANT: Osman, Yehia A.  
APPLICANT: Madkour, Magdy A.  
APPLICANT: Bulla, Lee A.  
TITLE OF INVENTION: BACILLUS THURINGIENSIS ISOLATES WITH  
TITLE OF INVENTION: BROAD SPECTRUM ACTIVITY  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: W. Murray Spruill (Alston & Bird, LLP)  
STREET: 3605 Glenwood Ave. Suite 310  
CITY: Raleigh  
STATE: NC  
COUNTRY: US  
ZIP: 27622  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/003,217  
FILING DATE:  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Spruill, W. Murray  
REGISTRATION NUMBER: 32,943  
REFERENCE/DOCKET NUMBER: 5718-3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 919 420 2202  
TELEFAX: 919 881 3175  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 719 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-003-217-2

Query Match 88.8%; Score 3341; DB 2; Length 719;  
Best Local Similarity 89.2%; Pred. No. 5.8e-295;  
Matches 642; Conservative 35; Mismatches 41; Indels 2; Gaps 2;  
QY 1 M K L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y E N V E F V S A S T I 60  
DB 1 M K L K N P D K H Q T L S S N A K V D K I A T D S L K N E T D I E L K N M N E D Y L R M S E H S I D P F V S A S T I 60  
QY 61 Q T G I G I A G K I L G T L G V F F A G Q V A S L Y S F I L G E L W P K G K N Q W E I L F M E H V E E - I N Q K I S T Y 119  
DB 61 Q T G I G I A G K I L G T L G V F F A G Q V A S L Y S F I L G E L W P K G K S Q W E I - F M E H V E A I I N K I S T Y 119  
QY 120 A R N K A L T D L K G L G D A L A V Y H D S L E S W G V G N R N N T R A R S V V R S Q Y I A L E L M F V Q K L P S F A V S 179  
DB 120 A R N K A L T D L K G L G D A L A V Y H S L E S W G V G N R N N T R A R S V V K N Q Y I A L E L M F V Q K L P S F A V S 179  
QY 180 G E E V P L L P I Y A Q A N L H L L R D A S I F G K E W G L S S S E I S T F Y N R Q V E R A G D Y S D H C V K W Y 239

Db 180 GEEVPLPIYAQAANLHLLLRDASIFPKNGGLSASEISTFYNRQVTRDYSYHCVKWN 239  
Qy 240 STGLNLRGTNAESWRYNQFRDMTLMVLVLFPSYDTQMPYIKTTAQLTREVYTD 299  
Db 240 NGLNLRATNGQSWRYNQFRDKIELMVLVLFPSYDTQMPYIKTTAQLTREVYTD 299  
Qy 300 IGTVPHPSPSTTTWNNAPSAIEAAVVRNPHLLDFLEQVITYSLLSRWSNTQYMM 359  
Db 300 IGTVPNQALRSTTTWNNAPSAIEAAVVRNPHLLDFLEQVITYSLLSRWSNTQYMM 359  
Qy 360 WGHKLEPRTIGTGLNISTQSTNTSINPVTLPFTSRDVRYSAGLNLFLTPQVNGVP 419  
Db 360 WGHLESRPICGALNTSTQSTNTSINPVTLPFTSRDVRYSAGLNLFLTPQVNGVP 419  
Qy 420 RYDFHMKFVTHPIASDNFYIYAGYIGTQLODSENELPEATGPNVYESYSHRSHIGLI 479  
Db 420 RYDFHMKFVTHPIASDNFYIYAGYIGTQLODSENELPEATGPNVYESYSHRSHIGLI 479  
Qy 480 SASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGHILRT 539  
Db 480 SASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGHILRT 539  
Qy 540 NTGTGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDL 599  
Db 540 KSGTFGHIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDL 599  
Qy 600 KTFRTVGTFTTSPFSDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEK 659  
Db 600 KTFRTVGTFTTSPFSDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEK 659  
Qy 660 VTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDELXKRELFVVKAKQIHIERNM 719  
Db 660 VTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDELXKRELFVVKAKQIHIERNM 719

## RESULT 5

US-09-218-942-2  
; Sequence 2, Application US/09218942  
; Patent No. 6232439  
; GENERAL INFORMATION:  
; APPLICANT: Osman, Yehia  
; TITLE OF INVENTION: Bacillus Thuringiensis Isolates with Broad Spectrum  
; FILE REFERENCE: C7Y1  
; CURRENT APPLICATION NUMBER: US/09/218,942  
; CURRENT FILING DATE: 1998-12-22  
; EARLIER APPLICATION NUMBER: 60/035,361  
; EARLIER FILING DATE: 1997-01-10  
; EARLIER APPLICATION NUMBER: 09/003,217  
; EARLIER FILING DATE: 1998-01-06  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: Patent in Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 719  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
US-09-218-942-2

Query Match 88.7%; Score 3336; DB 3; Length 719;  
Best Local Similarity 89.2%; Pred. No. 1.7e-294;  
Matches 642; Conservative 35; Mismatches 41; Indels 2; Gaps 2;

Qy 1 MKLKNQDKHQSFSSNAKVDKISTLSKNETDIELQNIHEDCLMSEYENVEPVVSASTI 60  
Db 1 MKLKNPDKHQTLSSNAKVDKISTLSKNETDIELKNNWNNEDYLEMSEHSIDFVSASTI 60  
Qy 61 QTGIGIAGKIIGTGVPPAGQVASYLFIIGELMPKGNQWELFMEHVEE-INQKISTY 119  
Db 61 QTGIGIAGKIIGTGVPPAGQVASYLFIIGELMPKGNQWELFMEHVEE-INQKISTY 119  
Qy 120 ARNKALTDLKGIGDALAVYHDSLSWGNRNNTARSVRSQYIALELMPVQKLPSPAVS 179  
Db 120 ARNKALTDLKGIGDALAVYHDSLSWGNRNNTARSVRSQYIALELMPVQKLPSPAVS 179

Qy 180 GEEVPLPIYAQAANLHLLLRDASIFPKNGGLSASEISTFYNRQVTRDYSYHCVKWN 239  
Db 180 GEEVPLPIYAQAANLHLLLRDASIFPKNGGLSASEISTFYNRQVTRDYSYHCVKWN 239  
Qy 240 STGLNLRGTNAESWRYNQFRDMTLMVLVLFPSYDTQMPYIKTTAQLTREVYTD 299  
Db 240 NGLNLRATNGQSWRYNQFRDKIELMVLVLFPSYDTQMPYIKTTAQLTREVYTD 299  
Qy 300 IGTVPHPSPSTTTWNNAPSAIEAAVVRNPHLLDFLEQVITYSLLSRWSNTQYMM 359  
Db 300 IGTVPNQALRSTTTWNNAPSAIEAAVVRNPHLLDFLEQVITYSLLSRWSNTQYMM 359  
Qy 360 WGHKLEPRTIGTGLNISTQSTNTSINPVTLPFTSRDVRYSAGLNLFLTPQVNGVP 419  
Db 360 WGHLESRPICGALNTSTQSTNTSINPVTLPFTSRDVRYSAGLNLFLTPQVNGVP 419  
Qy 420 RYDFHMKFVTHPIASDNFYIYAGYIGTQLODSENELPEATGPNVYESYSHRSHIGLI 479  
Db 420 RYDFHMKFVTHPIASDNFYIYAGYIGTQLODSENELPEATGPNVYESYSHRSHIGLI 479  
Qy 480 SASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGHILRT 539  
Db 480 SASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGHILRT 539  
Qy 540 NTGTGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDL 599  
Db 540 KSGTFGHIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDL 599  
Qy 600 KTFRTVGTFTTSPFSDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEK 659  
Db 600 KTFRTVGTFTTSPFSDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEK 659  
Qy 660 VTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDELXKRELFVVKAKQIHIERNM 719  
Db 660 VTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDELXKRELFVVKAKQIHIERNM 719

## RESULT 6

US-08-286-870A-6  
; Sequence 6, Application US/08286870A  
; Patent No. 6063605  
; GENERAL INFORMATION:  
; APPLICANT: ELY, S  
; APPLICANT: TAILOR, RH  
; APPLICANT: TIPPETT, JM  
; APPLICANT: BLENN, RG  
; TITLE OF INVENTION: BACTERIAL GENES  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CUSHMAN DABY & CUSHMAN  
; ADDRESSEE: Intellectual Property Group of  
; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP  
; STREET: 1100 New York Avenue, N.W.  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3918  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/286,870A  
; FILING DATE: 05-AUG-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/520228  
; FILING DATE: 09-MAY-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 8910624.9  
; FILING DATE: 09-MAY-1989

ATTORNEY/AGENT INFORMATION:  
NAME: PAUL N. KOKULIS  
REGISTRATION NUMBER: 16,773  
REFERENCE/DOCKET NUMBER: 70608/220720  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 861-3000  
TELEFAX: (202) 822-0944  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 535 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-286-870A-6

Query Match 73.8%; Score 2776; DB 3; Length 535;  
Best Local Similarity 99.4%; Pred. No. 9.5e-244;  
Matches 533; Conservative 1; Mismatches 0; Indels 2; Gaps 2;

QY 1 MKLNQDKHOSFSSNAKVDKISTDSLNKQETDIELONINHEDECLKMSEYENVEFPVSASTI 60  
DB 1 MKLNQDKHOSFSSNAKVDKISTDSLNKQETDIELONINHEDECLKMSEYENVEFPVSASTI 60

QY 61 QTGIGIAGKILGTIGVFPAGQVASYLFGELWPKGNQWEILFMEHVEE-INQKISTY 119  
DB 61 QTGIGIAGKILGTIGVFPAGQVASYLFGELWPKGNQWEILFMEHVEEIIINQKISTY 119

QY 120 ARNKALTDLKGIDALAVHDSLESVGNENNRASVVRSOYIALELMFVQKLPFAVS 179  
DB 120 ARNKALTDLKGIDALAVHDSLESVGNENNRASVVRSOYIALELMFVQKLPFAVS 179

QY 180 GEEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISITFYNRQVERAGDSDHCVKWY 239  
DB 180 GEEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISITFYNRQVERAGDSDHCVKWY 239

QY 240 STGLNLRGNTASWRYNQFRDMTLMVLALPSPDYTMQYPIKTTAQLTREYVYTD 299  
DB 240 STGLNLRGNTASWRYNQFRDMTLMVLALPSPDYTMQYPIKTTAQLTREYVYTD 299

QY 300 IGTVHPHPSFTSTWYNNNAPSFAIEAAVVRPHLLDFLEQVTIYSLSRWNTQYMM 359  
DB 300 IGTVHPHPSFTSTWYNNNAPSFAIEAAVVRPHLLDFLEQVTIYSLSRWNTQYMM 359

QY 360 WGGHKLFRITGTLNISTQGSTNNTSINPVLTPFTSRDVRTSLAGNLFLTPQVNGVP 419  
DB 360 WGGHKLFRITGTLNISTQGSTNNTSINPVLTPFTSRDVRTSLAGNLFLTPQVNGVP 419

QY 420 RVDPHKFWTHPIASDNFYFYGAGIGTQLODSNELPPEATQPNYESYSHLSHIGLI 479  
DB 420 RVDPHKFWTHPIASDNFYFYGAGIGTQLODSNELPPEATQPNYESYSHLSHIGLI 479

QY 480 SASHVKALVSWTHRSADRTNITPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDI 535  
DB 480 SASHVKALVSWTHRSADRTNITPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDI 535

RESULT 7  
US-08-100-709-4  
Sequence 4, Application US/08100709  
Patent No. 5322687  
GENERAL INFORMATION:  
APPLICANT: Donovan, William P.  
APPLICANT: Tan, Yiping  
APPLICANT: Jan, Christine S.  
APPLICANT: Gonzalez Jr., Jose M.  
TITLE OF INVENTION: BACILLUS THURINGIENSIS CRYE4 AND CRYE5  
TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.  
ADDRESS: Nadel  
STREET: 1601 Market Street, 36th Floor  
CITY: Philadelphia

STATE: Pennsylvania  
COUNTRY: U.S.A.  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/100,709  
FILING DATE: 19930729  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Egolf, Christopher  
REGISTRATION NUMBER: 27633  
REFERENCE/DOCKET NUMBER: 7205-49  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-757-1590  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1229 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-100-709-4

Query Match 64.3%; Score 2417.5; DB 1; Length 1229;  
Best Local Similarity 65.3%; Pred. No. 1.6e-210;  
Matches 469; Conservative 90; Mismatches 140; Indels 19; Gaps 8;

QY 13 SSNAKVDKISTDSLNK-ETDIELQ-NINHEDECLKMSEYENVEFPVSASTIQTGIGIAGKI 70  
DB 7 NENEIINALSITVSNPSTQMNLSPDARIEDSLCAEVNNDIPFVSASTVQTGINAGRI 66

QY 71 LGTLGVFPAGQVASYLFGELWPKGNQWEILFMEHVEE-INQKISTYARNKALTDLK 129  
DB 67 LGVLGVFPAGQVASYLFGELWPKGNQWEILFMEHVEEQLIRQVNTENTTAIRLE 125

QY 130 GLGDALAVHDSLESVGNENNRASVVRSOYIALELMFVQKLPSPAVSEEVPLLPYI 189  
DB 126 GLGRGVRYSQQALETWLDNRNDARSILERYVALELDITTAIPFRIRNEEVEPLLMVY 185

QY 190 AQAANLHLLLRDASIFGKEWGLSSSEISITFYNRQVERAGDSDHCVKWYSTGLNLRGT 249  
DB 186 AQAANLHLLLRDASIFGKEWGLSSSEISITFYNRQVERAGDSDHCVKWYSTGLNLRGT 245

QY 250 NAESVVRVNRQFRDMTLMVLALPSPDYTMQYPIKTTAQLTREYVYTDALGTVHPHPSF 309  
DB 246 NAESVVRVNRQFRDMTLMVLALPSPDYTMQYPIKTTAQLTREYVYTDALGTVHPHPSF 305

QY 310 TSTTWNNAFSAIEAAVVRPHLLDFLEQVTIYSLSRWNTQYMMWGGHKLFRIT 369  
DB 306 ASTNMFNNAPSFAIEAAVVRPHLLDFLEQVTIYSLSRWNTQYMMWGGHKLFRIT 365

QY 370 IGGTLNISTQGST-NTSINPVLTPFTSRDVRTSLAGNLFLTPQVNGVPVRDHPHFW 428  
DB 366 IGGTLNISTQGST-NTSINPVLTPFTSRDVRTSLAGNLFLTPQVNGVPVRDHPHFW 422

QY 429 THPIASDNFYFYGAGIGTQLODSNELPPEATQPNYESYSHLSHIGLI 481  
DB 423 ---INPQNIYERGATTSYQYQGVIGLFDSETELPETTERPNYESYSHLSHIGLI 479

QY 482 SHVKALVSWTHRSADRTNITPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNT 541  
DB 480 NTLRPAVSWTHRSADRTNITPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNT 539

QY 542 GTFGDIRVNNPPFAQRVVRIRYASTDQLQHTSINKAINQGNFSAITMNGEDLDYKT 601  
DB 540 GTFGDIRVNNPPFAQRVVRIRYASTDQLQHTSINKAINQGNFSAITMNGEDLDYKT 599

QY 602 FRTVGTFTPFSLDQSTFTICANNFSSGNEVVIDRIEFPVVEYEAIDFEKAQEKVT 661  
DB 600 FRTVGTFTPFSLDQSTFTICANNFSSGNEVVIDRIEFPVVEYEAIDFEKAQEKVT 658

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QY 662 ALFTSTNPRGLKTDVYKHIDOVSNLVSLSDEFLVDEKRELFEIVKYANLHIERNM 719
Db 659 ALFTSTNPRRLKTDVTDYHIDQVSNMVACLSDFLDEKRELFEIVKYAKLSDERNL 716

RESULT 8
US-08-176-865-4
; Sequence 4, Application US/08176865
; Patent No. 5616319
; GENERAL INFORMATION:
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yiping
; APPLICANT: Jany, Christine S.
; APPLICANT: Gonzalez Jr., Jose M.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS CYET4 AND CYET5
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
; ADDRESSEE: Nadel
; STREET: 1601 Market Street, 36th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/176,865
; FILING DATE: 30-DEC-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/100,709
; FILING DATE: 29-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Egolf, Christopher
; REGISTRATION NUMBER: 27633
; REFERENCE/DOCKET NUMBER: 7205-49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-757-1590
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1229 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-176-865-4

Query Match 64.3%; Score 2417.5; DB 1; Length 1229;
Best Local Similarity 65.3%; Pred. No. 1.6e-210;
Matches 469; Conservative 90; Mismatches 140; Indels 19; Gaps 8;

QY 13 SSNAKVDSIKSTDSLKN-ETDLEQ-NINHEPCLKMSVENVEPVFVSASTTGTGTGIAGKI 70
Db 7 NENEINLSIPTVSNPSTQNLSFDARIEDSLCVAENVNIDPVFVSASTVQTGINIAGRI 66

QY 71 LGTLGVFPAGVASYLSPILGELWPKGNQWEILFMEHVEE-INQKISTYARNKALFDLK 129
Db 67 LGVLGVFPAGLASFYSPLVGLWFGSDPWEI-FLEHVEQLIRQVQVTRNTAIARLE 125

QY 130 GLGDAVAYHDSLSWGNRNNTARSVVRQYITALELMPVQKLPSFVSGEVEVPLPIY 189
Db 126 GLGGRYSYQQALETWLDNRNDRSRIILERYVALELDITTAIPLRIEVEVPLLMVY 185

QY 190 QAANLHLLLRDASIFGKWEGLSSSISTIPYNRQVERAGDYSCHVKWYSTGNNLRGT 249
Db 186 QAANLHLLLRDASLFGSEGMASDDVQYQIRYTEYSNHCVCQWNTGLNLRGT 245

QY 250 NAESWRVYNQFRDMLMVLDELVALFPSSYDTQMTYPIKTAQLTREVYTDALGTVHPHPSF 309

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Db 246 NAESWRVYNQFRDMLGVLDELVALFPSSYDTQMTYPIKTAQLTREVYTDALGTVHPHPSF 305
QY 310 TSTWYNNNAPSFAIEAAVVRNPHLLDLEQVITYLSLSRWSNTQYMMWGHKLEPRT 369
Db 306 ASTNWFNNAPSFAIEAAIFRPPHLLDPPEQLTIYSASSRWSSTQHMYNMYVGHRLNFRP 365
QY 370 IGGTLNISTOGST-NTSINPVTLPFTSRDVTYTESLAGLNLFLTOPVNGVPRVDSHMKVEV 428
Db 366 IGGTLNISTOGTLNNTSINPVTLPFTSRDVTYTESNAGTNILFTTPVNGVPRVWARFNF 422
QY 429 THEIASDNFYPG-----YAGITGLQDSDSENELPPEATGQFNYESYSHRLSHIGLISA 481
Db 423 ---INPQNIYERGATTYSQYQGVIGLFDSETLPPEPETERPYESYSHRLSHIGLIIG 479
QY 482 SHVKALVYSWTHRSADRTWTIEPNSITQIPLVKAFLNSGAAVVRGPGTGGDILRRNT 541
Db 480 NTLRAPVYSWTHRSADRTWTIGENRITQIPLVKAFLNSGAAVVRGPGTGGDILRRNT 539
QY 542 GTFGDIRVNIINPPFAQRYVRIRYASTTDLQPHTSINGKAINQGNFSAIMRGEIDLKYT 601
Db 540 GTFGDIRLINIVPLSQRYVRIRYASTTDLQPHTSINGKAINQGNFSAIMRGEIDLKYT 599
QY 602 FRTVGTTPFSLDQSTFTIGAMNPSGNEVYIDRIEFPVPEVVEYEAHYDEKAEKQVKT 661
Db 600 FRTAGFSTPFNLAQSTFTLGAQFSN-QEYVIDRVEFVPAEVTFEAYDILERAQKAVN 658
QY 662 ALFTSTNPRGLKTDVYKHIDOVSNLVSLSDEFLVDEKRELFEIVKYANLHIERNM 719
Db 659 ALFTSTNPRRLKTDVTDYHIDQVSNMVACLSDFLDEKRELFEIVKYAKLSDERNL 716

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## RESULT 9

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US-08-474-038-4
; Sequence 4, Application US/08474038
; Patent No. 5679343
; GENERAL INFORMATION:
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yiping
; APPLICANT: Jany, Christine S.
; APPLICANT: Gonzalez Jr., Jose M.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS CYET4 AND CYET5
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
; ADDRESSEE: Nadel
; STREET: 1601 Market Street, 36th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,038
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/176,865
; FILING DATE: 30-DEC-1993
; APPLICATION NUMBER: US 08/100,709
; FILING DATE: 29-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Egolf, Christopher
; REGISTRATION NUMBER: 27633
; REFERENCE/DOCKET NUMBER: 7205-49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-757-1590
; INFORMATION FOR SEQ ID NO: 4:

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SEQUENCE CHARACTERISTICS:  
 LENGTH: 1229 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-474-038-4

Query Match 64.3%; Score 2417.5; DB 1; Length 1229;  
 Best Local Similarity 65.3%; Pred. No. 1.6e-210;  
 Matches 469; Conservative 90; Mismatches 140; Indels 19; Gaps 8;

QY 13 SSNAKVDKISTSLKN-ETDIELQ-NINHEDECLKMEYENVEPVASSTIQTGIGIAGKI 70  
 DB 7 NENEIINALSIPTVNSPSTQNLSPDARIEDSLCAEVNNDIPFVSASTVQTGINAGRI 66

QY 71 LGTLGVPPAGQVASYFLIGELWPKGNQWELFMEHVEE-INQKISTYARKNALTDLK 129  
 DB 67 LGVLGVPPAGQVASYFLIGELWPKGNQWELFMEHVEE-INQKISTYARKNALTDLK 125

QY 130 GLGDALAVYHDSLESVGNRNTRARSVRSQVIALMLFVQKLPFAVSGEVPLPIY 189  
 DB 126 GLGRGYSYQQALETWLDNRDARSIIILERYVALELDITTAIPLFRINEEVPLLMVY 185

QY 190 AQAANLHLLLRDASIFGKESGLSSSEISTFYNRQVERAGDYSDHCVKYSTGLNLRGT 249  
 DB 186 AQAANLHLLLRDASIFGKESGLSSSEISTFYNRQVERAGDYSDHCVKYSTGLNLRGT 245

QY 250 NAEWVRYNQFRRDMLVLDLVALFSPYDTQMYPIKTTAQLTREYVTDAGTVHPHPSF 309  
 DB 246 NAEWVRYNQFRRDMLVLDLVALFSPYDTQMYPIKTTAQLTREYVTDAGTVHPHPSF 305

QY 310 TSTTWNYNAPSFAIEAAVVRNPHLDLFLQVYTSLLSEWNTQYMMNMGHKLFRFT 369  
 DB 306 ASTNFWNNAPSFAIEAAVVRNPHLDLFLQVYTSLLSEWNTQYMMNMGHKLFRFT 365

QY 370 IGGTLNISTQGST-NTSINPVTLPFTSRDVRRTESLAGNLFLLTPQVNGVPRVDFHWKFV 428  
 DB 366 IGGTLNISTQGST-NTSINPVTLPFTSRDVRRTESLAGNLFLLTPQVNGVPRVDFHWKFV 422

QY 429 THPTASDNFYYPG-----YAGTGTQDSENELPPEATGQPNYESYSHRSLHIGLISA 481  
 DB 423 ---INPQNIYERGATTYSQYQGVGIQLFDSSTELPPTTERPNYESYSHRSLHIGLIG 479

QY 482 SHVKALVYSWTHRSADRTNTEPNISITQIPLVKANLSSGAAVVRGPGTGGDILRRNT 541  
 DB 480 NTLRAPVYSWTHRSADRTNTEPNISITQIPLVKANLSSGAAVVRGPGTGGDILRRNT 539

## RESULT 10

US-08-779-046-4  
 ; Sequence 4, Application US/08779046  
 ; Patent No. 5854053  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Donovan, William P.  
 ; APPLICANT: Tan, Yiping  
 ; APPLICANT: Jan, Christine S.  
 ; APPLICANT: Gonzalez Jr., Jose M.  
 ; TITLE OF INVENTION: BACILLUS THURINGIENSIS CRYET4 AND CRYET5  
 ; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS  
 ; NUMBER OF SEQUENCES: 5  
 ; CORRESPONDENCE ADDRESS:

ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.  
 ADDRESSEE: Nadel  
 STREET: 1601 Market Street, 36th Floor  
 CITY: Philadelphia  
 STATE: Pennsylvania  
 COUNTRY: U.S.A.  
 ZIP: 19103

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/779,046  
 FILING DATE: 06-JAN-1997  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/100,709  
 FILING DATE: 29-JUL-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Egolf, Christopher  
 REGISTRATION NUMBER: 27633  
 REFERENCE/DOCKET NUMBER: 7205-49  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 215-757-1590  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1229 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-779-046-4

Query Match 64.3%; Score 2417.5; DB 2; Length 1229;

Best Local Similarity 65.3%; Pred. No. 1.6e-210;  
 Matches 469; Conservative 90; Mismatches 140; Indels 19; Gaps 8;

QY 13 SSNAKVDKISTSLKN-ETDIELQ-NINHEDECLKMEYENVEPVASSTIQTGIGIAGKI 70  
 DB 7 NENEIINALSIPTVNSPSTQNLSPDARIEDSLCAEVNNDIPFVSASTVQTGINAGRI 66

QY 71 LGTLGVPPAGQVASYFLIGELWPKGNQWELFMEHVEE-INQKISTYARKNALTDLK 129  
 DB 67 LGVLGVPPAGQVASYFLIGELWPKGNQWELFMEHVEE-INQKISTYARKNALTDLK 125

QY 130 GLGDALAVYHDSLESVGNRNTRARSVRSQVIALMLFVQKLPFAVSGEVPLPIY 189  
 DB 126 GLGRGYSYQQALETWLDNRDARSIIILERYVALELDITTAIPLFRINEEVPLLMVY 185

QY 190 AQAANLHLLLRDASIFGKESGLSSSEISTFYNRQVERAGDYSDHCVKYSTGLNLRGT 249  
 DB 186 AQAANLHLLLRDASIFGKESGLSSSEISTFYNRQVERAGDYSDHCVKYSTGLNLRGT 245

QY 250 NAEWVRYNQFRRDMLVLDLVALFSPYDTQMYPIKTTAQLTREYVTDAGTVHPHPSF 309  
 DB 246 NAEWVRYNQFRRDMLVLDLVALFSPYDTQMYPIKTTAQLTREYVTDAGTVHPHPSF 305

QY 310 TSTTWNYNAPSFAIEAAVVRNPHLDLFLQVYTSLLSEWNTQYMMNMGHKLFRFT 369  
 DB 306 ASTNFWNNAPSFAIEAAVVRNPHLDLFLQVYTSLLSEWNTQYMMNMGHKLFRFT 365

QY 370 IGGTLNISTQGST-NTSINPVTLPFTSRDVRRTESLAGNLFLLTPQVNGVPRVDFHWKFV 428  
 DB 366 IGGTLNISTQGST-NTSINPVTLPFTSRDVRRTESLAGNLFLLTPQVNGVPRVDFHWKFV 422

QY 429 THPTASDNFYYPG-----YAGTGTQDSENELPPEATGQPNYESYSHRSLHIGLISA 481  
 DB 423 ---INPQNIYERGATTYSQYQGVGIQLFDSSTELPPTTERPNYESYSHRSLHIGLIG 479

QY 482 SHVKALVYSWTHRSADRTNTEPNISITQIPLVKANLSSGAAVVRGPGTGGDILRRNT 541  
 DB 480 NTLRAPVYSWTHRSADRTNTEPNISITQIPLVKANLSSGAAVVRGPGTGGDILRRNT 539

QY 542 GTFGDIRVNPFAQRYVRIRYASTTDLQPHTSINGKAINOGNFSATMRGDLDYKT 601  
DB 540 GTFGDIRVNPFSQRYVRIRYASTTDLQPHTSINGKAINOGNFSATMRGDLDYKT 599  
QY 602 FTFTGTPFSDVQSTFTTIGAMNFSNGEYVYIDRIEFPVVEVTEAYEYDFEKAQKVT 661  
DB 600 FTFTGTPFSDVQSTFTTIGAMNFSNGEYVYIDRIEFPVVEVTEAYEYDFEKAQKVT 658  
QY 662 ALFTSTNPRGLKTDVYKHIDQVSNLVSLSDEFVLDKRELFVYKYNELHIERNM 719  
DB 659 ALFTSTNPRGLKTDVYKHIDQVSNLVSLSDEFVLDKRELFVYKYNELHIERNM 716

RESULT 11  
US-08-881-340-4  
; Sequence 4, Application US/08081340  
; Patent No. 5942658  
; GENERAL INFORMATION:  
; APPLICANT: Donovan, William P.  
; APPLICANT: Tan, Yiping  
; APPLICANT: Jany, Christine S.  
; APPLICANT: Gonzalez Jr., Jose M.  
; TITLE OF INVENTION: BACILLUS THURINGIENSIS cVYET4 AND cVYET5  
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Panith Schwarze Jacobs & Nadel c/o A.S.  
; ADDRESSER: Nadel  
; STREET: 1601 Market Street, 36th Floor  
; CITY: Philadelphia  
; STATE: Pennsylvania  
; COUNTRY: U.S.A.  
; ZIP: 19103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/881.340  
; FILING DATE: 24-JUN-1997  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/100,709  
; FILING DATE: 29-JUL-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Egolf, Christopher  
; REGISTRATION NUMBER: 27633  
; REFERENCE/DOCKET NUMBER: 7205-49  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 215-757-1590  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1229 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-881-340-4

Query Match 64.3%; Score 2417.5; DB 2; Length 1229;  
Best Local Similarity 65.3%; Pred. No. 1.6e-210;  
Matches 469; Conservative 90; Mismatches 140; Indels 19; Gaps 8;

QY 13 SSNAKVDKISDLSKN-ETDIELQ-NINHEDECLMSEVENVEPVASSTIQTGTGIAGKI 70  
DB 7 NENEINALSIPTVNSPSTQNNLSPDARIEDSLCAEWNIDPVSASTVQTGINIAGRI 66  
QY 71 LGTGVPPAGVAGSLYSPFILGELMPKGNQHEILFMHEVEE-INQKISTYARNKALTDLK 129  
DB 67 LGVLGVPAGVAGSLYSPFILGELMPKGNQHEILFMHEVEE-INQKISTYARNKALTDLK 125  
QY 130 GLGDALAVYHDSLSWGNRNNTARSVVRQYIALELMFVQKLPSFAVSGEVPLPIY 199

DB 126 GLGRGYRSYQQALETWLDNRNDARSIIILERYVALELDITTAIPLFIRNEEVPPLVMY 185  
QY 190 AQANLHLLLRDASIFGKENGWLSSEISTFNRQVERAGDYSDEHCVKYSTGLANLRGT 249  
DB 186 AQANLHLLLRDASIFGKENGWLSSEISTFNRQVERAGDYSDEHCVKYSTGLANLRGT 245  
QY 250 NAEWSVRYNQFQRRDMLVLDLVALPPSYDQWPIKTTAQTREYVYDAITGVHPHPSF 309  
DB 246 NAEWSVRYNQFQRRDMLVLDLVALPPSYDQWPIKTTAQTREYVYDAITGVHPHPSF 305  
QY 310 TSTTWNANPAPSAIEAAVAVRNPHLLDLEQVITYSLLSRWSNTQYMMWGGCHLEPRT 369  
DB 306 ASTNWFNNAPSAIEAAVAVRNPHLLDLEQVITYSLLSRWSNTQYMMWGGCHLEPRT 365  
QY 370 IGGTLNISTQGST-NTSINPVTLPFTSRDVTYTESLAGNLNLTQPVNGVPRVDPMKVF 428  
DB 366 IGGTLNISTQGST-NTSINPVTLPFTSRDVTYTESLAGNLNLTQPVNGVPRVDPMKVF 422  
QY 429 THPIASDNFYYPG-----YAGIGTQODSNEIPLPEATGPNYESYSHRSLHIGLISA 481  
DB 423 ---INPQNIYERGATTSQYQGVGQLFDSSETLPPETTERPNYESYSHRSLHIGLIIG 479  
QY 482 SHVKALVYSWTHRSADRTNTEPNSTIQLPKAFNLSSGAARVPGPGTGGDIILRRNT 541  
DB 480 NTLRAPVYSWTHRSADRTNTEPNSTIQLPKAFNLSSGAARVPGPGTGGDIILRRNT 539  
QY 542 GTFGDIRVNPFAQRYVRIRYASTTDLQPHTSINGKAINOGNFSATMRGDLDYKT 601  
DB 540 GTFGDIRVNPFSQRYVRIRYASTTDLQPHTSINGKAINOGNFSATMRGDLDYKT 599  
QY 602 FTFTGTPFSDVQSTFTTIGAMNFSNGEYVYIDRIEFPVVEVTEAYEYDFEKAQKVT 661  
DB 600 FTFTGTPFSDVQSTFTTIGAMNFSNGEYVYIDRIEFPVVEVTEAYEYDFEKAQKVT 658  
QY 662 ALFTSTNPRGLKTDVYKHIDQVSNLVSLSDEFVLDKRELFVYKYNELHIERNM 719  
DB 659 ALFTSTNPRGLKTDVYKHIDQVSNLVSLSDEFVLDKRELFVYKYNELHIERNM 716

RESULT 12  
US-08-448-170-10  
; Sequence 10, Application US/08448170  
; Patent No. 5723758  
; GENERAL INFORMATION:  
; APPLICANT: Payne, Jewel  
; APPLICANT: Cummings, David A.  
; APPLICANT: Cannon, Raymond J.C.  
; APPLICANT: Narva, Kenneth E.  
; APPLICANT: Stelman, Steve  
; TITLE OF INVENTION: No. 5723758el Bacillus thuringiensis Isolate Denoted  
; TITLE OF INVENTION: B.t. PS156C2, Active Against Lepidopteran Pests, and Genes  
; TITLE OF INVENTION: Encoding Lepidopteran-Active Toxins  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David R. Saliwanchik  
; STREET: 2421 N.W. 41st. Street, Suite A-1  
; CITY: Gainesville  
; STATE: Florida  
; COUNTRY: USA  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/448,170  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/069,902  
; FILING DATE: 01-JUNE-1993  
; CLASSIFICATION: 424

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/759,247  
FILING DATE: 13-SEPT-1991  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Saiiwanichik, David R.  
REGISTRATION NUMBER: 31,794  
REFERENCE/DOCKET NUMBER: M/S 102D.C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (904) 375-8100  
TELEFAX: (904) 372-5800  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 488 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-448-170-10

Query Match 61.6%; Score 2318.5; DB 1; Length 488;  
Best Local Similarity 89.4%; Pred. No. 3.6e-202;  
Matches 445; Conservative 13; Mismatches 29; Indels 11; Gaps 3;

Qy 1 MCLKQDKHQSFSNAKVDKISTDSLKNETDIELQNHEDCLKMSYENVEPVSASTI 60  
Db 1 MSKNQNHQSLSNATVDKNTGSLNNTNTELQNFH-----EGIEPFSVSTI 51  
Qy 61 QTGIGIAGKILGTGVPPAGQVASYFILGELMPKGNQWEILFMEHVEE-INQKISTY 119  
Db 52 QTGIGIVGKILGNLGVPPAGQVASYFILGELMPKGSQWEI-FMEHVEELINQKISTY 110  
Qy 120 ARNKALTDLKLGDALAVYHDSLESWGNNRTRSVRSOYIALMLFVQKLPSPAVS 179  
Db 111 ARNKALADLKLGDALAVYHESLESWIENRNTTRSVKQSYITLMLFVQSLPSPAVS 170  
Qy 180 GEEVPLLPPIYAQAANLHLLLRDASIFGKXWGLSDSEISTFYNNRQSGKSEYSDHCVKWY 239  
Db 171 GEEVPLLPPIYAQAANLHLLLRDASIFGKXWGLSDSEISTFYNNRQSGKSEYSDHCVKWY 230  
Qy 240 STGLNNLRGTNAESWRYNQFRDMLVLDLVALFPSYDTQMPYPIKTTAQLTREVYTD 299  
Db 231 NTGLNRLMGNNAESWRYNQFRDMLVLDLVALFPSYDTQMPYPIKTTAQLTREVYTD 290  
Qy 300 IGTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDLEQVITYSLLSRWNSQYMMN 359  
Db 291 IGTVHPHPSFTSTTWYNNAPSFSTIEAAVVRNPHLLDLEQVITYSLLSRWNSQYMMN 350  
Qy 360 WGGHKLFRITGTLNISTQGSTNTSINPVTLPFTRSDVYRTESLAGLNFLTPQVNGVP 419  
Db 351 WGGHKLFRITGTLNISTQGSTNTSINPVTLPFTRSDVYRTESLAGLNFLTPQVNGVP 410  
Qy 420 RVDFFHWKPVTHPIASDNFYYPGYAGIGTQLODSNELPPEATGQPNYESYSHRLSHIGLI 479  
Db 411 RVDFFHWKPVTHPIASDNFYYPGYAGIGTQLODSNELPPEATGQPNYESYSHRLSHIGLI 470  
Qy 480 SASHWKALVYSWTHRSAD 497  
Db 471 SASHWKALVYSWTHRSAD 488

RESULT 13  
US-08-961-803-10  
Sequence 10, Application US/08961803  
Patent No. 6150589  
GENERAL INFORMATION:  
APPLICANT: Payne, Jewel  
APPLICANT: Cummings, David A.  
APPLICANT: Cannon, Raymond J.C.  
APPLICANT: Narva, Kenneth E.  
APPLICANT: Stelman, Steve  
TITLE OF INVENTION: No. 6150589a1 Bacillus thuringiensis Isolate Denoted  
; TITLE OF INVENTION: B.t. PS158Cz, Active Against Lepidopteran Pests, and Genes

TITLE OF INVENTION: Encoding Lepidopteran-Active Toxins  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jay M. Sanders  
STREET: 2421 N.W. 41st Street, Suite A-1  
CITY: Gainesville  
STATE: Florida  
COUNTRY: USA  
ZIP: 32606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/961,803  
FILING DATE: 31-OCT-1997  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/069,902  
FILING DATE: 01-JUNE-1993  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/759,247  
FILING DATE: 13-SEPT-1991  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/448,170  
FILING DATE: 23-MAY-1995  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Sanders, Jay M.  
REGISTRATION NUMBER: 39,355  
REFERENCE/DOCKET NUMBER: M/S 102DCD1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (352) 375-8100  
TELEFAX: (352) 372-5800  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 488 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-961-803-10

Query Match 61.6%; Score 2318.5; DB 3; Length 488;  
Best Local Similarity 89.4%; Pred. No. 3.6e-202;  
Matches 445; Conservative 13; Mismatches 29; Indels 11; Gaps 3;

Qy 1 MCLKQDKHQSFSNAKVDKISTDSLKNETDIELQNHEDCLKMSYENVEPVSASTI 60  
Db 1 MSKNQNHQSLSNATVDKNTGSLNNTNTELQNFH-----EGIEPFSVSTI 51  
Qy 61 QTGIGIAGKILGTGVPPAGQVASYFILGELMPKGNQWEILFMEHVEE-INQKISTY 119  
Db 52 QTGIGIVGKILGNLGVPPAGQVASYFILGELMPKGSQWEI-FMEHVEELINQKISTY 110  
Qy 120 ARNKALTDLKLGDALAVYHDSLESWGNNRTRSVRSOYIALMLFVQKLPSPAVS 179  
Db 111 ARNKALADLKLGDALAVYHESLESWIENRNTTRSVKQSYITLMLFVQSLPSPAVS 170  
Qy 180 GEEVPLLPPIYAQAANLHLLLRDASIFGKXWGLSDSEISTFYNNRQSGKSEYSDHCVKWY 239  
Db 171 GEEVPLLPPIYAQAANLHLLLRDASIFGKXWGLSDSEISTFYNNRQSGKSEYSDHCVKWY 230  
Qy 240 STGLNNLRGTNAESWRYNQFRDMLVLDLVALFPSYDTQMPYPIKTTAQLTREVYTD 299  
Db 231 NTGLNRLMGNNAESWRYNQFRDMLVLDLVALFPSYDTQMPYPIKTTAQLTREVYTD 290  
Qy 300 IGTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDLEQVITYSLLSRWNSQYMMN 359  
Db 291 IGTVHPHPSFTSTTWYNNAPSFSTIEAAVVRNPHLLDLEQVITYSLLSRWNSQYMMN 350

QY 360 WGHGKLEFRTIGTGLNISTQSTNTSINPVTLPFTSRDVRTESLAGLNLFLTQPVNGVP 419  
 Db 351 WGHGKLEFRTIGTGLNISTQSTNTSINPVTLPFTSRDVRTESLAGLNLFLTQPVNGVP 410  
 QY 420 RYDFHKKFVTHPIADNFYPPYAGIGTQLODSENELPPEATGQPNYESYSHRSLHIGLI 479  
 Db 411 RYDFHKKFVTHPIADNFYPPYAGIGTQLODSENELPPEATGQPNYESYSHRSLHIGLI 470  
 QY 480 SASHVKALVYSWTHRSAD 497  
 Db 471 SASHVKALVYSWTHRSAD 488

RESULT 14

US-07-951-715A-7  
 ; Sequence 7, Application US/07951715A  
 ; Patent No. 5625136

GENERAL INFORMATION:

APPLICANT: Koziel, Michael G.  
 APPLICANT: Desai, Nalini M.  
 APPLICANT: Lewis, Kelly S.  
 APPLICANT: Kramer, Vance C.  
 APPLICANT: Warren, Gregory W.  
 APPLICANT: Evola, Stephen V.  
 APPLICANT: Crossland, Lyle D.  
 APPLICANT: Wright, Martha S.  
 APPLICANT: Merlin, Ellis J.  
 APPLICANT: Launis, Karen L.  
 APPLICANT: Rothstein, Steven J.  
 APPLICANT: Bowman, Cindy G.  
 APPLICANT: Dawson, John L.  
 APPLICANT: Dunder, Erik M.  
 APPLICANT: Pace, Gary M.  
 APPLICANT: Suttie, Janet L.

TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
 TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE

NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:

ADDRESSES: CIBA-GEIGY Corporation  
 STREET: 7 Skyline Drive  
 CITY: Hawthorne  
 STATE: New York  
 COUNTRY: USA  
 ZIP: 10532

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30B  
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/951,715A

FILING DATE: 25-SEP-1992

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/772,027

FILING DATE: 04-OCT-1991

ATTORNEY/AGENT INFORMATION:

NAME: Spruill, W. Murray

REGISTRATION NUMBER: 32,943

REFERENCE/DOCKET NUMBER: S-18805/A/CGC 1577/CIP

TELECOMMUNICATION INFORMATION:

TELEPHONE: (919)541-8615

TELEFAX: (919)541-8689

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 1207 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-07-951-715A-7

Query Match

59.5%; Score 2236.5; DB 1; Length 1207;

Best Local Similarity 64.1%; Pred. No. 4.7e-194;  
 Matches 441; Conservative 76; Mismatches 156; Indels 15; Gaps 7;  
 QY 40 EDCLEKSEVENPEPVSASTIOTIGIAGKILCTIGVFPAGOVASLYSIFILGELWPKGN 99  
 Db 10 EDCLEKSEVENPEPVSASTIOTIGIAGKILCTIGVFPAGOVASLYSIFILGELWPKGN 99  
 QY 100 QWEILFMEHVEE-INQKISTYARNKALTDKLGDLALAVYHDSLSWGNRNNTARSVV 158  
 Db 70 QWEI-FLEHVEQLINQOITENARNTALARLQGLGDSFRAYQOQSLDLENRDASTRVL 128  
 QY 159 RSOYIALELMFYQKLPSEFAVSGEVEPLPIYAQAANLHLLLRDASIFGKENGSLASSEIS 218  
 Db 129 YTOYIALELDPLNAMPFAIRQOEVPFLMWYQAANLHLLLRDASIFGSEFGLTSQELIQ 188  
 QY 219 TFYNRQVERAGDYSCHVCWYSTGLNLRGTNAESWVRYNQFRDRMTLMVLDLVLFPSY 278  
 Db 189 RYVERQVERTRDYSYCVIEWYNTGLNLRGTNAESWVRYNQFRDRMTLMVLDLVLFPSY 248  
 QY 279 DTOMYDIKTTAQLTRVYTTDAIGTVHPHPSFTSTWYANNAPSESAIEAAVVRNPHLDF 338  
 Db 249 DRTYPTINTSAQLTRVYTTDAIGAT--GVNMAWMWYNNNAPSFSAIEAAVVRNPHLDF 306  
 QY 339 LEQVTIYSLLSRWNTQVYMMMGHKLPRITIGGTINISTOGSTNTSINPVTLPFTSRDV 398  
 Db 307 LEQVTIYSLLSRWNTQVYMMMGHKLPRITIGGTINISTOGSTNTSINPVTLPFTSRDV 366  
 QY 399 YRTESLAGLNLFP--LTQPVNGVPRVDVFWKFWTHP-----IASDNFYYPGYAGIGTQLOD 451  
 Db 367 YRTESYAGVLLMGYILEPIHGVPTVRNF--TNPQNISDRGTANYSQP--YESPGLQLKD 422  
 QY 452 SENELPPEATGQPNYESYSHRSLHIGLI SASHVKALVYSWTHRSADRTNITPNSITQIP 511  
 Db 423 SETELPPTETERPYESYSHRSLHIGLI ILOSVNVPVYSWTHRSADRTNITPNSITQIP 482  
 QY 512 LVKAFNLSSGAADVPGFTGGDILERTNTGTFDIRVNVINPPFAQVRVIRIYASTDL 571  
 Db 483 MVKASELPQGTTVVRGPGFTGGDILERTNTGTFDIRVNVINPPFAQVRVIRIYASTDL 542  
 QY 572 QFHTSINGRAINGNFSATMNGEDLDYKTFRTVGTFTTPTFSDVQSTFTICAMFNSSGN 631  
 Db 543 DFFVSRGGTTVNNFRFLRTNNSGDELYKGNFVRATFTPTFTQIDIRTSIQGLSGNG 602  
 QY 632 EYIDRIEFVPEVTEYAEYDFEKAQKVTAFTSTNPRGLKTDVYKHIDQVSNLVSFL 691  
 Db 603 EYIDKIEIIPVTATFEASYDLERAQEAVALFTNTNPRKLTVDYHIDQVSNLVAFL 662  
 QY 692 SDEFYLDKRELFPEIVKYANELHIERNM 719  
 Db 663 SDEFYLDKRELFPEIVKYANELHIERNM 690

RESULT 15

US-08-459-448A-7  
 ; Sequence 7, Application US/08459448A

Patent No. 5859336

GENERAL INFORMATION:

APPLICANT: Koziel, Michael G.

APPLICANT: Desai, Nalini M.

APPLICANT: Lewis, Kelly S.

APPLICANT: Kramer, Vance C.

APPLICANT: Warren, Gregory W.

APPLICANT: Evola, Stephen V.

APPLICANT: Crossland, Lyle D.

APPLICANT: Wright, Martha S.

APPLICANT: Merlin, Ellis J.

APPLICANT: Launis, Karen L.

APPLICANT: Rothstein, Steven J.

APPLICANT: Bowman, Cindy G.

APPLICANT: Dawson, John L.

APPLICANT: Dunder, Erik M.

APPLICANT: Pace, Gary M.

APPLICANT: Suttie, Janet L.







GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 28, 2004, 17:52:12 ; Search time 98.4365 Seconds  
(without alignments)  
4202.652 Million cell updates/sec

Title: US-10-019-823B-58

Perfect score: 3761

Sequence: 1 MKLNQDKHQSFSNAKVDK.....KRELFEIVKYANELHIERNM 719

Scoring table: BLOSUM62

Gapop 10.0 ; Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 02.1\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3733	99.3	719	2	CAC85964
2	3724	99.0	719	1	C1A8_BACTK
3	3724	99.0	719	2	O6X151
4	3724	99.0	719	2	AAP85782
5	3719	98.9	719	2	Q33N55
6	3718	98.9	719	2	O85796
7	3589	95.4	719	2	O8KY61
8	3517	93.5	719	2	Q9F0P8
9	3484	92.6	719	1	C1IB_BACTE
10	3363	89.4	719	1	C1ID_BACTU
11	3341	88.8	719	1	C1IC_BACTU
12	2417.5	64.3	1229	1	C1BB_BACTU
13	2417.5	64.3	1233	2	C1BC_BACTM
14	2250.5	59.8	1228	2	Q93775
15	2248.5	59.8	1228	1	C1BA_BACTK
16	2240.5	59.6	1228	2	Q93NM5
17	2166.5	57.6	849	2	O6PYW8
18	2166.5	57.6	849	2	AAS93797
19	2166.5	57.6	1227	1	C1BE_BACTU
20	2083.5	55.4	1231	2	Q8KNY2
21	2078.5	55.3	1231	2	C1BD_BACT2
22	1971.5	52.4	1215	1	C1KA_BACTM
23	1876	49.9	381	2	Q45740
24	1643.5	43.7	1157	1	C8AA_BACUK
25	1630	43.3	1144	2	Q8KZL7
26	1466	39.0	1157	1	C9CA_BACTO
27	1460.5	38.8	1169	1	C8BA_BACTU
28	1458.5	38.8	1166	1	C1CA_BACTU
29	1455	38.7	1169	1	C1FB_BACTM
30	1451	38.6	1167	1	C1JA_BACTU
31	1449	38.5	1174	2	Q45749

32	1443	38.4	1155	1	C1AB_BACTK	P06578 bacillus th
33	1443	38.4	1155	2	Q7BE98	Q7BE98 bacillus th
34	1443	38.4	1155	2	Q9F296	Q9F296 bacillus th
35	1443	38.4	1155	2	AAN76494	AAN76494 bacillus
36	1443	38.4	1155	2	AAC13302	AAC13302 bacillus
37	1441	38.3	1118	2	Q9AM83	Q9AM83 bacillus th
38	1438	38.2	1156	2	Q6GUA7	Q6GUA7 bacillus th
39	1433	38.1	1177	2	Q6EIX3	Q6EIX3 bacillus th
40	1431	38.0	1155	2	Q93T21	Q93T21 bacillus th
41	1430.5	38.0	793	2	O6PYW7	Q6PYW7 bacillus th
42	1430.5	38.0	793	2	AAS93798	AAS93798 bacillus
43	1430.5	38.0	1180	2	Q9S5V8	Q9S5V8 bacillus th
44	1429.5	38.0	1176	2	Q7WZT9	Q7WZT9 bacillus th
45	1425.5	37.9	1181	1	C1AE_BACTL	Q03748 bacillus th

## ALIGNMENTS

### RESULT 1

CAC85964 PRELIMINARY; PRT; 719 AA.  
ID CAC85964 AC CAC85964;  
DT 02-MAR-2004 (Tremblrel. 27, Created)  
DT 02-MAR-2004 (Tremblrel. 27, Last sequence update)  
DT 02-MAR-2004 (Tremblrel. 27, Last annotation update)  
DE Delta-endotoxin.  
GN CRYIIA.  
OS Bacillus thuringiensis (subsp. kurstaki).  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;  
OC Bacillus cereus group; Bacillus thuringiensis.  
OX NCBI\_TaxID=29339;  
RN [1]\_TaxID=29339;  
RP SEQUENCE FROM N.A.  
RC STRAIN=ENS3;  
RA Tounsi S., Zouari N., Jacua S.;  
RT "Cloning and study of the expression of a novel cryIIa-type gene from  
Bacillus thuringiensis subsp. kurstaki.";  
RL J. Appl. Microbiol. 95:23-28(2003).  
DR EMBL, AJ315121; CAC85964.1;  
SQ SEQUENCE 719 AA; 81203 MW; 8676ESA6C25DAFE8 CRC64;

Query Match 99.3%; Score 3733; DB 2; Length 719;

Best Local Similarity 99.6%; Pred. No. 4.5e-253;

Matches 717; Conservative 1; Mismatches 0; Indels 2; Gaps 2;

QY 1 MKLNQDKHQSFSNAKVDKISTDSLKNETDIELQININHEDCCLKMSEYENVEPVSASTI 60

DB 1 MKLNQDKHQSFSNAKVDKISTDSLKNETDIELQININHEDCCLKMSEYENVEPVSASTI 60

QY 61 QTGIGTAGKILGTGVPPAGQVASYLSFTLGELWPKGNQWEILFMEHVEE-INQKISTY 119

DB 61 QTGIGTAGKILGTGVPPAGQVASYLSFTLGELWPKGNQWEILFMEHVEE-INQKISTY 119

QY 120 ARNKALTDLKGDLALAVYHDSLESWGNGNNTNRARSVRSYIALELMFVKLPSFAVS 179

DB 120 ARNKALTDLKGDLALAVYHDSLESWGNGNNTNRARSVRSYIALELMFVKLPSFAVS 179

QY 180 GBEVPLLPYAAANLHLLLRDASIFGKEWGLSSSEISTFYNNQVERAGDYSCHVKWY 239

DB 180 GBEVPLLPYAAANLHLLLRDASIFGKEWGLSSSEISTFYNNQVERAGDYSCHVKWY 239

QY 240 STGLNNLRGTNAESWVRYNQFRDMLVLDLVALFPDYDTOMYPIKTTAQJTRREYIDA 299

DB 240 STGLNNLRGTNAESWVRYNQFRDMLVLDLVALFPDYDTOMYPIKTTAQJTRREYIDA 299

QY 300 IGVTHPHPSFTTWTNNNAPSFAIEAAVVRNPHLLDFLEQVTTYSLLSRNSNTQYNNM 359

DB 300 IGVTHPHPSFTTWTNNNAPSFAIEAAVVRNPHLLDFLEQVTTYSLLSRNSNTQYNNM 359

QY 360 WGGHKLFEFTTIGTGLNISTQGSTNTSINPVTLPFTSRDYRTESLAGNLFITQPVNGVP 419

DB 360 WGGHKLFEFTTIGTGLNISTQGSTNTSINPVTLPFTSRDYRTESLAGNLFITQPVNGVP 419

QY 420 RVDHFWKFTVTHPIASDNFYPGYAGIGTQLODSENELPEATGPNVSYSHRSLHIGLI 479  
 Db |||||  
 QY 420 RVDHFWKFTVTHPIASDNFYPGYAGIGTQLODSENELPEATGPNVSYSHRSLHIGLI 479  
 Db |||||  
 QY 480 SASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFLNLSGAAVVRGPGTGGDILRR 539  
 Db |||||  
 QY 480 SASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFLNLSGAAVVRGPGTGGDILRR 539  
 Db |||||  
 QY 540 NNGTGDIVNINPFAQYRIRVASTDLOHFTSINGKAINQGNFSAFMNREGDLDY 599  
 Db |||||  
 QY 540 NNGTGDIVNINPFAQYRIRVASTDLOHFTSINGKAINQGNFSAFMNREGDLDY 599  
 Db |||||  
 QY 600 KIFRTVGTTPSFDFLDVQSTFTIGAWNFSSGNEVYIDRIEFPVVEVYAEYDFEKAQEK 659  
 Db |||||  
 QY 600 KIFRTVGTTPSFDFLDVQSTFTIGAWNFSSGNEVYIDRIEFPVVEVYAEYDFEKAQEK 659  
 Db |||||  
 QY 660 VTALTSNPRGLKTDVQYHIDQVNSLVESLSDBFYLDKRGELFEIVKYANELHIERNM 719  
 Db |||||  
 QY 660 VTALTSNPRGLKTDVQYHIDQVNSLVESLSDBFYLDKRGELFEIVKYANELHIERNM 719  
 Db |||||

## RESULT 2

CLIA\_BACTK STANDARD: PRT: 719 AA.  
 AC Q45752; P71092; Q45750; Q45751; Q45756;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Pestidical crystal protein cryIIa (insecticidal delta-endotoxin  
 DE CryII(a)) (Crystalline entomocidal protoxin) (81 kDa crystal protein).  
 GN Name=cryIIa; Synonyms=cryII(a), cryV, cryVI, CCcryV;  
 OS Bacillus thuringiensis (subsp. kurstaki).  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=29339;  
 RN [1]  
 RC SEQUENCE FROM N.A.  
 RC STRAIN=DSIR732;  
 RX MEDLINE=93298009; PubMed=8517758;  
 RA Gleave A.P., Williams R., Hedges R.J.;  
 RT "Screening by polymerase chain reaction of Bacillus thuringiensis  
 RT serotypes for the presence of cryV-like insecticidal protein genes and  
 RT characterization of a cryV gene cloned from B. thuringiensis subsp.  
 RT kurstaki";  
 RL Appl. Environ. Microbiol. 59:1683-1687(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RP STRAIN=JHCC4835;  
 RX MEDLINE=92269582; PubMed=1588820;  
 RA Taylor R., Tippet J., Gibb G., Pells S., Pike D., Jordan L., Ely S.;  
 RT "Identification and characterization of a novel Bacillus thuringiensis  
 RT delta-endotoxin entomocidal to coleopteran and lepidopteran larvae";  
 RL Mol. Microbiol. 5:1211-1217(1992).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RP STRAIN=HD-1;  
 RX MEDLINE=95314293; PubMed=7793960;  
 RA Shin B.-S., Park S.-H., Choi S.-K., Koo B.T., Lee S.T., Kim J.I.;  
 RT "Distribution of cryV-type insecticidal protein genes in Bacillus  
 RT thuringiensis and cloning of cryV-type genes from Bacillus  
 RT thuringiensis subsp. kurstaki and Bacillus thuringiensis subsp.  
 RT entomocidus";  
 RL Appl. Environ. Microbiol. 61:2402-2407(1995).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RP STRAIN=AB88;  
 RX MEDLINE=96178985; PubMed=8606196;  
 RA Kostichka K., Warren G.W., Mullins M., Mullins A.D., Palekar N.V.,  
 RA Craig J.A., Koziel M.G., Estruch J.J.;  
 RT "Cloning of a cryV-type insecticidal protein gene from Bacillus  
 RT thuringiensis: the cryV-encoded protein is expressed early in  
 RT stationary phase";  
 RL J. Bacteriol. 178:2141-2144(1996).

RN SEQUENCE FROM N.A.  
 RP STRAIN=61;  
 RA Selvapandian A., Bhatnagar R.K.;  
 RT "Isolation, cloning and expression of cryV gene";  
 RL Submitted (Oct-1996) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Promotes colloidotomic lysis by binding to the midgut  
 CC epithelial cells of certain coleopteran and lepidopteran species.  
 CC Active on pluteella xylostella and Bombyx mori.  
 CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during  
 CC sporulation and is accumulated both as an inclusion and as part of  
 CC the spore coat.  
 CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-  
 CC terminus.  
 CC -!- SIMILARITY: Belongs to the delta endotoxin family.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
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 CC or send an email to license@isb-sib.ch).  
 CC  
 CC EMBL; M98544; AAA22354.1; -  
 CC EMBL; X2821; CAA44633.1; -  
 CC EMBL; L36338; AAC36999.1; -  
 CC EMBL; L49391; AAB00958.1; -  
 CC EMBL; Y08920; CAA70124.1; -  
 CC PIR; I39815; I39815.  
 CC PIR; S25383; S25383.  
 CC HSSP; P02965; ICIV.  
 CC InterPro; IPR001178; Endotoxin.  
 CC InterPro; IPR005638; endotoxin\_C.  
 CC InterPro; IPR005639; endotoxin\_N.  
 CC InterPro; IPR008979; Gal\_bind\_like.  
 CC Pfam; PF03944; Endotoxin\_C; 1.  
 CC Pfam; PF00555; Endotoxin\_M; 1.  
 CC Pfam; PF03945; Endotoxin\_N; 1.  
 CC Sporulation; Toxin. 159  
 CC VARIANT 159 159 K -> R (in strain 61).  
 CC VARIANT 233 233 D -> Y (in strain JHCC4835 and strain HD-  
 CC 1).  
 CC VARIANT 443 443 A -> V (in strain AB88).  
 CC VARIANT 711 712 KQ -> NE (in strain HD-1 and strain 61).  
 CC SEQUENCE 719 AA; 81216 MW; 3627ESA6C25DAFF5 CRC64;  
 CC  
 CC Query Match 99.0%; Score 3724; DB 1; Length 719;  
 CC Best Local Similarity 99.3%; Pred. No. 1.9e-252;  
 CC Matches 715; Conservative 2; Mismatches 1; Indels 2; Gaps 2;  
 CC  
 CC QY 1 MKLKNQDKHQSFSNAKVDKISTDLKNETDTELQNIHEDCLKMSYENVEPFSASTI 60  
 CC Db 1 MKLKNQDKHQSFSNAKVDKISTDLKNETDTELQNIHEDCLKMSYENVEPFSASTI 60  
 CC  
 CC QY 61 QTGIGIAGKILGTGVFPAGQVASYLSFILGELWPKGNQWEILFMEHVEE-INOKISTY 119  
 CC Db 61 QTGIGIAGKILGTGVFPAGQVASYLSFILGELWPKGNQWEILFMEHVEEINOKISTY 119  
 CC  
 CC QY 120 ANKALTDLKGIDALAVVHDSLESWGNRNTRARSVVRQYIALELMFVKLPSPAVS 179  
 CC Db 120 ANKALTDLKGIDALAVVHDSLESWGNRNTRARSVVRQYIALELMFVKLPSPAVS 179  
 CC  
 CC QY 180 GEEVPLLPYIAQAANLHLLLRDASIFGKWLSSSEISTFTYRQVERAGYSVHCWKY 239  
 CC Db 180 GEEVPLLPYIAQAANLHLLLRDASIFGKWLSSSEISTFTYRQVERAGYSVHCWKY 239  
 CC  
 CC QY 240 STGLNNLRGTNAESVVRNQFRDMLVLDLVALFPSYDTQMYPIKTAQTREVVYDA 299  
 CC Db 240 STGLNNLRGTNAESVVRNQFRDMLVLDLVALFPSYDTQMYPIKTAQTREVVYDA 299  
 CC  
 CC QY 300 ICTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMM 359  
 CC Db 300 ICTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMM 359

Db 300 IGVHPHPSFTSTWYNNAPSAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMMN 359  
 QY 360 WGHKLEPRTIGTGLNISTQSTNTSINPVTLPFTSRDVRVRESLAGLNLFLOPVNGVP 419  
 Db 360 WGHKLEPRTIGTGLNISTQSTNTSINPVTLPFTSRDVRVRESLAGLNLFLOPVNGVP 419  
 QY 420 RVDHFWKFTVTHPIASDNFYPGYAGIGTQLODSSENLPEATGPNYESYSHRLSHIGLI 479  
 Db 420 RVDHFWKFTVTHPIASDNFYPGYAGIGTQLODSSENLPEATGPNYESYSHRLSHIGLI 479  
 QY 480 SASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRT 539  
 Db 480 SASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRT 539  
 QY 540 NTGTFGDIRVNIWPPFAQRYRIRYASTTDLOQHTSINGKAINQGNFSATMNRGEGDLY 599  
 Db 540 NTGTFGDIRVNIWPPFAQRYRIRYASTTDLOQHTSINGKAINQGNFSATMNRGEGDLY 599  
 QY 600 KTFRTVGFTTFFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEK 659  
 Db 600 KTFRTVGFTTFFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEK 659  
 QY 660 VTALFTSTNPRGLKTDVKDHYDQVSNLVSLSDEFYLDKRELFEIVKAKQLHIERNM 719  
 Db 660 VTALFTSTNPRGLKTDVKDHYDQVSNLVSLSDEFYLDKRELFEIVKAKQLHIERNM 719

## RESULT 3

Q6X181 PRELIMINARY; PRT; 719 AA.  
 ID Q6X181  
 AC Q6X181  
 DT 05-JUL-2004 (TremBLrel. 27, Created)  
 DT 05-JUL-2004 (TremBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TremBLrel. 27, Last annotation update)  
 DE Crv11  
 GN Bacillus thuringiensis.  
 OS Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OC NCBI\_TaxID=1428;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Espindola R., Lemos M.V.F., Lemos E.G.M., Sena J.A.D.;  
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY262167; AAP86782.1; -  
 DR InterPro; IPR001178; Endotoxin.  
 DR InterPro; IPR005638; endotoxin C.  
 DR InterPro; IPR005639; endotoxin N.  
 DR InterPro; IPR008979; Gal bind like.  
 DR Pfam; PF03944; Endotoxin\_C\_1.  
 DR Pfam; PF00555; Endotoxin\_M\_1.  
 DR Pfam; PF03945; Endotoxin\_N\_1.  
 DR PF03945; Endotoxin\_N\_1.  
 SQ SEQUENCE 719 AA; 81216 MW; 3627B5A6C25DAFF5 CRC64;

Query Match 99.0%; Score 3724; DB 2; Length 719;  
 Best Local Similarity 99.3%; Pred. No. 1.9e-252;  
 Matches 715; Conservative 2; Mismatches 1; Indels 2; Gaps 2;

QY 1 MCLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKXSEYENVEPVSASTI 60  
 Db 1 MCLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKXSEYENVEPVSASTI 60  
 QY 61 QTGIGIAGKILGTGVPPAGQVASLYSFLGELMPKGNQWEILFMEHVEE-INQKISTY 119  
 Db 61 QTGIGIAGKILGTGVPPAGQVASLYSFLGELMPKGNQWEILFMEHVEE-INQKISTY 119  
 QY 120 ARNKALTDKGLGDALAVYHDSLESWGNRNTRARSVRSQYIALELMFVKQLPSFAVS 179  
 Db 120 ARNKALTDKGLGDALAVYHDSLESWGNRNTRARSVRSQYIALELMFVKQLPSFAVS 179  
 QY 180 GEEVPLLPYQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHVKWY 239  
 Db 180 GEEVPLLPYQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHVKWY 239

QY 240 STGLNNLRGTNAESVRYNQPRDMTLMVLDLVALPPSYDTQWPIKTTAQLTREVYTDA 299  
 Db 240 STGLNNLRGTNAESVRYNQPRDMTLMVLDLVALPPSYDTQWPIKTTAQLTREVYTDA 299  
 QY 300 IGVHPHPSFTSTWYNNAPSAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMMN 359  
 Db 300 IGVHPHPSFTSTWYNNAPSAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMMN 359  
 QY 360 WGHKLEPRTIGTGLNISTQSTNTSINPVTLPFTSRDVRVRESLAGLNLFLOPVNGVP 419  
 Db 360 WGHKLEPRTIGTGLNISTQSTNTSINPVTLPFTSRDVRVRESLAGLNLFLOPVNGVP 419  
 QY 420 RVDHFWKFTVTHPIASDNFYPGYAGIGTQLODSSENLPEATGPNYESYSHRLSHIGLI 479  
 Db 420 RVDHFWKFTVTHPIASDNFYPGYAGIGTQLODSSENLPEATGPNYESYSHRLSHIGLI 479  
 QY 480 SASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRT 539  
 Db 480 SASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRT 539  
 QY 540 NTGTFGDIRVNIWPPFAQRYRIRYASTTDLOQHTSINGKAINQGNFSATMNRGEGDLY 599  
 Db 540 NTGTFGDIRVNIWPPFAQRYRIRYASTTDLOQHTSINGKAINQGNFSATMNRGEGDLY 599  
 QY 600 KTFRTVGFTTFFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEK 659  
 Db 600 KTFRTVGFTTFFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEK 659  
 QY 660 VTALFTSTNPRGLKTDVKDHYDQVSNLVSLSDEFYLDKRELFEIVKAKQLHIERNM 719  
 Db 660 VTALFTSTNPRGLKTDVKDHYDQVSNLVSLSDEFYLDKRELFEIVKAKQLHIERNM 719

## RESULT 4

AAP86782 PRELIMINARY; PRT; 719 AA.  
 ID AAP86782  
 AC AAP86782  
 DT 02-MAR-2004 (TremBLrel. 27, Created)  
 DT 02-MAR-2004 (TremBLrel. 27, Last sequence update)  
 DT 02-MAR-2004 (TremBLrel. 27, Last annotation update)  
 DE Crv11  
 GN Crv11  
 OS Bacillus thuringiensis.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;  
 OC Bacillus cereus group.  
 OC NCBI\_TaxID=1428;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=T01 328;  
 RA Espindola R., Lemos M.V.F., Lemos E.G.M., Sena J.A.D.;  
 RT "Complete sequence of crv11 gene of isolate T01 328 from Bacillus  
 RL thuringiensis from Cubatao (SP - Brazil) soil."  
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY262167; AAP86782.1; -  
 SQ SEQUENCE 719 AA; 81216 MW; 3627E5A6C25DAFF5 CRC64;

Query Match 99.0%; Score 3724; DB 2; Length 719;  
 Best Local Similarity 99.3%; Pred. No. 1.9e-252;  
 Matches 715; Conservative 2; Mismatches 1; Indels 2; Gaps 2;

QY 1 MCLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKXSEYENVEPVSASTI 60  
 Db 1 MCLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKXSEYENVEPVSASTI 60  
 QY 61 QTGIGIAGKILGTGVPPAGQVASLYSFLGELMPKGNQWEILFMEHVEE-INQKISTY 119  
 Db 61 QTGIGIAGKILGTGVPPAGQVASLYSFLGELMPKGNQWEILFMEHVEE-INQKISTY 119  
 QY 120 ARNKALTDKGLGDALAVYHDSLESWGNRNTRARSVRSQYIALELMFVKQLPSFAVS 179  
 Db 120 ARNKALTDKGLGDALAVYHDSLESWGNRNTRARSVRSQYIALELMFVKQLPSFAVS 179  
 QY 180 GEEVPLLPYQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHVKWY 239

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180 GEEVPLLPPIAQAANLHLLLDASIFGKEWGLSSSEISTFYNRQVERAGYSDHCWKY 239
QY
240 STGLANLRGTNAESWRYNQFRDMTLMVLDLVALPSPYDQMPYIKTTAQITREVTYDA 299
Db
240 STGLANLRGTNAESWRYNQFRDMTLMVLDLVALPSPYDQMPYIKTTAQITREVTYDA 299
QY
300 IGTVHPHPSFTTWTYNNNAPSFAIEAAVVRNPHLLDLEQVTTIYSLLSWSNTQYNNM 359
Db
300 IGTVHPHPSFTTWTYNNNAPSFAIEAAVVRNPHLLDLEQVTTIYSLLSWSNTQYNNM 359
QY
360 WGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESTAGLNLFLOPVNGVP 419
Db
360 WGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESTAGLNLFLOPVNGVP 419
QY
420 RYDFHKKFVTHPIASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRSLHIGLI 479
Db
420 RYDFHKKFVTHPIASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRSLHIGLI 479
QY
480 SASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT 539
Db
480 SASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT 539
QY
540 NTGTGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATWNRGEDLDY 599
Db
540 NTGTGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATWNRGEDLDY 599
QY
600 KTRFTVGTTPPSFLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVTEAYEDFEKAQEK 659
Db
600 KTRFTVGTTPPSFLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVTEAYEDFEKAQEK 659
QY
660 VTALFTSTNPRGLKTDVKDHYDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719
Db
660 VTALFTSTNPRGLKTDVKDHYDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 5
Q93NJ5 PRELIMINARY; PRT; 719 AA.
ID Q93NJ5
AC Q93NJ5
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE CryIIa.
GN Name=cryIIa;
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RA Song F., Zhang J., Gu A., Huang D., Li G.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AF373207; AK66742.1; -
DR HSSP; P02965; 1CIY.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal_bind_like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF03955; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
SQ SEQUENCE 719 AA; 81225 MW; C629DF2C44827241 CRC64;

Query Match 98.9%; Score 3719; DB 2; Length 719;
Best Local Similarity 99.2%; Pred. No. 4, 3e-252;
Matches 714; Conservative 2; Mismatches 2; Indels 2; Gaps 2;
QY 1 MKLKNQDKHQSFSSNAKVDKISTSLKNETDIELQINIHEDCLKMSYENVEPVSASTI 60
Db 1 MKLKNQDKHQSFSSNAKVDKISTSLKNETDIELQINIHEDCLKMSYENVEPVSASTI 60

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61 QTGIGTAGKILGTLPVFPAGQVASYLSFTLGBELWPKGNQWILFMEHVEE-INOKISTY 119
Db
61 QTGIGTAGKILGTLPVFPAGQVASYLSFTLGBELWPKGNQWILFMEHVEE-INOKISTY 119
QY
120 ARNKALTDLKGLGDALAVYHDSLESWVGNRNTRARSVVRQVIALELMFVOKLSPFAVS 179
Db
120 ARNKALTDLKGLGDALAVYHDSLESWVGNRNTRARSVVRQVIALELMFVOKLSPFAVS 179
QY
180 GEEVPLLPPIAQAANLHLLLDASIFGKEWGLSSSEISTFYNRQVERAGYSDHCWKY 239
Db
180 GEEVPLLPPIAQAANLHLLLDASIFGKEWGLSSSEISTFYNRQVERAGYSDHCWKY 239
QY
240 STGLANLRGTNAESWRYNQFRDMTLMVLDLVALPSPYDQMPYIKTTAQITREVTYDA 299
Db
240 STGLANLRGTNAESWRYNQFRDMTLMVLDLVALPSPYDQMPYIKTTAQITREVTYDA 299
QY
300 IGTVHPHPSFTTWTYNNNAPSFAIEAAVVRNPHLLDLEQVTTIYSLLSWSNTQYNNM 359
Db
300 IGTVHPHPSFTTWTYNNNAPSFAIEAAVVRNPHLLDLEQVTTIYSLLSWSNTQYNNM 359
QY
360 WGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESTAGLNLFLOPVNGVP 419
Db
360 WGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESTAGLNLFLOPVNGVP 419
QY
420 RYDFHKKFVTHPIASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRSLHIGLI 479
Db
420 RYDFHKKFVTHPIASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRSLHIGLI 479
QY
480 SASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT 539
Db
480 SASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT 539
QY
540 NTGTGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATWNRGEDLDY 599
Db
540 NTGTGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATWNRGEDLDY 599
QY
600 KTRFTVGTTPPSFLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVTEAYEDFEKAQEK 659
Db
600 KTRFTVGTTPPSFLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVTEAYEDFEKAQEK 659
QY
660 VTALFTSTNPRGLKTDVKDHYDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719
Db
660 VTALFTSTNPRGLKTDVKDHYDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 6
O85796 PRELIMINARY; PRT; 719 AA.
ID O85796
AC O85796;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Insecticidal protein.
GN Name=cryVI01;
OS Bacillus thuringiensis (subsp. kurstaki).
OG Plasmid large plasmid.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=29339;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=8101.
RA Zhong Q., Deng R., Long Q., Yuan M., Pang Y., Wang X.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AF076953; AAC26910.1; -
DR HSSP; P02965; 1CIY.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal_bind_like.

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DR Pfam; PF03944; Endotoxin\_C; 1.  
DR Pfam; PF00555; Endotoxin\_M; 1.  
DR Pfam; PF03945; Endotoxin\_N; 1.  
KW PfamId.  
SQ SEQUENCE 719 AA; 81230 MW; 42746D478359BBA7 CRC64;  
  
Query Match 98.9%; Score 3718; DB 2; Length 719;  
Best Local Similarity 99.2%; Pred. No. 5.1e-252;  
Matches 714; Conservative 2; Mismatches 2; Indels 2; Gaps 2;  
  
QY 1 MKLKNQKHQSFSSNAKVDKISTSLKNETDIELQININHEDCMKSEYENVEPVSASTI 60  
Db 1 MKLKNQKHQSFSSNAKVDKISTSLKNETDIELQININHEDCMKSEYENVEPVSASTI 60  
  
QY 61 QTGIGIAGKILGTGVPFAGQVASYLFIKELWPKGNQWEILFMEHVEE-INQIKISTY 119  
Db 61 QTGIGIAGKILGTGVPFAGQVASYLFIKELWPKGNQWEI-FMEHVEEIIINQIKISTY 119  
  
QY 120 ARNKALTDLKGDLALAVYHDSLESWGNRNTRARSVRSQYIALELMFVQKLPFAVS 179  
Db 120 ARNKALTDLKGDLALAVYHDSLESWGNRNTRARSVRSQYIALELMFVQKLPFAVS 179  
  
QY 180 GEEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWY 239  
Db 180 GEEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWY 239  
  
QY 240 STGLNNLRGTNAESWRYNQFRDMTLMVLDLVALFPSYDTQMPYIKTTAQLTREYVYDA 299  
Db 240 STGLNNLRGTNAESWRYNQFRDMTLMVLDLVALFPSYDTQMPYIKTTAQLTREYVYDA 299  
  
QY 300 IGTVHPHPSFTTWWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYMMN 359  
Db 300 IGTVHPHPSFTTWWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYMMN 359  
  
QY 360 WGHKLEFRITGTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNFLTQPVNGVP 419  
Db 360 WGHKLEFRITGTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNFLTQPVNGVP 419  
  
QY 420 RVDPHWKVTHPIASDNFYPGYAGIGTQLODSNELPPEATGQPNYESYSHRLSHIGLI 479  
Db 420 RVDPHWKVTHPIASDNFYPGYAGIGTQLODSNELPPEATGQPNYESYSHRLSHIGLI 479  
  
QY 480 SASHVKALVSWTHRSADRTNIBPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT 539  
Db 480 SASHVKALVSWTHRSADRTNIBPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT 539  
  
QY 540 NTGTFGDIRVNIINPPFAQRVRYRYASTTDLPQHTSINGKAINQGNFSATMNRGEDLDY 599  
Db 540 NTGTFGDIRVNIINPPFAQRVRYRYASTTDLPQHTSINGKAINQGNFSATMNRGEDLDY 599  
  
QY 600 KTFRTVGTFTPFSLDVQSTFTIGAWNFSSNGNEVYIDRIEFVPEVYEAEDFEKAQEK 659  
Db 600 KTFRTVGTFTPFSLDVQSTFTIGAWNFSSNGNEVYIDRIEFVPEVYEAEDFEKAQEK 659  
  
QY 660 VTALFTSTNPRGLTKTDVKYHIDQVSNLVESLSEDFYLDKRELFEIVKYAKQLHIERNM 719  
Db 660 VTALFTSTNPRGLTKTDVKYHIDQVSNLVESLSEDFYLDKRELFEIVKYAKQLHIERNM 719

## RESULT 7

Q8KY61  
ID Q8KY61 PRELIMINARY; PRT; 719 AA.  
AC Q8KY61;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Cry.  
OS Bacillus thuringiensis.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=1428;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Porcar M., Martinez C., Caballero P.;

RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF278797; AAM73516.1; -.  
DR EIR; B42459; B42459.  
DR HSSP; P02985; IC1Y.  
DR GO; GO:0005102; F:receptor binding; IEA.  
DR GO; GO:0006952; P:defense response; IEA.  
DR GO; GO:0009405; P:pathogenesis; IEA.  
DR InterPro; IPR001178; Endotoxin.  
DR InterPro; IPR005638; endotoxin\_C.  
DR InterPro; IPR008979; Gal\_bind\_like.  
DR Pfam; PF03944; Endotoxin\_C; 1.  
DR Pfam; PF00555; Endotoxin\_M; 1.  
DR Pfam; PF03945; Endotoxin\_N; 1.  
SQ SEQUENCE 719 AA; 80984 MW; 84F1287246264473 CRC64;

Query Match 95.4%; Score 3589; DB 2; Length 719;  
Best Local Similarity 95.6%; Pred. No. 5.8e-243;  
Matches 688; Conservative 14; Mismatches 16; Indels 2; Gaps 2;

QY 1 MKLKNQKHQSFSSNAKVDKISTSLKNETDIELQININHEDCMKSEYENVEPVSASTI 60  
Db 1 MKLKNQKHQSFSSNAKVDKISTSLKNETDIELQININHEDCMKSEYENVEPVSASTI 60  
  
QY 61 QTGIGIAGKILGTGVPFAGQVASYLFIKELWPKGNQWEILFMEHVEE-INQIKISTY 119  
Db 61 QTGIGIAGKILGTGVPFAGQVASYLFIKELWPKGNQWEI-FMEHVEEIIINQIKISTY 119  
  
QY 120 ARNKALTDLKGDLALAVYHDSLESWGNRNTRARSVRSQYIALELMFVQKLPFAVS 179  
Db 120 ARNKALTDLKGDLALAVYHDSLESWGNRNTRARSVRSQYIALELMFVQKLPFAVS 179  
  
QY 180 GEEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWY 239  
Db 180 GEEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWY 239  
  
QY 240 STGLNNLRGTNAESWRYNQFRDMTLMVLDLVALFPSYDTQMPYIKTTAQLTREYVYDA 299  
Db 240 STGLNNLRGTNAESWRYNQFRDMTLMVLDLVALFPSYDTQMPYIKTTAQLTREYVYDA 299  
  
QY 300 IGTVHPHPSFTTWWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYMMN 359  
Db 300 IGTVHPHPSFTTWWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYMMN 359  
  
QY 360 WGHKLEFRITGTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNFLTQPVNGVP 419  
Db 360 WGHKLEFRITGTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNFLTQPVNGVP 419  
  
QY 420 RVDPHWKVTHPIASDNFYPGYAGIGTQLODSNELPPEATGQPNYESYSHRLSHIGLI 479  
Db 420 RVDPHWKVTHPIASDNFYPGYAGIGTQLODSNELPPEATGQPNYESYSHRLSHIGLI 479  
  
QY 480 SASHVKALVSWTHRSADRTNIBPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT 539  
Db 480 SASHVKALVSWTHRSADRTNIBPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT 539  
  
QY 540 NTGTFGDIRVNIINPPFAQRVRYRYASTTDLPQHTSINGKAINQGNFSATMNRGEDLDY 599  
Db 540 NTGTFGDIRVNIINPPFAQRVRYRYASTTDLPQHTSINGKAINQGNFSATMNRGEDLDY 599  
  
QY 600 KTFRTVGTFTPFSLDVQSTFTIGAWNFSSNGNEVYIDRIEFVPEVYEAEDFEKAQEK 659  
Db 600 KTFRTVGTFTPFSLDVQSTFTIGAWNFSSNGNEVYIDRIEFVPEVYEAEDFEKAQEK 659  
  
QY 660 VTALFTSTNPRGLTKTDVKYHIDQVSNLVESLSEDFYLDKRELFEIVKYAKQLHIERNM 719  
Db 660 VTALFTSTNPRGLTKTDVKYHIDQVSNLVESLSEDFYLDKRELFEIVKYAKQLHIERNM 719

## RESULT 8

Q9F0P8  
ID Q9F0P8 PRELIMINARY; PRT; 719 AA.  
AC Q9F0P8;

DT 01-VAR-2001 (TREMELrel. 16, Created)  
 DT 01-VAR-2001 (TREMELrel. 16, Last sequence update)  
 DT 01-VAR-2004 (TREMELrel. 26, Last annotation update)  
 DE CrvII.  
 GN Name=crvII;  
 OS Bacillus thuringiensis.  
 OG Plasmid pBVC19.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1428;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BTCC007;  
 RA Song F., Zhang J., Gu A., Wu Y., Han L., He K., Chen Z., Yao J.,  
 RA Hu Y., Li G., Huang D.;  
 RT "Identification of crvII-type genes from Bacillus thuringiensis  
 RT strains and characterization of a novel crvII-type gene."  
 RL Appl. Environ. Microbiol. 69:5207-5211(2003).  
 DR EMBL; AF211190; AAG43526.1; --  
 DR HSP; P02965; 1CIV.  
 DR GO; GO:0005102; P:receptor binding; IEA.  
 DR GO; GO:0006952; P:defense response; IEA.  
 DR GO; GO:0009405; P:pachogenesis; IEA.  
 DR InterPro; IPR001178; Endotoxin.  
 DR InterPro; IPR005638; endotoxin C.  
 DR InterPro; IPR008979; Gal bind like.  
 DR Pfam; PF03944; Endotoxin\_C; 1.  
 DR Pfam; PF00555; Endotoxin\_M; 1.  
 DR Pfam; PF03945; Endotoxin\_N; 1.  
 KW Plasmid.  
 SQ SEQUENCE 719 AA; 81024 MW; 7E17481922C435E6 CRC64;

Query Match 93.5%; Score 3517; DB 2; Length 719;  
 Best Local Similarity 93.1%; Pred. No. 6.5e-238;  
 Matches 670; Conservative 27; Mismatches 21; Indels 2; Gaps 2;

QY 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKNSEYENVPFVSASTI 60  
 DB 1 MKLKNPDKHQSLSSNAKVDKIATDSLKNETDIELKNINHEDFLMSSEHSDIPVSASTI 60

QY 61 QTGIGIAGKIITGLVPPAGOVASLYSPILGELPKGNQWEILFMEHVEE-INQKISTY 119  
 DB 61 QTGIGIAGKIITGLVPPAGQIASLYSPILGELPKGKQWEI-FMEHVEELIDQKISTY 119

QY 120 ARNKALTDLKGIDGALAYVHDSLESWGNRNTRARSQYIALBELMFVKLPSPAVS 179  
 DB 120 ARNIALADLKGIDGALAYVHDSLESWIKRNARATSVKRQYIALBELLFVKLPSPAVS 179

QY 180 GEEVPLLPYQAANLHLLILDASIFGKEWGLSSBSISFYNRQVERAGDSDHCYKMY 239  
 DB 180 GEEVPLLPYQAANLHLLILDASVFGKEWGLSNQISITFYNRQVERTSDYSDHCYKMY 239

QY 240 STGLANLRGTNAESVVRNQFRDMTLMVLDLVALFPSSYDTQMPYIKTTAQLTRVYTD 299  
 DB 240 STGLANLRGTNAESVVRNQFRKDWTLMLVLDLIALFPSSYDTLVYPIKTTAQLTRVYTD 299

QY 300 IGVHPHPSFTSTWYNNAPSPAIEAUVVRNPHLLDFLEQVYIYLLSRWSNTQMMN 359  
 DB 300 IGVHPNAPSPASTTWYNNAPSPAIESAVVRNPHLLDFLEQVYIYLLSRWSNTQMMN 359

QY 360 WGHKLEPRTIGGLINISTQGSTNTSNPVLPTSDVVRTESLAGNLFLTPQVNGVP 419  
 DB 360 WGHRLPRTIGGLVNLSTQGSTNTSNPVLPTSDVVRTESLAGNLFLTPQVNGVP 419

QY 420 RVDPHKVPHTPIASDNPYPGAGIGTQLODSNELPPBATGPNTYESHRLSHIGLI 479  
 DB 420 RVDPHKVPHTPIASDNPYLYGAGVGTQLODSNELPPETGQPNYESHRLSHIGLI 479

QY 480 SASHVKALVYSWTHRSADRTNTPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT 539  
 DB 480 SASHVKALVYSWTHRSADRTNTPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT 539

QY 540 NTCTFGDIRVNIAPPQAQRYRVRIRYASTTDLOPHTSINGKAINQGNFSATNRCGEDLDY 599  
 DB 540 NTCTFGDIRVNIAPPQAQRYRVRIRYASTTDLOPHTSINGKAINQGNFSATNRCGEDLDY 599

QY 600 KTFRTVGFTTPFSFLDVQSTFTIGAWNFSSGNEVIDRIEFVFPVETVEAEYDFEKAQEK 659  
 DB 600 KTFRTVGFTTPFSFSDVQSTFTIGAWNFSSGNEVIDRIEFVFPVETVEAEYDFEKAQEK 659

QY 660 VTALFTSTNPRGLKTDVQYHIDQVSNLVESLSDPYLDEKRELFEIVKYNELHIERNM 719  
 DB 660 VTALFTSTNPRGLKTDVQYHIDQVSNLVESLSDPYLDEKRELFEIVKYNELHIERNM 719

## RESULT 9

CLIB\_BACTE STANDARD; PRT; 719 AA.  
 AC Q45709;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Pesticidal crystal protein crvIIb (Insecticidal delta-endotoxin  
 DE CrvII(b)) (Crystalline entomocidal protoxin) (81 kDa crystal protein).  
 GN Name=crvIIb; Synonyms=crvII(b), cryV, cryV465;  
 OS Bacillus thuringiensis (subsp. entomocidus).  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1436;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BP485;  
 RX MEDLINE=95314293; PubMed=7793960;  
 RA Shin B.-S., Park S.-H., Choi S.-K., Koo B.T., Lee S.T., Kim J.I.;  
 RT "Distribution of cryV-type insecticidal protein genes in Bacillus  
 RT thuringiensis and cloning of cryV-type genes from Bacillus  
 RT thuringiensis subsp. kurstaki and Bacillus thuringiensis subsp.  
 RT entomocidus";  
 RL Appl. Environ. Microbiol. 61:2402-2407(1995).  
 CC -!- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut  
 CC epithelial cells of certain coleopteran and lepidopteran species.  
 CC Active on Plutella xylostella but not on Bombyx mori.  
 CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during  
 CC sporulation and is accumulated both as an inclusion and as part of  
 CC the spore coat.  
 CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-  
 CC terminus.  
 CC -!- SIMILARITY: Belongs to the delta endotoxin family.

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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; U07642; AAA82114.1; --  
 CC IPR; I40590; I40590.  
 CC HSP; P02965; 1CIV.  
 CC InterPro; IPR001178; Endotoxin.  
 CC InterPro; IPR005638; endotoxin C.  
 CC InterPro; IPR005639; endotoxin N.  
 CC InterPro; IPR008979; Gal bind like.  
 CC Pfam; PF03944; Endotoxin\_C; 1.  
 CC Pfam; PF00555; Endotoxin\_M; 1.  
 CC Pfam; PF03945; Endotoxin\_N; 1.  
 CC Sporulation; Toxin;  
 KW SEQUENCE 719 AA; 81295 MW; E8210ABAE97688E CRC64;

Query Match 92.6%; Score 3484; DB 1; Length 719;  
 Best Local Similarity 92.2%; Pred. No. 1.3e-235;  
 Matches 664; Conservative 33; Mismatches 21; Indels 2; Gaps 2;

QY 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKNSEYENVPFVSASTI 60  
 DB 1 MKLKNPDKHQSLSSNAKVDKIATDSLKNETDIELKNINHEDFLMSSEHSDIPVSASTI 60



Db 1 MLLKNDPKHQSLSNKAVDKIATDSLKNEDTIELKXNVEDYLRMSSEHSIDPVSASTI 60  
 Qy 61 QTGIGIAGKILGTGVFPAGQVASYLFIQELWPKQKQWELFMHVEE-INOKISTY 119  
 Db 61 QTGIGIAGKILGTGVFPAGQVASYLFIQELWPKQKQWELFMHVEE-INOKISTY 119  
 Qy 120 ARNKALTDKLGGLDALAVYHDSLESWGNRNNTARSVRSOYIALELMFVKLPSPAVS 179  
 Db 120 ARNKALDRLGGLDALAVYHDSLESWGNRNNTARSVRSOYIALELMFVKLPSPAVS 179  
 Qy 180 GEEVPLLPPIYAQAANLHLLLRDASIFGKMWGLSSSEISTFYNNQVRAGDYSDHCWKY 239  
 Db 180 GEEVPLLPPIYAQAANLHLLLRDASIFGKMWGLSSSEISTFYNNQVRAGDYSDHCWKY 239  
 Qy 240 STGLNLRGNTNAESWRYNQPRDMLVLDLVALFYSYDTOMYPIKTTAQLTREVYTD 299  
 Db 240 NTGLNLRGNTNAESWRYNQPRDMLVLDLVALFYSYDTOMYPIKTTAQLTREVYTD 299  
 Qy 300 IGTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVITYLLSRWSNTQYMMN 359  
 Db 300 IGTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVITYLLSRWSNTQYMMN 359  
 Qy 360 WGGHKLFRITIGTINISQGSTNTSINPVTLPFTSRDVRATESLAGLNLFLTPQVNGVP 419  
 Db 360 WGGHKLFRITIGTINISQGSTNTSINPVTLPFTSRDVRATESLAGLNLFLTPQVNGVP 419  
 Qy 420 RVDHFWKFTVTHPIASDNFYYPGAGVGTQLODSNELPPATGPNVSEYSHRLSHIGLI 479  
 Db 420 RVDHFWKFTVTHPIASDNFYYPGAGVGTQLODSNELPPATGPNVSEYSHRLSHIGLI 479  
 Qy 480 SASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT 539  
 Db 480 SASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT 539  
 Qy 540 NTGTFGDIRVNINPPFAQRVRIYASTDLOQHTSINGKAINQGNFSATMNRGEDLDY 599  
 Db 540 NTGTFGDIRVNINPPFAQRVRIYASTDLOQHTSINGKAINQGNFSATMNRGEDLDY 599  
 Qy 600 KTFRTVGTFTTSPESFLDVOSTFTIGAWNFSNGNEVDRIEFVPEVTVTEAEYDFEKAQEK 659  
 Db 600 KTFRTVGTFTTSPESFLDVOSTFTIGAWNFSNGNEVDRIEFVPEVTVTEAEYDFEKAQEK 659  
 Qy 660 VTALFTSTNPRGLKTDVKRHDQVSNLVSLSDEFYLDKRELFEIVKYAKQIHERNN 719  
 Db 660 VTALFTSTNPRGLKTDVKRHDQVSNLVSLSDEFYLDKRELFEIVKYAKQIHERNN 719

RESULT 10

CLID BACTU STANDARD; PRT; 719 AA.  
 AC Q9XDL1;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Pesticidal crystal protein cryII (insecticidal delta-endotoxin  
 DE CryII(d)) (Crystalline entomocidal protoxin) (81 kDa crystal protein).  
 GN Name=cryII; Synonyms=cryII(d), Nrcryv;  
 OS Bacillus thuringiensis.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1428;  
 RN [1]  
 RC SEQUENCE FROM N.A.  
 RC STRAIN=BR30;  
 RX MEDLINE=20374042; PubMed=10919402;  
 RA Choi S.-K., Shin B.-S., Kong E.-M., Rho H.M., Park S.-H.;  
 RT "Cloning of a new Bacillus thuringiensis cryII-type crystal protein  
 RT gene."  
 RL Curr. Microbiol. 41:65-69(2000).  
 CC -!- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut  
 CC epithelial cells of many lepidopteran larvae. Active on Plutella  
 CC xylostella and on Bombyx mori.  
 CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during  
 CC sporulation and is accumulated both as an inclusion and as part of

CC the spore coat.  
 CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-terminus.  
 CC -!- SIMILARITY: Belongs to the delta endotoxin family.  
 CC -----  
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 CC -----  
 CC EMBL: AF047579; AAD44366.1; -;  
 DR HSSP: P02965; 1CIV;  
 DR InterPro: IPR001178; Endotoxin.  
 DR InterPro: IPR005638; Endotoxin\_C.  
 DR InterPro: IPR005639; Endotoxin\_N.  
 DR InterPro: IPR008979; Gal bind like.  
 DR Pfam: PF03944; Endotoxin\_C; 1.  
 DR Pfam: PF00555; Endotoxin\_M; 1.  
 DR Pfam: PF03945; Endotoxin\_N; 1.  
 KW Sporulation; Toxin.  
 SQ SEQUENCE 719 AA; 81403 MW; F335F5689D3B0C45 CRC64;

Query Match 89.4%; Score 3363; DB 1; Length 719;  
 Best Local Similarity 89.3%; Pred. No. 4.2e-227;  
 Matches 643; Conservative 36; Mismatches 39; Indels 2; Gaps 2;

Qy 1 MLLKNDPKHQSLSNKAVDKIATDSLKNEDTIELKXNVEDYLRMSSEHSIDPVSASTI 60  
 Db 1 MLLKNDPKHQSLSNKAVDKIATDSLKNEDTIELKXNVEDYLRMSSEHSIDPVSASTI 60  
 Qy 61 QTGIGIAGKILGTGVFPAGQVASYLFIQELWPKQKQWELFMHVEE-INOKISTY 119  
 Db 61 QTGIGIAGKILGTGVFPAGQVASYLFIQELWPKQKQWELFMHVEE-INOKISTY 119  
 Qy 120 ARNKALTDKLGGLDALAVYHDSLESWGNRNNTARSVRSOYIALELMFVKLPSPAVS 179  
 Db 120 ARNKALTDKLGGLDALAVYHDSLESWGNRNNTARSVRSOYIALELMFVKLPSPAVS 179  
 Qy 180 GEEVPLLPPIYAQAANLHLLLRDASIFGKMWGLSSSEISTFYNNQVRAGDYSDHCWKY 239  
 Db 180 GEEVPLLPPIYAQAANLHLLLRDASIFGKMWGLSSSEISTFYNNQVRAGDYSDHCWKY 239  
 Qy 240 STGLNLRGNTNAESWRYNQPRDMLVLDLVALFYSYDTOMYPIKTTAQLTREVYTD 299  
 Db 240 STGLNLRGNTNAESWRYNQPRDMLVLDLVALFYSYDTOMYPIKTTAQLTREVYTD 299  
 Qy 300 IGTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVITYLLSRWSNTQYMMN 359  
 Db 300 IGTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVITYLLSRWSNTQYMMN 359  
 Qy 360 WGGHKLFRITIGTINISQGSTNTSINPVTLPFTSRDVRATESLAGLNLFLTPQVNGVP 419  
 Db 360 WGGHKLFRITIGTINISQGSTNTSINPVTLPFTSRDVRATESLAGLNLFLTPQVNGVP 419  
 Qy 420 RVDHFWKFTVTHPIASDNFYYPGAGVGTQLODSNELPPATGPNVSEYSHRLSHIGLI 479  
 Db 420 RVDHFWKFTVTHPIASDNFYYPGAGVGTQLODSNELPPATGPNVSEYSHRLSHIGLI 479  
 Qy 480 SASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT 539  
 Db 480 SASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT 539  
 Qy 540 NTGTFGDIRVNINPPFAQRVRIYASTDLOQHTSINGKAINQGNFSATMNRGEDLDY 599  
 Db 540 NTGTFGDIRVNINPPFAQRVRIYASTDLOQHTSINGKAINQGNFSATMNRGEDLDY 599  
 Qy 600 KTFRTVGTFTTSPESFLDVOSTFTIGAWNFSNGNEVDRIEFVPEVTVTEAEYDFEKAQEK 659  
 Db 600 KTFRTVGTFTTSPESFLDVOSTFTIGAWNFSNGNEVDRIEFVPEVTVTEAEYDFEKAQEK 659

QY 660 VTALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDFYLDKRELFEIVKYANELHIERNM 719  
 Db 660 ITAMFTSTNLRKLTNTVDCHIDQVSNLVESLSDFYLDKRELFEIVKYAKQNIERNM 719  
 RESULT 11  
 C1BB BACTU STANDARD; PRT: 719 AA.  
 AC 087404;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Pesticidal crystal protein cryIc (insecticidal delta-endotoxin  
 DE CryII(c) (crystalline entomocidal protoxin) (81 kDa crystal protein).  
 GN Name=cryIc; Synonyms=cryII(c);  
 OS Bacillus thuringiensis.  
 OG Plasmid.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1428;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C18 / Egypt.  
 RA Osman Y.A., Madkour M.A., Bulla L.A. Jr.;  
 Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.  
 RL  
 CC -!- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut  
 CC epithelial cells of insects.  
 CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during  
 CC sporulation and is accumulated both as an inclusion and as part of  
 CC the spore coat.  
 CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-  
 CC terminus.  
 CC -!- SIMILARITY: Belongs to the delta endotoxin family.  
 CC  
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 CC  
 CC EMBL; AF056933; AAC62933.1; -  
 DR HSP; P02965; 1C1Y.  
 DR InterPro; IPR001178; Endotoxin.  
 DR InterPro; IPR005638; endotoxin C.  
 DR InterPro; IPR005639; endotoxin N.  
 DR InterPro; IPR008979; Gal bind like.  
 DR Pfam; PF03944; Endotoxin C; 1.  
 DR Pfam; PF00555; Endotoxin M; 1.  
 DR Pfam; PF03945; Endotoxin N; 1.  
 KW Plasmid; Sporulation; Toxin.  
 SQ SEQUENCE 719 AA; 81210 MW; 8370BP06B905DFF CRC64;  
 Query Match 88.8%; Score 3341; DB 1; Length 719;  
 Best Local similarity 89.2%; Pred. No. 1.5e-225;  
 Matches 642; Conservative 35; Mismatches 41; Indels 2; Gaps 2;  
 QY 1 MKLKNQDQHSFSSNAKYDKISTDLSKNETDIELQNTINHDCLKMSVENVEPVSASTI 60  
 Db 1 MKLKNPDKHQTLSSNAKYDKIATDLSKNETDIELQNTINHDCLKMSHESIDPVSASTI 60  
 QY 61 QTGIGIAGKILGTLCVPPAGQVASYLSFILGELPKGNQWEILFMHEVER-INQKISTY 119  
 Db 61 QTGIGIAGKILGTLCVPPFGQIASYLSFILGELPKGKQWEI-FMEHVEALINRKISTY 119  
 QY 120 ARNKALTDLKLGDALAYTHDSLSWGNRNNTARSVVRQYIALELMFVKQLPSFAVS 179  
 Db 120 ARNKALTDLKLGDALAYTHDSLSWGNRNNTARSVVRQYIALELMFVKQLPSFAVS 179  
 QY 180 GBEVPLLPYQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHVKWY 239  
 Db 180 GBEVPLLPYQAANLHLLLRDASIFPKNGLSASEISTFYNRQVERTRDYSYHCVKWN 239

QY 240 STGLNNLRGTNAESWRYNQPRRDMTLMVLDLVLPSPSYDTOMYPIKTTAQLTREYVYDA 299  
 Db 240 NTGLNNLRATNGSWRYNQPRFKDIELMWLDLVRVFPSTYDTLVYPIKTTSLQTLTREYVYDA 299  
 QY 300 IGTVHPHPSFTSTTWYNNNAPSFAIAEAAVVRNPHLLDFLEQVTTYSLLSRWSNTQYMMN 359  
 Db 300 IGTVDNQLARSTTWYNNNAPSFAIAEAAVIRSPHLLDFLEKVTYSLLSRWSNTQYMMN 359  
 QY 360 WGGHLEFETIGTGLNISTQGSTNTSINPTLPFTSRDVRSTESLAGLNLFLTQPVNGVP 419  
 Db 360 WGGHRLDESPIGALNTSTQGSTNTSINPTLQFTSRDYRTESWAGLNLFLTQPVNGVP 419  
 QY 420 RVDFFHKVFTPIASDNFYYPGAGIGTQLODSENELPEPATGQPNYESYSHRLSHIGLI 479  
 Db 420 RVDFFHKVFTPIASDNFYVLGAGVGTQLODSENELPEPATGQPNYESYSHRLSHIGLI 479  
 QY 480 SASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAANVRGPGFTGGILRRT 539  
 Db 480 SASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAANVRGPGFTGGILRRT 539  
 QY 540 NTGTFGDIRVNINPPPAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATWNRGEDLDY 599  
 Db 540 KSGTFGHIRVNINPPPAQRYRVRMSYASTTDLQFHTSINGKAINQGNFSATWNRGEDLDY 599  
 QY 600 KTFRTVGTFTPTPSFLDVQSTFTIGAWNFSNGNEVDRIEFVPEVTEAEYDFEKAQEK 659  
 Db 600 KTFRTVGTFTPTPSFLDVQSTFTIGAWNFSNGNEVIGRIEFVPEVTEAEYDFEKAQEK 659  
 QY 660 VTALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDFYLDKRELFEIVKYANELHIERNM 719  
 Db 660 VTALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDFYLDKRELFEIVKYAKQNIERNM 719  
 RESULT 12  
 C1BB BACTU STANDARD; PRT: 1229 AA.  
 ID C1BB BACTU STANDARD; PRT: 1229 AA.  
 AC 045739;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Pesticidal crystal protein cryIBb (insecticidal delta-endotoxin  
 DE CryIB(b)) (crystalline entomocidal protoxin) (140 kDa crystal protein).  
 GN Name=cryIBb; Synonyms=cryIB(b), cryET5;  
 OS Bacillus thuringiensis.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1428;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NRL B-21110 / EG5847;  
 RA Donovan W.P., Tan Y., Jany C.S., Gonzalez J.M. Jr.;  
 RT "Bacillus thuringiensis cryet4 and cryet5 toxin genes and proteins  
 RT toxic to lepidopteran insects";  
 RL patent number US5322887, 21-JUN-1994.  
 CC -!- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut  
 CC epithelial cells of many lepidopteran larvae.  
 CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during  
 CC sporulation and is accumulated both as an inclusion and as part of  
 CC the spore coat.  
 CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-  
 CC terminus.  
 CC -!- SIMILARITY: Belongs to the delta endotoxin family.  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL; L32020; AAA22344.1; -  
 DR HSP; P02965; 1C1Y.  
 DR InterPro; IPR001178; Endotoxin.

DR InterPro; IPR005638; endotoxin C.  
DR InterPro; IPR005639; endotoxin N.  
DR InterPro; IPR008979; Gal bind like.  
DR Pfam; PF03944; Endotoxin C; 1.  
DR Pfam; PF00555; Endotoxin M; 1.  
DR Pfam; PF03945; Endotoxin N; 1.  
KW Sporulation; Toxin.  
SQ SEQUENCE 1229 AA; 139769 MW; A4C949DB675C3269 CRC64;

Query Match 64.3%; Score 2417.5; DB 1; Length 1229;  
Best Local Similarity 65.3%; Pred. No. 2e-160;  
Matches 469; Conservative 90; Mismatches 140; Indels 19; Gaps 8;

QY 13 SSNAKVDKISTDSLKN-ETDIELQ-NINHEDCIKMSEVENVEPVFVSGASTIQTGIGIAGKI 70  
DB 7 NENEINALSIFTVNPSFTQMLSPDARIEDSLCAEVNNDIPFVSASTVQTGINAGRI 66  
QY 71 LGTLGVPPFAQVASYLFIIGELMPKGNQWELFMEHVEE-INQKISTYARKALTDLK 129  
DB 67 LGVLGVPPFAQVASYLFIIGELMPKGNQWELFMEHVEE-INQKISTYARKALTDLK 125  
QY 130 GLGDALAVYHDSLESVGNENNRARSVRSOYIALELMFVKLPFAVSGEVPPLPIY 189  
DB 126 GLGRGYSYQQALETWLDNRDARSIIILERYVALELDITTAIPLFRINREVEPLLMVY 185  
QY 190 AQANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKYSTGLNNLRGT 249  
DB 186 AQANLHLLLRDASIFGSEWGMASDVNQYQEQIRYTEYSNHCQWNTGLNNLRGT 245  
QY 250 NAESWRYNQFRDMLTMDLVALFPSYDTQMYPIKTTAQLTRVYTDAGTVHHPSP 309  
DB 246 NAESWRYNQFRDMLTMDLVALFPSYDTQMYPIKTTAQLTRVYTDAGTVHHPSP 305  
QY 310 TSTWYNNAPSFSAIEAAVVRNPHLADLEQVITYSLSRWSNTQYMMWVGKLEFRT 369  
DB 306 ASTWYNNAPSFSAIEAAVVRNPHLADLEQVITYSLSRWSNTQYMMWVGKLEFRT 365  
QY 370 IGGTLNISTQGST-NTSINPVTLPFTSRDVTYTESLAGNLFLTOPVNGVPRVDFHWKFV 428  
DB 366 IGGTLNISTQGST-NTSINPVTLPFTSRDVTYTESLAGNLFLTOPVNGVPRVDFHWKFV 422  
QY 429 THPTASDNFYYPG-----YAGIGTQLODSSENLPPPEATGQPNVESYSHRLSHIGLISA 481  
DB 423 ---INQNIYERGATTSYQYQGVIGLFDSETELPPTETERNVESYSHRLSHIGLIIIG 479  
QY 482 SHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILARTNT 541  
DB 480 NTLRPVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILARTNT 539  
QY 542 GTFGDIRVNPFAQYRVRIRYASTTDLOFHTSINGKAINQGNPSTATNRGDEDLYKT 601  
DB 540 GTFGDIRVNPFAQYRVRIRYASTTDLOFHTSINGKAINQGNPSTATNRGDEDLYKT 599  
QY 602 FRTVGTTPRFLDQSTFTIGAMNFGSGNEVYIDRIEFYVPEVITYEAEYDFEKAQEKVT 661  
DB 600 FRTAGFTTFNFLNAQSTFTLGAQSFN-QEVIYIDRIEFYVPEVITYEAEYDFEKAQEKVT 658  
QY 662 ALFTSTNPRGLTKDVKYHIDQVSNLVESGDEFYDKRELFEIVKYANELHIERNM 719  
DB 659 ALFTSTNPRGLTKDVKYHIDQVSNLVESGDEFYDKRELFEIVKYANELHIERNM 716

RESULT 13  
CIBC\_BACTM STANDARD; PRT; 1233 AA.  
ID CIBC\_BACTM  
AC Q45774;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Pesticidal crystal protein cryIc (insecticidal delta-endotoxin)  
DE CryI(Bc) (Crystalline entomocidal protoxin) (140 kDa crystal protein).  
GN Name=cryIc; Synonyms=cryI(Bc), cryI(Bc);  
OS Bacillus thuringiensis (subsp. morrisoni).

Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
NCBI\_TaxID=1441;  
[1]  
SEQUENCE FROM N.A.  
Bishop A.H., Bone E.J., Ellar D.J.;  
"Cloning of novel Bacillus thuringiensis delta-endotoxin.";  
Submitted (Nov-1994) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: Promotes colloid osmotic lysis by binding to the midgut  
epithelial cells of insects.  
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during  
sporulation and is accumulated both as an inclusion and as part of  
the spore coat.  
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-  
terminus.  
CC -!- SIMILARITY: Belongs to the delta endotoxin family.  
-----  
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EMBL; Z46442; CAA86568.1; -;  
DR HSSP; P02965; 1CIY.  
DR InterPro; IPR001178; Endotoxin.  
DR InterPro; IPR005638; endotoxin C.  
DR InterPro; IPR005639; endotoxin N.  
DR InterPro; IPR008979; Gal\_bind\_like.  
DR Pfam; PF03944; Endotoxin C; 1.  
DR Pfam; PF00555; Endotoxin M; 1.  
DR Pfam; PF03945; Endotoxin N; 1.  
KW Sporulation; Toxin.  
SQ SEQUENCE 1233 AA; 140451 MW; 7318382413529F21 CRC64;

Query Match 64.3%; Score 2417.5; DB 1; Length 1233;  
Best Local Similarity 65.3%; Pred. No. 2e-160;  
Matches 469; Conservative 90; Mismatches 140; Indels 19; Gaps 8;

QY 13 SSNAKVDKISTDSLKN-ETDIELQ-NINHEDCIKMSEVENVEPVFVSGASTIQTGIGIAGKI 70  
DB 7 NENEINALSIFTVNPSFTQMLSPDARIEDSLCAEVNNDIPFVSASTVQTGINAGRI 66  
QY 71 LGTLGVPPFAQVASYLFIIGELMPKGNQWELFMEHVEE-INQKISTYARKALTDLK 129  
DB 67 LGVLGVPPFAQVASYLFIIGELMPKGNQWELFMEHVEE-INQKISTYARKALTDLK 125  
QY 130 GLGDALAVYHDSLESVGNENNRARSVRSOYIALELMFVKLPFAVSGEVPPLPIY 189  
DB 126 GLGRGYSYQQALETWLDNRDARSIIILERYVALELDITTAIPLFRINREVEPLLMVY 185  
QY 190 AQANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKYSTGLNNLRGT 249  
DB 186 AQANLHLLLRDASIFGSEWGMASDVNQYQEQIRYTEYSNHCQWNTGLNNLRGT 245  
QY 250 NAESWRYNQFRDMLTMDLVALFPSYDTQMYPIKTTAQLTRVYTDAGTVHHPSP 309  
DB 246 NAESWRYNQFRDMLTMDLVALFPSYDTQMYPIKTTAQLTRVYTDAGTVHHPSP 305  
QY 310 TSTWYNNAPSFSAIEAAVVRNPHLADLEQVITYSLSRWSNTQYMMWVGKLEFRT 369  
DB 306 ASTWYNNAPSFSAIEAAVVRNPHLADLEQVITYSLSRWSNTQYMMWVGKLEFRT 365  
QY 370 IGGTLNISTQGST-NTSINPVTLPFTSRDVTYTESLAGNLFLTOPVNGVPRVDFHWKFV 428  
DB 366 IGGTLNISTQGST-NTSINPVTLPFTSRDVTYTESLAGNLFLTOPVNGVPRVDFHWKFV 422  
QY 429 THPTASDNFYYPG-----YAGIGTQLODSSENLPPPEATGQPNVESYSHRLSHIGLISA 481  
DB 423 ---INQNIYERGATTSYQYQGVIGLFDSETELPPTETERNVESYSHRLSHIGLIIIG 479  
QY 482 SHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILARTNT 541  
DB 480 NTLRPVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILARTNT 539  
QY 542 GTFGDIRVNPFAQYRVRIRYASTTDLOFHTSINGKAINQGNPSTATNRGDEDLYKT 601  
DB 540 GTFGDIRVNPFAQYRVRIRYASTTDLOFHTSINGKAINQGNPSTATNRGDEDLYKT 599  
QY 602 FRTVGTTPRFLDQSTFTIGAMNFGSGNEVYIDRIEFYVPEVITYEAEYDFEKAQEKVT 661  
DB 600 FRTAGFTTFNFLNAQSTFTLGAQSFN-QEVIYIDRIEFYVPEVITYEAEYDFEKAQEKVT 658  
QY 662 ALFTSTNPRGLTKDVKYHIDQVSNLVESGDEFYDKRELFEIVKYANELHIERNM 719  
DB 659 ALFTSTNPRGLTKDVKYHIDQVSNLVESGDEFYDKRELFEIVKYANELHIERNM 716

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Db 480 NTERAPVSVWTHRSADRTNIGPNRITQPLVKALNLSGVTVGGPGFTGGDILRRNT 539
QY 542 GTFGDIRVNPFPFAQRVVRIRYASTTDLQFHTSINGKAINQGNFSATMNGEDLDYKT 601
Db 540 GTFGDIRLNVNPLSQRYVRIRYASTTDLQFHTSINGKAINQGNFSATMNGEDLDYKT 599
QY 602 FETVGTFTPFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTVYEAEDFEKAQKVT 661
Db 600 FRTAGFSPFNLNQAQSTFTLGAQGSN-QEYVIDRVEFPAEVTFEAYDLERAQKAVN 658
QY 662 ALFTSTNPRGLKTDVKDHYDQVSNLVESLSEDFYLDKRELFETIKYANLHIERNM 719
Db 659 ALFTSTNPRGLKTDVTDYHIDQVSNVACLSEDFCLDEKRELFETIKYAKLSDERNL 716

RESULT 14
Q93T75
ID Q93T75 PRELIMINARY; PRT; 1228 AA.
AC Q93T75;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Delta-endotoxin CryIaBa2.
GN Name=CryIaBa2;
OS Bacillus thuringiensis (subsp. entomocidus).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1436;
RN [1]_TaxID=1436;
RP SEQUENCE FROM N.A.
RC STRAIN=HD-9;
RA Mahadi M.A.F., Mahadi N.M.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF363025; AAK51084.1; -
DR HSSP; P07130; 1DLC.
DR GO; GO:0005102; P:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin C.
DR InterPro; IPR005639; endotoxin N.
DR InterPro; IPR008979; Gal bind like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
SQ SEQUENCE 1228 AA; 139620 MW; 3DA2A4DBF59C95C3 CRC64;

Query Match
Best Local Similarity 62.5%; Pred. No. 1.1e-148;
Matches 448; Conservative 78; Mismatches 164; Indels 27; Gaps 8;

QY 23 TDSLKNVTDIELQNIH-----EDCLKSEVENVEPVFVASTTQTGTGIAGKI 70
Db 2 TSNRKNENEIINAVNSHAQMDLLPDARIEDSLCAEGNIDPFVASTVQTGINIAGRI 61
QY 71 LGTLGVPPAGVVASLYSIFGELWPKGNOWEILFMHEVB-INOKISTVARNKALTDLK 129
Db 62 LGVLGVPPAGVVASLYSIFGELWPKGNOWEILFMHEVB-INOKISTVARNKALTDLK 120
QY 130 GLGDALAYHDSLESWGNRNNTARRSVRSQYIALELMFVQKLPSPAVSGEEVPLPIY 189
Db 121 GLGDSFRAYQCSLEWLENRDARTSVLHQTALDLEFLNAPLFAIRNQEVEPLLMVY 180
QY 190 ACAANLHLLLRDASIFCKEGLASSETSTFYNQVSRAGYSDHCVKYSTGNLRGT 249
Db 191 ACAANLHLLLRDASIFCKEGLASSETSTFYNQVSRAGYSDHCVKYSTGNLRGT 240
QY 250 NAESVVRNQFRDRLTMVLVDLVALFSPYDQYPIKTAQLTREVYTDAGTGVHPSPF 309
Db 241 NAASVVRNQFRDRLTMVLVDLVALFSPYDQYPIKTAQLTREVYTDAGTGVHPSPF 298
QY 310 TSTTWYNNAPSFSAIEAIVRNPHLLDFLEQVITYLSLLSEWNTQYMMWGGHLEFRT 369

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Db 299 ASMWYNNAPSFSAIEAIIIRSPHLLDFLEQITIPFSASRWSNTRHMTYWRGHTIQSRP 358
QY 370 IGTALNISQSTNTSINPVTLPTFSRDVYRTESLAGNLF--LTQPVNGVPRVDFHMKF 427
Db 359 IGGGLTSTHGATNTSINPVTLPTFSRDVYRTESLAGNLF--LTQPVNGVPRVDFHMKF 416
QY 428 VTHP-----IASDNVYVPGVAGIGTQLODSENELPEATGQPNYESYSHRLSHIGLISAS 482
Db 417 -TNPQNISRGATANYSQP-YESFGLQKDSLETLPETTERPNYESYSHRLSHIGLISAS 474
QY 483 HVKALYVSWTHRSADRTNIPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILARTNTG 542
Db 475 RVNVVYVSWTHRSADRTNIPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILARTNTG 534
QY 543 TFGDIRVNPFPFAQRVVRIRYASTTDLQFHTSINGKAINQGNFSATMNGEDLDYKT 602
Db 535 GFGDIRVNPFPFAQRVVRIRYASTTDLQFHTSINGKAINQGNFSATMNGEDLDYKT 594
QY 603 RTVGFTTSPFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTVYEAEDFEKAQKVT 662
Db 595 VRRFTTPTFTTQIQDIIRTSIQGLSGNGEVYIDRIEFVPEVTVYEAEDFEKAQKVT 654
QY 663 LFTSTNPRGLKTDVKDHYDQVSNLVESLSEDFYLDKRELFETIKYANLHIERNM 719
Db 655 LFTSTNPRGLKTDVTDYHIDQVSNLVACLSEDFCLDEKRELFETIKYAKLSDERNL 711

RESULT 15
CLIB_BACTX
ID CLIB_BACTX STANDARD; PRT; 1228 AA.
AC P05517; Q45731;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pesticidal crystal protein cryIa (Insecticidal delta-endotoxin
DE CryIa(a)) (Crystalline entomocidal protoxin) (140 kDa crystal protein).
GN Name=CryIa; Synonyms=cryIa(a), cryA4;
OS Bacillus thuringiensis (subsp. kurstaki), and
OS Bacillus thuringiensis (subsp. entomocidus).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=29339, 1436;
RN [1]_TaxID=29339, 1436;
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.kurstaki; STRAIN=HD-2;
RX MEDLINE=88203216; PubMed=3362680;
RA Brizzard B.L., Whiteley H.R.;
RT "Nucleotide sequence of an additional crystal protein gene cloned from
RL Bacillus thuringiensis subsp. thuringiensis.";
RN Nucleic Acids Res. 16:2723-2723(1988).
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.entomocidus; STRAIN=HD-110;
RA Soetaert P.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut
CC epithelial cells of insects.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -!- SIMILARITY: Belongs to the delta endotoxin family.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X06711; CAA29898.1; -
DR EMBL; X95704; CAA65003.1; -

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DR PIR; S00873; S00873.  
DR HSP; P07130; IDLC.  
DR InterPro; IPR001178; Endotoxin.  
DR InterPro; IPR005638; endotoxin\_C.  
DR InterPro; IPR005639; endotoxin\_N.  
DR InterPro; IPR008979; Gal bind\_Like.  
DR Pfam; PF03944; Endotoxin\_C; 1.  
DR Pfam; PF00555; Endotoxin\_M; 1.  
DR Pfam; PF03945; Endotoxin\_N; 1.  
KW Sporulation; Toxin.  
FT VARIANT 150 150 Y -> H (in strain HD-110).  
SQ SEQUENCE 1228 AA; 139647 MW; C8E3A19FB5D98575 CRC64;

Query Match 59.8%; Score 2248.5; DB 1; Length 1228;  
Best Local Similarity 62.5%; Pred. No. 1.5e-148;  
Matches 448; Conservative 78; Mismatches 164; Indels 27; Gaps 8;

QY 23 TDSLKNETDIELOQNH-----EDCLKMSEYENVEPFVSASTIQTGIGIAGKI 70  
DB 2 TSNRKNENEIINAVNSHSAQMDLLPDARIEDSLCIAEGNNDIPFVSASTVQTGINIAGRI 61  
QY 71 LGTLGVFPAGQVSLYSFIILGELWPKGNQWELFMEHVEE-INOKISTYARNKALTDLK 129  
DB 62 LGVLGVFPAGQLASFYSLVGEIWMGRDQWEI-FLEHVEQLINQOITENARNTALARQ 120  
QY 130 GLGDALAVYHDSLESWGNENNRARSVRSQVIALFELMFVQKLPFAVSGSEVPLPIY 189  
DB 121 GLGDSFRAYQCSLEWLENRDDARTSRVLYQTQIALDELFLNAMPLEFARNQEVPLIMVY 180  
QY 190 AQANLHLLLRDASIFGKKGWJSSSEISTFYNRQVERAGDYSCHCVKWTSTGLNNLRGT 249  
DB 181 AQANLHLLLRDASLFGSFGSLTSQEIQRYRQVERTRDYSYCVIEWYNTGLNSLRGT 240  
QY 250 NAESWVYVNOFRDMTAVLDLVALFSPYDTQVPIKTTAQLTRVYVTDAGTGVHPHPSF 309  
DB 241 NAASWVYVNOFRDLTGVLDLVALFSPYDTQVPIKTTAQLTRVYVTDAGT--GVNM 298  
QY 310 TSTTYNNNAFSAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMMNMGCKLEFRT 369  
DB 299 ASMNWYNNNAFSAIEAAIRSPHLLDFLEQVTIYSLSRWSNTQYMMNMGCKLEFRT 358  
QY 370 IGGTLNSTQGSTWTSINPVTLPTSDVDYRTESLAGNLF--LTQPVNGVPRVDPHWK 427  
DB 359 IGGGLNSTHGATNTSINPVTLPRASRDYRTESYAGVLLWGIYLEPIHGVPTVRFNF-- 416  
QY 428 VTHP-----IASDNFYPGVAGIGTQLQDSNELPPEATGQPNYESYSHLSHIGLISAS 482  
DB 417 -TNFQNTSDRCTANYSQP-YESPOLQKDSSETLPPTETPRPNYESYSHLSHIGILQS 474  
QY 483 HVKALVSWTHRSADRNNTIEPNSITQIPLVKAENLSSGAAVRGPQFTGCDILRRNTG 542  
DB 475 RVNVPVSWTHRSADRNNTIGPNRITQIPVKASELFQGTTVVRGPQFTGCDILRRNTG 534  
QY 543 TFGDIRVNIINPPFAQRYVRIRYASTTDLOPHTSINGKAINOGNFSATMARGEDLDYKF 602  
DB 535 GFGPIRVTVNGPLTQRIQRIYASTVDPDFVSRGGTTVNNFRFLTMNSGDELKYNF 594  
QY 603 RTVGFTTFFSLDVQSTFTIGAMNFSNGEYVIDRIEFVPEVTEYAEYDFEXAQEKVTA 662  
DB 595 VRRFTTPTFTQIDIRTSIQGLSGNGEYVIDKIEIIPVTATFEAEYDLERAQEAUNA 654  
QY 663 LFTSTNREGLTKYDKHIDQVSNVESLSDEFYLDKRELFELVYKYNELHIERNM 719  
DB 655 LFTNTNPRRLKTDVTDYHIDQVSNVACLSDDEFCLDEKRELEKVKYAKRLSDERNL 711

Search completed: October 28, 2004, 18:30:09  
Job time : 105.579 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 28, 2004, 18:10:58 ; Search time 65.6795 Seconds  
(without alignments)  
3549.224 Million cell updates/sec

Title: US-10-019-823B-58

Perfect score: 3761  
Sequence: 1 MKLNQDQHQSSNAKVDK.....KRELFEIVKYANELHIERNM 719

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1370721 seqs, 324215800 residues

Total number of hits satisfying chosen parameters: 1370721

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pcp.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pcp.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pcp.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pcp.\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pcp.\*
- 6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pcp.\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pcp.\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pcp.\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pcp.\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pcp.\*
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- 13: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pcp.\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pcp.\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pcp.\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pcp.\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pcp.\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pcp.\*
- 19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pcp.\*
- 20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3724	99.0	719	17	US-10-782-020-10
2	3724	99.0	719	17	US-10-782-141-8
3	3724	99.0	719	17	US-10-782-096-10
4	3724	99.0	719	17	US-10-782-570-7
5	3442.5	91.5	710	14	US-10-428-961-42
6	2250.5	59.8	1228	16	US-10-809-953-10
7	2236.5	59.5	1207	10	US-09-988-462-7
8	2157.5	57.4	1227	14	US-10-428-961-63
9	2142.5	57.0	1186	9	US-09-836-660-23
10	2087	55.5	1228	14	US-10-428-961-38
11	2087	55.5	1228	15	US-10-614-524-2
12	1909.5	50.8	643	9	US-09-826-660-25
13	1694.5	45.1	1167	14	US-10-089-678-1

14	1658.5	44.1	653	14	US-10-428-961-6	Sequence 6, Appli
15	1643.5	43.7	1157	17	US-10-782-141-16	Sequence 16, Appl
16	1643.5	43.7	1157	17	US-10-782-096-17	Sequence 17, Appl
17	1643.5	43.7	1157	17	US-10-782-570-13	Sequence 13, Appl
18	1485	39.5	1206	13	US-10-032-717-2	Sequence 2, Appli
19	1485	39.5	1206	14	US-10-414-637-2	Sequence 2, Appli
20	1485	39.5	1206	15	US-10-606-320-2	Sequence 2, Appli
21	1485	39.5	1206	17	US-10-746-914-2	Sequence 2, Appli
22	1469	39.1	1210	13	US-10-032-717-4	Sequence 4, Appli
23	1469	39.1	1210	14	US-10-414-637-4	Sequence 4, Appli
24	1469	39.1	1210	15	US-10-606-320-4	Sequence 4, Appli
25	1469	39.1	1210	17	US-10-746-914-4	Sequence 4, Appli
26	1459.5	38.8	1156	14	US-10-099-285-72	Sequence 72, Appl
27	1459.5	38.8	1156	14	US-10-428-961-28	Sequence 28, Appl
28	1443	38.4	1155	9	US-09-756-643-2	Sequence 2, Appli
29	1443	38.4	1155	10	US-09-988-462-9	Sequence 9, Appli
30	1443	38.4	1155	14	US-10-136-998A-2	Sequence 2, Appli
31	1443	38.4	1177	14	US-10-035-060-6	Sequence 6, Appli
32	1443	38.4	1181	10	US-09-988-462-11	Sequence 11, Appl
33	1443	38.4	1181	10	US-09-988-462-13	Sequence 13, Appl
34	1443	38.4	1181	10	US-09-988-462-15	Sequence 15, Appl
35	1443	38.4	1181	10	US-09-988-462-17	Sequence 17, Appl
36	1443	38.4	1181	10	US-09-988-462-28	Sequence 28, Appl
37	1443	38.4	1181	14	US-10-136-998A-4	Sequence 4, Appli
38	1443	38.4	1181	14	US-10-136-998A-8	Sequence 8, Appli
39	1443	38.4	1181	14	US-10-136-998A-10	Sequence 10, Appl
40	1443	38.4	1181	14	US-10-136-998A-12	Sequence 12, Appl
41	1438	38.2	1177	14	US-10-035-060-2	Sequence 2, Appli
42	1436	38.2	1177	14	US-10-035-060-8	Sequence 8, Appli
43	1435	38.2	1177	14	US-10-102-469-24	Sequence 24, Appl
44	1419.5	37.7	1176	17	US-10-782-141-6	Sequence 6, Appli
45	1419.5	37.7	1176	17	US-10-782-096-7	Sequence 7, Appli

#### ALIGNMENTS

#### RESULT 1

US-10-782-020-10  
; Sequence 10, Application US/10782020  
; Publication No. US20040197916A1  
; GENERAL INFORMATION:  
; APPLICANT: Carozzi, Nadine  
; APPLICANT: Hargiss, Tracy  
; APPLICANT: Koziel, Michael G.  
; APPLICANT: Duck, Nicholas B.  
; APPLICANT: Carr, Brian  
; TITLE OF INVENTION: AXMI-004, A Delta-Endotoxin Gene and  
; TITLE OF INVENTION: Methods for Its Use  
; FILE REFERENCE: 045600/274139  
; CURRENT APPLICATION NUMBER: US/10/782,020  
; CURRENT FILING DATE: 2004-02-19  
; PRIOR APPLICATION NUMBER: 60/448,810  
; PRIOR FILING DATE: 2003-02-20  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 719  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
US-10-782-020-10

Query Match 99.0%; Score 3724; DB 17; Length 719;

Best Local Similarity 99.3%; Pred. No. 1e-305; Indels 2; Gaps 2;

Matches 715; Conservative 2; Mismatches 1;

QY 1 MKLNQDQHQSSNAKVDKISTDSLKNETDTLQKINHEDCIKMSEYENVPFVSASTI 60

Db 1 MKLNQDQHQSSNAKVDKISTDSLKNETDTLQKINHEDCIKMSEYENVPFVSASTI 60

QY 61 QTGIGIAGKILGTGLGVFPFAGQVASYLSYFILGELWPKGNQWEILPMEHVEE-INOKISTY 119

Db 61 QTGIGIAGKILGTGLGVFPFAGQVASYLSYFILGELWPKGNQWEILPMEHVEE-INOKISTY 119

QY 120 ARNKALTDLKGGLDALAVYHDSLEWVGNNRNNTRARSVVRQYIALELMFYQKLPSPFAVS 179  
 Db 120 ARNKALTDLKGGLDALAVYHDSLEWVGNNRNNTRARSVVRQYIALELMFYQKLPSPFAVS 179  
 QY 180 GEEVPLLPPIYAQAANLHLLLDASIFGKEWGLSSSEISTFYNNQVERAGDYSCHCVKWY 239  
 Db 180 GEEVPLLPPIYAQAANLHLLLDASIFGKEWGLSSSEISTFYNNQVERAGDYSCHCVKWY 239  
 QY 240 STGLNNLRCTNAESVVRVYNNQFRDMLVLDLVALFPYSYDTQMPYIKTTAQLTREVVYDA 299  
 Db 240 STGLNNLRCTNAESVVRVYNNQFRDMLVLDLVALFPYSYDTQMPYIKTTAQLTREVVYDA 299  
 QY 300 IGTVHPHPSFTSTTWNNNAPSFAIEAAVVRNPHLLDFLEQVTTYSLLSRWSNTQYMMN 359  
 Db 300 IGTVHPHPSFTSTTWNNNAPSFAIEAAVVRNPHLLDFLEQVTTYSLLSRWSNTQYMMN 359  
 QY 360 WGGHKLERTIGTGLNISTQGSTNTSINPVTLPFTSRDVTETESLAGNLFLOTPVNGVP 419  
 Db 360 WGGHKLERTIGTGLNISTQGSTNTSINPVTLPFTSRDVTETESLAGNLFLOTPVNGVP 419  
 QY 420 RYDFHKKFVTHPIASDNFYPGYAGIGTQLODSENELPPEATGQPNYESYSHRSLHIGLI 479  
 Db 420 RYDFHKKFVTHPIASDNFYPGYAGIGTQLODSENELPPEATGQPNYESYSHRSLHIGLI 479  
 QY 480 SASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRT 539  
 Db 480 SASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRT 539  
 QY 540 NTGTGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDY 599  
 Db 540 NTGTGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDY 599  
 QY 600 KTFRTVGTTPPFLDVOSTTTIGAMNPFSSGNEVYIDRIEFVPEVVEVYEAEDPEKAQEK 659  
 Db 600 KTFRTVGTTPPFLDVOSTTTIGAMNPFSSGNEVYIDRIEFVPEVVEVYEAEDPEKAQEK 659  
 QY 660 VTALFTSNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYANLHIERNM 719  
 Db 660 VTALFTSNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYANLHIERNM 719

RESULT 2

US-10-782-141-8  
 ; Sequence 8, Application US/10782141  
 ; Publication No. US20040197917A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Carozzi, Nadine  
 ; APPLICANT: Hargiss, Tracy  
 ; APPLICANT: Kozziel, Michael G.  
 ; APPLICANT: Duck, Nicholas B.  
 ; APPLICANT: Carr, Brian  
 ; TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and  
 ; TITLE OF INVENTION: Methods for its Use  
 ; FILE REFERENCE: 045600/274143  
 ; CURRENT APPLICATION NUMBER: US/10782,141  
 ; PRIOR FILING DATE: 2004-02-20  
 ; PRIOR FILING DATE: 2003-02-20  
 ; NUMBER OF SEQ ID NOS: 23  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 8  
 ; LENGTH: 719  
 ; TYPE: PRT  
 ; ORGANISM: Bacillus thuringiensis  
 US-10-782-141-8

Query Match 99.0%; Score 3724; DB 17; Length 719;  
 Best Local Similarity 99.3%; Pred. No. 1e-305;  
 Matches 715; Conservative 2; Mismatches 1; Indels 2; Gaps 2;

Db 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHHEDCLKMSEYENVEPFFVSASTI 60  
 QY 61 QTGIGTAGKILGTGVPFAGOVASISYFTLGBLWPKGNQWEILFWEHVEE-INOKISITY 119  
 Db 61 QTGIGTAGKILGTGVPFAGOVASISYFTLGBLWPKGNQWEILFWEHVEE-INOKISITY 119  
 QY 120 ARNKALTDLKGGLDALAVYHDSLEWVGNNRNNTRARSVVRQYIALELMFYQKLPSPFAVS 179  
 Db 120 ARNKALTDLKGGLDALAVYHDSLEWVGNNRNNTRARSVVRQYIALELMFYQKLPSPFAVS 179  
 QY 180 GEEVPLLPPIYAQAANLHLLLDASIFGKEWGLSSSEISTFYNNQVERAGDYSCHCVKWY 239  
 Db 180 GEEVPLLPPIYAQAANLHLLLDASIFGKEWGLSSSEISTFYNNQVERAGDYSCHCVKWY 239  
 QY 240 STGLNNLRCTNAESVVRVYNNQFRDMLVLDLVALFPYSYDTQMPYIKTTAQLTREVVYDA 299  
 Db 240 STGLNNLRCTNAESVVRVYNNQFRDMLVLDLVALFPYSYDTQMPYIKTTAQLTREVVYDA 299  
 QY 300 IGTVHPHPSFTSTTWNNNAPSFAIEAAVVRNPHLLDFLEQVTTYSLLSRWSNTQYMMN 359  
 Db 300 IGTVHPHPSFTSTTWNNNAPSFAIEAAVVRNPHLLDFLEQVTTYSLLSRWSNTQYMMN 359  
 QY 360 WGGHKLERTIGTGLNISTQGSTNTSINPVTLPFTSRDVTETESLAGNLFLOTPVNGVP 419  
 Db 360 WGGHKLERTIGTGLNISTQGSTNTSINPVTLPFTSRDVTETESLAGNLFLOTPVNGVP 419  
 QY 420 RYDFHKKFVTHPIASDNFYPGYAGIGTQLODSENELPPEATGQPNYESYSHRSLHIGLI 479  
 Db 420 RYDFHKKFVTHPIASDNFYPGYAGIGTQLODSENELPPEATGQPNYESYSHRSLHIGLI 479  
 QY 480 SASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRT 539  
 Db 480 SASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRT 539  
 QY 540 NTGTGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDY 599  
 Db 540 NTGTGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDY 599  
 QY 600 KTFRTVGTTPPFLDVOSTTTIGAMNPFSSGNEVYIDRIEFVPEVVEVYEAEDPEKAQEK 659  
 Db 600 KTFRTVGTTPPFLDVOSTTTIGAMNPFSSGNEVYIDRIEFVPEVVEVYEAEDPEKAQEK 659  
 QY 660 VTALFTSNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYANLHIERNM 719  
 Db 660 VTALFTSNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYANLHIERNM 719

RESULT 3

US-10-782-096-10  
 ; Sequence 10, Application US/10782096  
 ; Publication No. US20040210964A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Carozzi, Nadine  
 ; APPLICANT: Hargiss, Tracy  
 ; APPLICANT: Kozziel, Michael G.  
 ; APPLICANT: Duck, Nicholas B.  
 ; APPLICANT: Carr, Brian  
 ; TITLE OF INVENTION: AXMI-009, A Delta-Endotoxin Gene and  
 ; TITLE OF INVENTION: Methods for its Use  
 ; FILE REFERENCE: 045600/274148  
 ; CURRENT APPLICATION NUMBER: US/10782,096  
 ; CURRENT FILING DATE: 2004-02-19  
 ; PRIOR APPLICATION NUMBER: 60/448,633  
 ; PRIOR FILING DATE: 2003-02-20  
 ; NUMBER OF SEQ ID NOS: 23  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 10  
 ; LENGTH: 719  
 ; TYPE: PRT  
 ; ORGANISM: Bacillus thuringiensis  
 US-10-782-096-10

Query Match 99.0%; Score 3724; DB 17; Length 719;



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Best Local Similarity 99.3%; Pred. No. 1e-305;
Matches 715; Conservative 2; Mismatches 1; Indels 2; Gaps 2;

QY 1 MKLNQDKHQSFSNNAKVDKISTDSLNKNETDIELQNIHEDCLKMGSEYENVEPFFVSASTI 60
DB 1 MKLNQDKHQSFSNNAKVDKISTDSLNKNETDIELQNIHEDCLKMGSEYENVEPFFVSASTI 60
QY 61 QTGIGTAGKILGTGVPFAGQVASLYSFIIGELMPKGNQWEILFMEHVEE-INQKISTY 119
DB 61 QTGIGTAGKILGTGVPFAGQVASLYSFIIGELMPKGNQWEILFMEHVEE-INQKISTY 119
QY 120 ARNKALTDLKGDLALAVYHDSLESWGNRNNTARSVRSQVIALELMPVQKLPSPFAVS 179
DB 120 ARNKALTDLKGDLALAVYHDSLESWGNRNNTARSVRSQVIALELMPVQKLPSPFAVS 179
QY 180 GEEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHVKWY 239
DB 180 GEEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHVKWY 239
QY 240 STGLNNLRGTNAESWVRYNQFRDMLTMLVDLVALPSPYDTQMPYIKTTAQLTREYVYDA 299
DB 240 STGLNNLRGTNAESWVRYNQFRDMLTMLVDLVALPSPYDTQMPYIKTTAQLTREYVYDA 299
QY 300 ICTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMMN 359
DB 300 ICTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMMN 359
QY 360 WGGHKLFRITGTLNISTOGSNTSINPVTLPFTSRDVRYSLAGLNLFLTPQVNGVP 419
DB 360 WGGHKLFRITGTLNISTOGSNTSINPVTLPFTSRDVRYSLAGLNLFLTPQVNGVP 419
QY 420 RVDPHKFWTHPIASDNFYFPGYAGIGTQLODSENELPPEATQPNYESYSHRLSHIGLI 479
DB 420 RVDPHKFWTHPIASDNFYFPGYAGIGTQLODSENELPPEATQPNYESYSHRLSHIGLI 479
QY 480 SASHVKALVSWTHRSADRNTNTEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRT 539
DB 480 SASHVKALVSWTHRSADRNTNTEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRT 539
QY 540 NTGTFGDIRVNNPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLDY 599
DB 540 NTGTFGDIRVNNPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLDY 599
QY 600 KTFRTVGFTTTPSFLDVQSTFTIGAWNFSNGNEVYIDRIEFVPEVTEAEYDFEKAQEK 659
DB 600 KTFRTVGFTTTPSFLDVQSTFTIGAWNFSNGNEVYIDRIEFVPEVTEAEYDFEKAQEK 659
QY 660 VTALFTSTNPRGLKTDVKDYHIDQVSNLVSLSDEFFYLDEKRELFEIVKYANLHERNM 719
DB 660 VTALFTSTNPRGLKTDVKDYHIDQVSNLVSLSDEFFYLDEKRELFEIVKYANLHERNM 719

RESULT 4
US-10-782-570-7
; Sequence 7, Application US/10782570
; Publication No. US20040210965A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-007, A Delta-Endotoxin Gene and
; Methods for Its Use
; FILE REFERENCE: 045600/274144
; CURRENT APPLICATION NUMBER: US/10/782,570
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: 60/448,812
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 719

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; TYPE: PRF
; ORGANISM: Bacillus thuringiensis
US-10-782-570-7

Query Match 99.0%; Score 3724; DB 17; Length 719;
Best Local Similarity 99.3%; Pred. No. 1e-305;
Matches 715; Conservative 2; Mismatches 1; Indels 2; Gaps 2;

QY 1 MKLNQDKHQSFSNNAKVDKISTDSLNKNETDIELQNIHEDCLKMGSEYENVEPFFVSASTI 60
DB 1 MKLNQDKHQSFSNNAKVDKISTDSLNKNETDIELQNIHEDCLKMGSEYENVEPFFVSASTI 60
QY 61 QTGIGTAGKILGTGVPFAGQVASLYSFIIGELMPKGNQWEILFMEHVEE-INQKISTY 119
DB 61 QTGIGTAGKILGTGVPFAGQVASLYSFIIGELMPKGNQWEILFMEHVEE-INQKISTY 119
QY 120 ARNKALTDLKGDLALAVYHDSLESWGNRNNTARSVRSQVIALELMPVQKLPSPFAVS 179
DB 120 ARNKALTDLKGDLALAVYHDSLESWGNRNNTARSVRSQVIALELMPVQKLPSPFAVS 179
QY 180 GEEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHVKWY 239
DB 180 GEEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHVKWY 239
QY 240 STGLNNLRGTNAESWVRYNQFRDMLTMLVDLVALPSPYDTQMPYIKTTAQLTREYVYDA 299
DB 240 STGLNNLRGTNAESWVRYNQFRDMLTMLVDLVALPSPYDTQMPYIKTTAQLTREYVYDA 299
QY 300 ICTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMMN 359
DB 300 ICTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMMN 359
QY 360 WGGHKLFRITGTLNISTOGSNTSINPVTLPFTSRDVRYSLAGLNLFLTPQVNGVP 419
DB 360 WGGHKLFRITGTLNISTOGSNTSINPVTLPFTSRDVRYSLAGLNLFLTPQVNGVP 419
QY 420 RVDPHKFWTHPIASDNFYFPGYAGIGTQLODSENELPPEATQPNYESYSHRLSHIGLI 479
DB 420 RVDPHKFWTHPIASDNFYFPGYAGIGTQLODSENELPPEATQPNYESYSHRLSHIGLI 479
QY 480 SASHVKALVSWTHRSADRNTNTEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRT 539
DB 480 SASHVKALVSWTHRSADRNTNTEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRT 539
QY 540 NTGTFGDIRVNNPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLDY 599
DB 540 NTGTFGDIRVNNPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLDY 599
QY 600 KTFRTVGFTTTPSFLDVQSTFTIGAWNFSNGNEVYIDRIEFVPEVTEAEYDFEKAQEK 659
DB 600 KTFRTVGFTTTPSFLDVQSTFTIGAWNFSNGNEVYIDRIEFVPEVTEAEYDFEKAQEK 659
QY 660 VTALFTSTNPRGLKTDVKDYHIDQVSNLVSLSDEFFYLDEKRELFEIVKYANLHERNM 719
DB 660 VTALFTSTNPRGLKTDVKDYHIDQVSNLVSLSDEFFYLDEKRELFEIVKYANLHERNM 719

RESULT 5
US-10-428-961-42
; Sequence 42, Application US/10428961
; Publication No. US20030237111A1
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Chu, Chih-Rei
; APPLICANT: Donovan, William P.
; APPLICANT: Gilmer, Amy J.
; APPLICANT: Ruper, Mark J.
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin
; Polynucleotides, Compositions, and Methods of Use (Amended)
; FILE REFERENCE: MECO201--1
; CURRENT APPLICATION NUMBER: US/10/428,961
; CURRENT FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: 09/661,322

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; PRIOR FILING DATE: 2000-09-13  
 ; PRIOR APPLICATION NUMBER: 60/153,995  
 ; PRIOR FILING DATE: 1999-09-15  
 ; NUMBER OF SEQ ID NOS: 63  
 ; SOFTWARE: Patent version 3.2  
 ; SEQ ID NO 42  
 ; LENGTH: 710  
 ; TYPE: PRT  
 ; ORGANISM: Bacillus thuringiensis  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: (2007)..(200)  
 ; OTHER INFORMATION: The 'Xaa' at location 200 stands for any naturally occurring amino acid  
 US-10-428-961-42

Query Match 91.5%; Score 3442.5; DB 14; Length 710;  
 Best Local Similarity 91.9%; Pred. No. 6.7e-282;  
 Matches 562; Conservative 16; Mismatches 31; Indels 11; Gaps 3;  
 QY 1 MKLNQKHQSPSSNAKVDKISTDLKNETDIEIQLNINHEDECLMKSYENVPEFVSASTI 60  
 DB 1 MKSKNQNHQSLNNATVDKNTGSLNNTNTELQNFH-----EGIEPFVSASTI 51  
 QY 61 QTGIGIAGKILGTLGVPAGQVASYSLFILGELWPKGNOWEILFMEHVEE-INOKISTY 119  
 DB 52 QTGIGIAGKILGTLGVPAGQVASYSLFILGELWPKGNOWEILFMEHVEEILNOKISTY 110  
 QY 120 ARNKALTDKLGDLALAVYHDSLESVGNRRNTRARSVRSQYIALELMFVQKLPSPAVS 179  
 DB 111 ARNKALADKLGDLALAVYHDSLESVGNRRNTRARSVRSQYIALELMFVQKLPSPAVS 170  
 QY 180 GEEVPLPIYQAQANLHLLLDASIFCKEWGLSSSEISTFYNQVVERAGDYSCHVKWY 239  
 DB 171 GEEVPLPIYQAQANLHLLLDASIFCKEWGLSSSEISTFYNQVVERAGDYSCHVKWY 230  
 QY 240 STGLNLRGTTNAESVRYNQFRDWTMLVLDLVALFSDYDTQMPYIKTTAQLTEVYTD 299  
 DB 231 NTGLNLRGTTNAESVRYNQFRDWTMLVLDLVALFSDYDTQMPYIKTTAQLTEVYTD 290  
 QY 300 IGTVPHPSPSTTWNNAFSAIEAAVVRNPHLLDFLEQVITYLLSRWSNTQNMN 359  
 DB 291 IGTVPHPSPSTTWNNAFSAIEAAVVRNPHLLDFLEQVITYLLSRWSNTQNMN 350  
 QY 360 WGGHKLERTTGGTLNISTQSTNTSINPVLPTSDRDVYRTESLAGLNLFTQPVNGVP 419  
 DB 351 WGGHKLERTTGGTLNISTQSTNTSINPVLPTSDRDVYRTESLAGLNLFTQPVNGVP 410  
 QY 420 RVDHFKVFTVPIASDNFYPGYAGIGTQLODSENELPPEATQPNYESYSHRLSHIGLI 479  
 DB 411 RVDHFKVFTVPIASDNFYPGYAGIGTQLODSENELPPEATQPNYESYSHRLSHIGLI 470  
 QY 480 SASHVKALVYSWTHRSADRTNTEIPNSITQPLVKAFLSSGAARVPGFTGDIILRR 539  
 DB 471 SASHVKALVYSWTHRSADRTNTEIPNSITQPLVKAFLSSGAARVPGFTGDIILRR 530  
 QY 540 NTGTFGDIRVNNPPFAQRYVRIRYASTTDLPHTSINGKAINQGNFSAATMRGEDLDY 599  
 DB 531 NTGTFGDIRVNNPPFAQRYVRIRYASTTDLPHTSINGKAINQGNFSAATMRGEDLDY 590  
 QY 600 KTEFTVGTTPFSDVQSTTICAWNFSSGNEVYIDRIEFVPEVYEAEDPEKAQEK 659  
 DB 591 KTEFTVGTTPFSDVQSTTICAWNFSSGNEVYIDRIEFVPEVYEAEDPEKAQEK 650  
 QY 660 VTALFTSTNPRGLKTDVKDHYHDQVSNLVESLSDEFYLDKRELFVIVKYANELHIERNM 719  
 DB 651 VTALFTSTNPRGLKTDVKDHYHDQVSNLVESLSDEFYLDKRELFVIVKYANELHIERNM 710

RESULT 6  
 US-10-809-953-10  
 ; Sequence 10, Application US/10809953  
 ; Publication No. US20040181825A1  
 ; GENERAL INFORMATION:

; APPLICANT: Van Mellaert, Herman  
 ; APPLICANT: Botterman, Johan  
 ; APPLICANT: Van Rie, Jeroen  
 ; APPLICANT: Joos, Henk  
 ; TITLE OF INVENTION: RECOMBINANT PLANT EXPRESSING NON-COMPETITIVELY BINDING Bc INSECTIC  
 ; FILE REFERENCE: 021565-078  
 ; CURRENT APPLICATION NUMBER: US/10/809,953  
 ; CURRENT FILING DATE: 2004-03-26  
 ; PRIOR APPLICATION NUMBER: US/09/661,016  
 ; PRIOR FILING DATE: 2000-09-13  
 ; PRIOR APPLICATION NUMBER: PCT/EP90/00905  
 ; PRIOR FILING DATE: 1990-05-30  
 ; PRIOR APPLICATION NUMBER: GB 89401499.2  
 ; PRIOR FILING DATE: 1989-05-31  
 ; NUMBER OF SEQ ID NOS: 10  
 ; SOFTWARE: Patent version 2.0  
 ; SEQ ID NO 10  
 ; LENGTH: 1228  
 ; TYPE: PRT  
 ; ORGANISM: Bacillus thuringiensis  
 ; US-10-809-953-10  
 Query Match 59.8%; Score 2250.5; DB 16; Length 1228;  
 Best Local Similarity 62.5%; Pred. No. 1.1e-180;  
 Matches 448; Conservative 78; Mismatches 164; Indels 27; Gaps 8;  
 QY 23 TDSLKNETDIEIQLNINH-----EDCLMKSEYENVPEFVSASTIQTGIGIAGKI 70  
 DB 2 TSNRKQNEIINAVSNHSAQMDLLPDARIEDSLCAEGNNDIPFVSASTVOTGIGIAGRI 61  
 QY 71 IGTLPVPAGQVASYSLFILGELWPKGNOWEILFMEHVEE-INOKISTYARNKALTDK 129  
 DB 62 LGVLGVPAGQVASYSLFILGELWPKGNOWEILFMEHVEEINOKISTYARNKALTDK 120  
 QY 130 GLGDALAVYHDSLESVGNRRNTRARSVRSQYIALELMFVQKLPSPAVSGEEVPLPIY 189  
 DB 121 GLGDSFRAVQOSLEDWLENRDARTSVLHTQYIALELDLFLNANPLFAIRQCEVPLLMVY 180  
 QY 190 AQANLHLLLDASIFCKEWGLSSSEISTFYNQVVERAGDYSCHVKWYSTGLNLRGT 249  
 DB 181 AQANLHLLLDASIFCKEWGLSSSEISTFYNQVVERAGDYSCHVKWYSTGLNLRGT 240  
 QY 250 NAESVRYNQFRDWTMLVLDLVALFSDYDTQMPYIKTTAQLTEVYTDALGTVHPHPSP 309  
 DB 241 NAESVRYNQFRDWTMLVLDLVALFSDYDTQMPYIKTTAQLTEVYTDALGTVHPHPSP 309  
 QY 310 TSTTWNNAFSAIEAAVVRNPHLLDFLEQVITYLLSRWSNTQNMNMGHKLERT 369  
 DB 299 ASMNWNNNAFSAIEAAVVRNPHLLDFLEQVITYLLSRWSNTQNMNMGHKLERT 358  
 QY 370 IGTLPVPAGQVASYSLFILGELWPKGNOWEILFMEHVEE-INOKISTYARNKALTDK 427  
 DB 359 IGTLPVPAGQVASYSLFILGELWPKGNOWEILFMEHVEEINOKISTYARNKALTDK 416  
 QY 428 VTHP-----IASDNFYPGYAGIGTQLODSENELPPEATQPNYESYSHRLSHIGLI 482  
 DB 417 -TNPQNISDRGTANYSQP-YESPGQLKXDSSETLPPTTERPNYESYSHRLSHIGLI 474  
 QY 483 HVKALVYSWTHRSADRTNTEIPNSITQPLVKAFLSSGAARVPGFTGDIILRRNTG 542  
 DB 475 RVNVVPIVSWTHRSADRTNTEIPNSITQPLVKAFLSSGAARVPGFTGDIILRRNTG 534  
 QY 543 TFGDIRVNNPPFAQRYVRIRYASTTDLPHTSINGKAINQGNFSAATMRGEDLDYKTF 602  
 DB 535 GFGPIRVVNGPLTQRYRIGFRYASTVDFDFVSRGGTTVNNFRFLRTMNSGDELKYNF 594  
 QY 603 RVVGTTPFSDVQSTTICAWNFSSGNEVYIDRIEFVPEVYEAEDPEKAQEKVTA 662  
 DB 595 VRAFTTPTTQIDTIRTSIQGLSGNGEYVYIDRIEFVPEVYEAEDPEKAQEKVTA 654  
 QY 663 LFTSTNPRGLKTDVKDHYHDQVSNLVESLSDEFYLDKRELFVIVKYANELHIERNM 719

Db 655 LFTNPNRLKTDVTDYHIDQVSNLVACLSDPFCLEKRELLKVKYAKRLSDERNL 711

RESULT 7

US-09-988-462-7

; Sequence 7, Application US/09988462

; Publication No. US20030046726A1

; GENERAL INFORMATION:

; APPLICANT: Koziel, Michael G.

; Desai, Nalini M.

; Lewis, Kelly S.

; Kramer, Vance C.

; Warren, Gregory W.

; Evola, Stephen V.

; Crossland, Lyle D.

; Wright, Martha S.

; Merlin, Ellis J.

; Lavis, Karen L.

; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED

; INSECTICIDAL ACTIVITY IN MAIZE

; NUMBER OF SEQUENCES: 34

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Syngenta Biotechnology, Inc.

; STREET: 3054 Cornwallis Road

; CITY: Research Triangle Park

; STATE: NC

; COUNTRY: USA

; ZIP: 27709

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: IBM PC compatible

; SOFTWARE: Patent in Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/988,462

; FILING DATE: 20-NO. US20030046726A1-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 09/547,422

; FILING DATE: 11-APR-2000

; APPLICATION NUMBER: US 08/459,504

; FILING DATE: 02-JUN-1995

; APPLICATION NUMBER: US 07/951,715

; FILING DATE: 25-SEP-1992

; APPLICATION NUMBER: US 07/772,027

; FILING DATE: 04-OCT-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Weigs, J. Timothy

; REGISTRATION NUMBER: 38,241

; REFERENCE/DOCKET NUMBER: S-188051

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (919)541-8587

; TELEFAX: (919)541-8689

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1207 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 7:

US-09-988-462-7

Query Match 59.5%; Score 2236.5; DB 10; Length 1207;

Best Local Similarity 64.1%; Pred. No. 1.6e-179;

Matches 441; Conservative 76; Mismatches 156; Indels 15; Gaps 7;

Qy 40 EDCLKMSYENVEPVASSTQTGTGAGKILGTGVFPAGQVASLYSFLIGELWPKGN 99

Db 10 EDSLCIAEGNIDFPVASTVGTGNTAGRLGVLGVFPAGQLASFYSFLVIGELWPKGRD 69

Qy 100 QWEILFMHEVBE-INQKISTYARNKALTDLKLGLDALVYHDSLESWVGNNRNTFASVV 158

Db 70 QWEI-FLFHVQLNQITENARNTALARLQGLGDSFRAYQQSLDLEWNRDDARTSVL 128

Qy 159 RSQYIALELMFVQKLPSFAVSGEEVPLPIYAAQANLHLLLRDASIFGKEWGLSSSEIS 218  
 Db 129 YTCYIALELDFLNAMPLFAIRNQEVPLLMVYAAQANLHLLLRDASLFGSEFGLTSQBIQ 188  
 Qy 219 TEVNEOVERAGDYSCHCYKWTSTGLNNLRGTNAESWVYNOFRDRTMLWLDLVALFPSY 278  
 Db 189 RYERQVETRDYSYCVWYNTGLNSLRGTNAESWVYNOFRDRTMLWLDLVALFPSY 248  
 Qy 279 DTQMPYIKTTAQLTREVVYTDAGTVHPHPSFTSTTNNNAPSFSABAAVVRNPHLLDF 338  
 Db 249 DTRTYPINTSAQLTREVVYTDAGT - GVNMAWMNNNAPSFSABAAVVRNPHLLDF 306  
 Qy 339 LEQVTIYSLLSWSNTQYMMNGHKLFRFTIGGLTGLNLSSTGTSNTSINPVTLPTSRDV 398  
 Db 307 LEQLTIFSASSWSNRHTMYRGHTIOSRPIGGLNTSTEGATNTSINPVTLPTSRDV 366  
 Qy 399 YRTESLAGLNF--LTQPVNGVPRVDFEKFVTHP-----IASDNFYYPGVAGICTQLQD 451  
 Db 367 YRTESYAGVLLWGIYLEPIHGVTVRNF--TNQNTSDRGNTANYSQP-YESPGQLKLD 422  
 Qy 452 SENELPPEATGPNYESYSHRSLHGLISASHVKALVYSWTHRSADRTNTEPNSITQIP 511  
 Db 423 SETELPPEATERPNYESYSHRSLH:GILOSRVNVVYSWTHRSADRTNTEPNSITQIP 482  
 Qy 512 LKFAFNLSGAAVVRGPGFTGGDILRRNTGTGDIRVNNINPPFAQRYRVRIRYASTTDL 571  
 Db 483 MVKASELPQGTTVVRGPGFTGGDILRRNTGTGDIRVNVGFLQRYRIRYASTVDF 542  
 Qy 572 QFHTSINGKAINOGNPSATMNGEDLDYKTPRTVGTFTPPFSLDVQSTFTTICAWNFSSGN 631  
 Db 543 DFFVSRGGTGVNFRFLRTMNSGDELKYNFVRRRAFTTPTFTQIQDIIRTSIQLSGNG 602  
 Qy 632 EYVIDRIEFPVPEVYEAEDPEKAEKVTAFTSTNPRGLKTDVKDHYHIDQVSNLVEGL 691  
 Db 603 EVIDKIEIIPVTAIPEAEYDLERAQEAVALFTNINPRLKTDVTHIDQVSNLVAQL 662  
 Qy 692 SDEFVLDEKRELFYVYKANELHIERNM 719  
 Db 663 SDEFCLDEKRELLKVKYAKRLSDERNL 690

RESULT 8

US-10-428-961-63

; Sequence 63, Application US/10428961

; Publication No. US20030237111A1

; GENERAL INFORMATION:

; APPLICANT: Baum, James A.

; APPLICANT: Chu, Chih-Rei

; APPLICANT: Donovan, William P.

; APPLICANT: Gilmer, Amy J.

; APPLICANT: Rupar, Mark J.

; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin

; FILE REFERENCE: MECO201--1

; CURRENT APPLICATION NUMBER: US/10/428,961

; CURRENT FILING DATE: 2003-05-02

; PRIOR APPLICATION NUMBER: 09/661,322

; PRIOR FILING DATE: 2000-09-13

; PRIOR APPLICATION NUMBER: 60/153,995

; PRIOR FILING DATE: 1999-09-15

; NUMBER OF SEQ ID NOS: 63

; SOFTWARE: Patent in version 3.2

; SEQ ID NO 63

; LENGTH: 1227

; TYPE: PRT

; ORGANISM: Bacillus thuringiensis

US-10-428-961-63

Query Match 57.4%; Score 2157.5; DB 14; Length 1227;

Best Local Similarity 59.0%; Pred. No. 7.8e-173;

Matches 422; Conservative 103; Mismatches 175; Indels 15; Gaps 5;

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QY 13 SNAKVDKISTDSLKN-----ETDIELQNIHEDCLMKSEYENVEPVFASTIQTGIG 65
Db 7 NENEINALSIPAVSHSQQMNLSTDAI-----EDSLCIAEGNIDPFVFASTVQTGIN 61
QY 66 IAGKILGTGVFPAGQVASYFLGELWPKGNQWEILFMEHVEE-INQKISTYARNKA 124
Db 62 IAGRILGVLPVFPAGQIASFYSLGELWPRGRDPWEI-FLEHVEHLIRQVVTENTRDTA 120
QY 125 LTDLKGGLDALAVYHDSLESWGNRNNTARVSRVSOYIALELMFVQKLPSFAVSGEVP 184
Db 121 LARLOGLGNFRAYQOSLEDWLENRDRDARTSVLYTQYIALELDFLNAMPLFAIRNQVEP 180
QY 185 LLEPIYAQAANLHLLLRDASIFGKMWGLSSSEISTFYNRQVERAGDYSCHVKWYSTGLN 244
Db 181 LLMVYAQAANLHLLLRDASLFGSEBGLTSQBIQRYRYERQVEKTRREYSDYCARWYNTGLN 240
QY 245 NLRGNTNAESWRYNQFRDMLTVALPVSYDTQMPYIKTTAQLTREYVYDAIGTVH 304
Db 241 NLRGNTNAESWRYNQFRDMLTVALPVSYDTQMPYIKTTAQLTREYVYDAIGTVH 300
QY 305 PHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLRWSNTOYMMNMGHGK 364
Db 301 APGSGFASTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLRWSNTOYMMNMGHGK 360
QY 365 LLEPRITGTLNISTOGSTNTSINPVTLPFTSDRVYRTESLAGNLFLTPQVNGVPRVDFH 424
Db 361 LESRTIRGSLSTWTHGNTNTSINPVTLPFTSDRVYRTESLAGNLFLTPQVNGVPRVDFH 420
QY 425 WKFTVTHPIASDNFYFPGYAGIGTQDSENELPPEATQPNYVESYSHRLSHIGLISASHV 484
Db 421 WENPLNSLRGSLYITIGYTGVTQTFDSETELPPTTERPNYESYSHRLSNIRLISGNTL 480
QY 485 KALVYSWTHRSADRTNTEPNISITQIPLVKAPNLSGGAUVVRGPGFTGCDILRNTNTGTF 544
Db 481 RAPVYSWTHRSADRTNTEPNISITQIPLVKAPNLSGGAUVVRGPGFTGCDILRNTNTGTF 540
QY 545 GDIRVNIINPPFAQRVRYRIRYASTTDLQPHTSINGKAINQGNFSAATNRGDLDYKTRT 604
Db 541 LSGMLFNNTSLQRYRVRVRYAASQTMVLRVTVGSGTTFDQGPSTGWSANESLTSQSFRF 600
QY 605 VGFTTFFSLDQSTFTTIGAMNFFSGNEVYIDRIEFVPEVYTYEAYDFEKAQEKVATLF 664
Db 601 AEFPPVGISASGSQ-TAGISISNNAGRQTFHPDKIEFIPITATFEAYDYLERAQAVNALF 659
QY 665 TSTNPRGLTKDYKHIDQVSNLVESLSDSEFVLDKRELFEIVKYANELHIERNM 719
Db 660 TTNPRRLKLTVDTHIDEVSNLVACLSDSEFCLDEKRELLEKVKYAKRLSDERNL 714

```

## RESULT 9

```

US-09-826-660-23
; Sequence 23, Application US/09826660
; Patent No. US20010026940A1
; GENERAL INFORMATION:
; APPLICANT: Cardineau, Guy A.
; APPLICANT: Stelman, Steven J.
; APPLICANT: Narva, Kenneth E.
; TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins
; CURRENT APPLICATION NUMBER: US/09/826,660
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/178,252
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: 60/065,215
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/076,445
; PRIOR FILING DATE: 1998-03-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 23
; LENGTH: 1186
; TYPE: PRT
; ORGANISM: Artificial Sequence

```

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; FEATURE:
; OTHER INFORMATION: Toxin encoded by synthetic B.t. gene
US-09-826-660-23

```

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Query Match 57.0%; Score 2142.5; DB 9; Length 1186;
Best Local Similarity 58.7%; Pred. No. 1.4e-171;
Matches 420; Conservative 106; Mismatches 174; Indels 15; Gaps 5;

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QY 13 SNAKVDKISTDSLKN-----ETDIELQNIHEDCLMKSEYENVEPVFASTIQTGIG 65
Db 7 NENEINALSIPAVSHSQQMNLSTDAI-----EDSLCIAEGNIDPFVFASTVQTGIN 61
QY 66 IAGKILGTGVFPAGQVASYFLGELWPKGNQWEILFMEHVEE-INQKISTYARNKA 124
Db 62 IAGRILGVLPVFPAGQIASFYSLGELWPRGRDPWEI-FLEHVEHLIRQVVTENTRDTA 120
QY 125 LTDLKGGLDALAVYHDSLESWGNRNNTARVSRVSOYIALELMFVQKLPSFAVSGEVP 184
Db 121 LARLOGLGNFRAYQOSLEDWLENRDRDARTSVLYTQYIALELDFLNAMPLFAIRNQVEP 180
QY 185 LLEPIYAQAANLHLLLRDASIFGKMWGLSSSEISTFYNRQVERAGDYSCHVKWYSTGLN 244
Db 181 LLMVYAQAANLHLLLRDASLFGSEBGLTSQBIQRYRYERQVEKTRREYSDYCARWYNTGLN 240
QY 245 NLRGNTNAESWRYNQFRDMLTVALPVSYDTQMPYIKTTAQLTREYVYDAIGTVH 304
Db 241 NLRGNTNAESWRYNQFRDMLTVALPVSYDTQMPYIKTTAQLTREYVYDAIGTVH 300
QY 305 PHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLRWSNTOYMMNMGHGK 364
Db 301 APGSGFASTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLRWSNTOYMMNMGHGK 360
QY 365 LLEPRITGTLNISTOGSTNTSINPVTLPFTSDRVYRTESLAGNLFLTPQVNGVPRVDFH 424
Db 361 LESRTIRGSLSTWTHGNTNTSINPVTLPFTSDRVYRTESLAGNLFLTPQVNGVPRVDFH 420
QY 425 WKFTVTHPIASDNFYFPGYAGIGTQDSENELPPEATQPNYVESYSHRLSHIGLISASHV 484
Db 421 WENPLNSLRGSLYITIGYTGVTQTFDSETELPPTTERPNYESYSHRLSNIRLISGNTL 480
QY 485 KALVYSWTHRSADRTNTEPNISITQIPLVKAPNLSGGAUVVRGPGFTGCDILRNTNTGTF 544
Db 481 RAPVYSWTHRSADRTNTEPNISITQIPLVKAPNLSGGAUVVRGPGFTGCDILRNTNTGTF 540
QY 545 GDIRVNIINPPFAQRVRYRIRYASTTDLQPHTSINGKAINQGNFSAATNRGDLDYKTRT 604
Db 541 LSGMLFNNTSLQRYRVRVRYAASQTMVLRVTVGSGTTFDQGPSTGWSANESLTSQSFRF 600
QY 605 VGFTTFFSLDQSTFTTIGAMNFFSGNEVYIDRIEFVPEVYTYEAYDFEKAQEKVATLF 664
Db 601 AEFPPVGISASGSQ-TAGISISNNAGRQTFHPDKIEFIPITATFEAYDYLERAQAVNALF 659
QY 665 TSTNPRGLTKDYKHIDQVSNLVESLSDSEFVLDKRELFEIVKYANELHIERNM 719
Db 660 TTSNQITGLTKDVTYHIDRVSNLVESLSDSEFCLDEKRELLEKVKYAKRLSDERNL 714

```

## RESULT 10

```

US-10-428-961-38
; Sequence 38, Application US/10428961
; Publication No. US20030237111A1
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Chu, Chih-Rei
; APPLICANT: Donovan, William P.
; APPLICANT: Gilmer, Amy J.
; APPLICANT: Rupar, Mark J.
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin
; FILE REFERENCE: MECO201-1
; CURRENT APPLICATION NUMBER: US/10/428,961
; CURRENT FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: 09/661,322

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; PRIOR FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: 607/153,995
; PRIOR FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
; LENGTH: 1228
; TYPE: PR1
; ORGANISM: Bacillus thuringiensis
; US-10-428-961-38

Query Match          55.5%; Score 2087; DB 14; Length 1228;
Best Local Similarity 59.2%; Pred. No. 7.2e-167;
Matches 423; Conservative 96; Mismatches 183; Indels 12; Gaps 9;

QY 13 SSNAKVDKISTSLKN-ETDIEIQ-NINHEDCUKMESEYENVEPFFVSASTIQTGTGIAGKI 70
DB 7 NENETINALSIPIAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGINIAGRI 66
QY 71 LGTLGVPPAGOVASLYSFLIGELWPKGKNOWELLFWEHVEE--INOKISFYARNKALTDLK 129
DB 67 LGVLGVPPAGQJAFYAFYFLVGEMLPGRGDQWEI-FLHEVQELINQIETENARNALARLQ 125
QY 130 GLGDALAVYHDSLESWGVGNRRNTRASVVRVSQVIALEMLFVKQLPSFVSGEEVPLPIY 189
DB 126 GLGDSFRAYQQSLBDMLENRDDARTRSVLTYQVIALELDFLNAEPLFAIRNQEVPLLMVY 185
QY 190 AQAAHLHLLLDASIECKEKGSLSSSEISTFYNNROVERAGDYSDCKVKWYSTGLNNLRGT 249
DB 186 AQAAHLHLLLDASLFGSEFGTSGIQIYRYERQVEQTRDSDYCVENYNTGLNSLRGT 245
QY 250 NAE5VRVYNQPRRDMTLMVLDLVALPFSYDTQMP-KTTAQLTREYVYTDALGTVHPHPSF 309
DB 246 NAA5VRVYNQPRRDLTLGLVDLVALPFSYDTRYPINTSAQLTREYVYTDALGT--GVNM 303
QY 310 TSTWYNNNAPSFAIEAAVVRAPHLLDLFLEQVYIISLLSRNSNTQYNMMGCHKLEPRT 369
DB 304 ASMNWYNNNAPSFAIETAVIRSPHLLDLFLEQVITFTSSRMSATRHMTYWRGHTIQSRP 363
QY 370 IGGTLNISTGSGTNTSINPVTLPDTSRDVRYTESLAGLNF--LTOPVNGVPRVDHMKF 427
DB 364 IGGGLNISTHSGTNTSINPVLSPFSDRDVYTESYAGVLLWGLIYLEPHGVPTVRFNFRN 423
QY 428 V--THPIASDNFYYPGAGIGTQLOQSENELPPEATGQPNYESYSHRSLSHIGLSASHVK 485
DB 424 PONTPEERGATNYSQP-YESPGLQLKQSETELPPEETTERPNYESYSHRSLSHIGLSIQRVH 482
QY 486 ALVYSWTHRSADRNTTIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILERTWTGFG 545
DB 483 VPVYSWTHRSADRNTTISSDISITQIPLVKSFLNLSGTSVVSQPGFTGGDIIRTNVNGSVL 542
QY 546 DIRVNNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYKTFRTV 605
DB 543 SMGLNFNNTSLQRYRVRVRYAASQTMVLRVTGGSSTTFDQGFSTMSANESLTSQSPREA 602
QY 606 GETTFPFLDVQSTFTTGAMNPSGNEVYIDRETFVPVEVTYEAEDYDEKAQEKYTALETF 665
DB 603 EPPVGISAGSQ--TAGISINNAGRQTFHFDKIEFIPITATFAEYDLERAQEAVALFT 661
QY 666 SNNPRLKTDVKVDYHIDQVSNLVSDESDFYLDKEKELFEIVKYANLHIERNM 719
DB 662 NTNPRRLKTDVTDYHIDQVSNVLACLSDFCLEKELLEKVKYAKLSDERNL 715

RESULT 11
US-10-614-524-2
; Sequence 2, Application US/10614524
; Publication No. US20040016020A1
; GENERAL INFORMATION:
; APPLICANT: Arnaut, Greta
; APPLICANT: Boets, Annemie
; APPLICANT: Damme, Nicole
; APPLICANT: Mathieu, Eva

```

RESULT 12  
US-09-826-660-25

```

; APPLICANT: Vanneste, Stijn
; APPLICANT: Van Rie, Jeroen
; TITLE OF INVENTION: Insecticidal proteins from Bacillus thuringiensis.
; FILE REFERENCE: NEWTUS2
; CURRENT APPLICATION NUMBER: US/10/614,524
; CURRENT FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: US/09/739,243
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/173387
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1228
; TYPE: PR1
; ORGANISM: Bacillus thuringiensis
; US-10-614-524-2

Query Match          55.5%; Score 2087; DB 15; Length 1228;
Best Local Similarity 59.2%; Pred. No. 7.2e-167;
Matches 423; Conservative 96; Mismatches 183; Indels 12; Gaps 9;

QY 13 SSNAKVDKISTDSLKN-ETDIEIQ-NINHEDCLKMEYENVEFVSASTTQTGIGIAGKI 70
DB 7 NENEINALSIFAVSNHSTQMDLSPARIEDSLCIAEGNNINPLVSASTVQTGINIAGRI 66
QY 71 LGTLGVPPAGQVASLYSFTILGELWPKGKQWEILFMEHVEE-INQKISTVARKNALTDLK 129
DB 67 LGVLGVPPAGQIASFYSLVGLWPRGRDQWEI-FLERVEQLINQQTENARNALTARLQ 125
QY 130 GLGDALAVYHDSLESVMGNRNNTFRASVRSQYIALELMFVQKLPSFAVSGEEVPLPIY 189
DB 126 GLGDSFRAQOQSLIEDWLENRDARTSVLYQTQYIALELDFLNAMPFLAIRNQEVPLLMVY 185
QY 190 AQAAHLHLLLRDASIFGKXEWGLSSSEISFTYNRQVERAGDYSDHCVKVYSTGLNNLRGT 249
DB 186 AQAAHLHLLLRDASLFGSEFGLTQSEIQRYERQVEQTRDSYCVWEYNTGLNSLRGT 245
QY 250 NAEWSRYNQFRDMLTLMVLDLVALPSPDYTMVPIKTTAQLTRREVYTDAGTGVHPHPSF 309
DB 246 NAASWRYNQFRDLTLGLVLDLVALPSPDYTRYPINTSAQLTRREVYTDAGT--GVNM 303
QY 310 TSTTWNNAAPGSAIEAAVVRNPHLLDFLEQVTIYSLLRWSNTQVMNMGHGKLEFR 369
DB 304 ASMNWNNNAAPGSAIEATAVIRSPHLLDFLEQLTIFSTSRWSATRHMTYWRGHTIQSRP 363
QY 370 IGGTLNISTGGSNTSINPVLPFTSRDYRYRTESLAGLNLF--LTQPVNGVPRVDHWF 427
DB 364 IGGTLNSTGGSNTSINPVRLSFFSRDYRYWTESYAGVLLWGVIYLBPIHGVPVTRFNFRN 423
QY 428 V--THPIASDNFYPGYAGIGTQLODSENELPPEATQPNQPNYESYSHRLSHIGLISASHVK 485
DB 424 PQNTFERGNTANYSQP--YESFGPLQKDSPELPEPPTERRPNYESYSHRLSHIGLISQSRVH 482
QY 486 ALVYSWTHRSADPTNIENSITQIPLVKAFNLSSGAAVVRGSGFTGGDLRLRNTCTFG 545
DB 483 VPVYSWTHRSADKNTISSDSITQIPLVKSFNLNSGTSVVGSGFTGGDLIRTNNGSVL 542
QY 546 DIRVNTNPPFAQRYRVRIRYASTDTQPHITSINGKAINQGNFSAATNMRGDLDYKTRTV 605
DB 543 SMGLNFNNTSLQRYRVRVRYAASQTVLVRVTVGGSITFDQGFPSSTYSANESLTSQSFRFA 602
QY 606 GFTPTPSFLDVQSTFTTIGAWNFSSGNEVIDRTEFPVPEVYTYAEYDFEKAQKVTALEFT 665
DB 603 EFPVGISAGSQ--TAGISNTNAGRTFFPKLEIFITATTFEAEYDLERAQEAVALFT 661
QY 666 STNPRGLKTDVQYHIDQVSNLVESLDESDFYLDKRELFEIVKYANELHTRNM 719
DB 662 NTNPRGLKTDVQYHIDQVSNLVACLSDFECLDKRELLEKVYAKRLSDERML 715

```

RESULT 12  
US-09-826-

; Sequence 25, Application US/09826660  
 ; Patent No. US20010026940A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cardineau, Guy A.  
 ; APPLICANT: Steelman, Steven J.  
 ; APPLICANT: Narva, Kenneth E.  
 ; TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins  
 ; FILE REFERENCE: MA-714XC2D1  
 ; CURRENT APPLICATION NUMBER: US/09/826,660  
 ; CURRENT FILING DATE: 2001-04-05  
 ; PRIOR APPLICATION NUMBER: 09/178,252  
 ; PRIOR FILING DATE: 1998-10-23  
 ; PRIOR APPLICATION NUMBER: 60/065,215  
 ; PRIOR FILING DATE: 1997-11-12  
 ; PRIOR APPLICATION NUMBER: 60/076,445  
 ; PRIOR FILING DATE: 1998-03-02  
 ; NUMBER OF SEQ ID NOS: 27  
 ; SOFTWARE: Patentin Ver. 2.0  
 ; SEQ ID NO 25  
 ; LENGTH: 643  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Toxin encoded by synthetic B.t. gene  
 US-09-826-660-25

Query Match 50.8%; Score 1909.5; DB 9; Length 643;  
 Best Local Similarity 57.6%; Pred. No. 2.7e-152;  
 Matches 371; Conservative 99; Mismatches 159; Indels 15; Gaps 5;  
 QY 13 SSNAKVDKISTDSLN-----EPDIELQINHEDCMKSEYENVPFVSASTIQTGIG 65  
 Db 7 NENEIALSPAVNHSAQWNLSTDARI-----EDSLCIAEGNNIDPFVSASTVQTGIN 61  
 QY 66 TAGKILGTLPFAQVACASLYSIFLGLWPKQKQWELFMHVEE-INQKISTYARKA 124  
 Db 62 IAGRILGLVGPFAQIASFSLVGLWLPGRGPWEI-FLHVEQLIRQOVTENTD 120  
 QY 125 LTDLGLGDALAVYHDSLESVGNRNTRARSVRSQVIALELMFVQKLPFAVSGSEVP 184  
 Db 121 LARLOGLNSFRAYQCSLEDLENRDDARTSVLYQTVIALELDFLNPMLFAIRNOEVP 180  
 QY 185 LPIYAQAANLHLLLRDASIFGKEMGLSSSEISTFYNRQVERAGDSDHCWKVYSTGLN 244  
 Db 181 LLWYAQAANLHLLLRDASIFGSEFGLTSQEIQRHYERQVEKREYSDYCARWYNTGLN 240  
 QY 245 NLRGTNABSWRYNQFRDMLMVLVALPSPYDQYKPKTQAUTREVYTDAGTVH 304  
 Db 241 NLRGTNABSWRYNQFRDMLMVLVALPSPYDQYKPKTQAUTREVYTDPIGRTN 300  
 QY 305 PHPSTSTWYNNNAPSATBAEAAVVRPHLLDLEQVITYSLSRWSNTQYNNMWGSHK 364  
 Db 301 APGFASTWYNNNAPSATBAEAAVVRPHLLDPEQLTIFSLSRWSNTQYNNMWGSHK 360  
 QY 365 LEFRTIGTLNISTOGSTNTSINPVLPTFTGRDYRTESLAGNLFLLTPQVNGVPRYDFH 424  
 Db 361 LESRTIRGSLSTSGTNTSINPVLPTFTGRDYRTESLAGNLFLLTPQVNGVPRYDFH 420  
 QY 425 WKFTVHTPASDNFYVPGAGIGTQLOSENELPPEATQPNYSEYSHLSHIGLISASHV 484  
 Db 421 WRNPLNSRGLSLLTYGTGVTGQTLFDSETLPPETTERPNYSEYSHLSHIGLISASHV 480  
 QY 485 KALVYSWTHRSADRNTTIEPNSITQIPLVKAFNLSGGAAVVRGPGFTGGDILRRNTGTG 544  
 Db 481 RAPVYSWTHRSADRNTTIEPNSITQIPLVKAFNLSGGSVVSVPFGFTGGDILRRNVGVS 540  
 QY 545 GDIRVNNPFAQRYRVRIRVASTITDLOFHTSINGKAINQGNFATMNRGEDLDYKTFRT 604  
 Db 541 LSMGLNFNTSLQRYRVRVRAAGQTMVLRVTVGSGSTTFDQGFPTMSANESLTSQSFRF 600  
 QY 605 VGFTTFFSFLDQVSTFTTICANFSGNEVYIDRIEFVPEVYIE 648  
 Db 601 AEFVPGISAGSQ-TAGISISNNAGROTFFHDKIEFIPITATLE 643

RESULT 13  
 US-10-089-678-1  
 ; Sequence 1, Application US/10089678  
 ; Publication No. US20030017967A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ASANO, Shinichiro  
 ; TITLE OF INVENTION: PROTEIN HAVING INSECTICIDAL ACTIVITY, DNA ENCODING THE PROTEIN, A  
 ; TITLE OF INVENTION: NOXIOUS ORGANISM-CONTROLLING AGENT AND METHOD  
 ; FILE REFERENCE: Q68821  
 ; CURRENT APPLICATION NUMBER: US/10/089,678  
 ; CURRENT FILING DATE: 2002-05-02  
 ; PRIOR APPLICATION NUMBER: JP 2000-236140  
 ; PRIOR FILING DATE: 2000-08-03  
 ; PRIOR APPLICATION NUMBER: PCT/JP01/06660  
 ; PRIOR FILING DATE: 2001-08-02  
 ; NUMBER OF SEQ ID NOS: 3  
 ; SOFTWARE: Patentin version 3.1  
 ; SEQ ID NO 1  
 ; LENGTH: 1167  
 ; TYPE: PRT  
 ; ORGANISM: Bacillus thuringiensis  
 US-10-089-678-1

Query Match 45.1%; Score 1694.5; DB 14; Length 1167;  
 Best Local Similarity 47.7%; Pred. No. 1.1e-133;  
 Matches 360; Conservative 125; Mismatches 219; Indels 51; Gaps 14;  
 QY 1 MKLNQDKHQ---SPSSNAKVDKISTDSLNKNETDIELQINHEDCMKSEYE-----NV 51  
 Db 1 MSPNNQVEIILDASSTSVSDNSVRYPLANDQTTTLQWNYKDYLRMSEGENPELFGNP 60  
 QY 52 EPFVSASTIQTGIGTAGKILGTLPFAQVACASLYSIFLGLWPKQKQWELFMHVEE 110  
 Db 61 ETPSSSTVQTGIGTAGKILGTLPFAQVACASLYSIFLGLWPKQKQWELFMHVEE 119  
 QY 111 E-INOKISTYARKAALTDLKGIDALAVYHDSLESVGNRNTRARSVRSQVIALELMF 169  
 Db 120 DLIDQKITSVKRTALAGLQGGDGLDVYQKSKWLENRNDTRARSVVVYQIALELDF 179  
 QY 170 VOKLPFAVSGSEVEPLPIYAQAANLHLLLRDASIFGKEMGLSSSEISTFYNRQVERAG 229  
 Db 180 VAKIPSAISGQEVPLLSVYAQAANLHLLLRDASIFGAEWGFTGCEISTFYDRQVTRTA 239  
 QY 230 DYSDHCWKVYSTGLNLRGTNABSWRYNQFRDMLMVLVALPSPYDQYKPKTQAUTREVYTDAGTVH 289  
 Db 240 QYSDYCVKRYNTGLDKLKGITNAASWLKYHQFRENTHLLVLDLVALFPNYDRTYPIETTA 299  
 QY 290 QLTREVYTDAGTVHVPHPSPFTSTWYNNNAPSATBAEAAVVRPHLLDLEQVITYSLLS 349  
 Db 300 QLTREVYTDPIVNRNRETSGFCRRWSLNSDISFSEVESAVIRSPHLDLSIEIFYTTTRA 359  
 QY 350 --RWSNTQNMNMGWGHKLEBFTIGTGLNISTOGSTNTSINPVLPTFTGRDYRTESLAGNLFLLTPQVNGVPRYDFH 406  
 Db 360 GLPLANTTELEYWVGHSHIKYKNTNASSALERNYGTITSNKIKYDLANKDKDFQVASLGAD 419  
 QY 407 LNLFLTQPVNGVPRYDFHVKFVTHPIASDNFYVPGAGIG-----TQLQDS 452  
 Db 420 LANYAQ-VYGVYASV-----TLDDKN---TGSGVGGFTYSPKHTTMQVCTQNTYNT 468  
 QY 453 ENELPPEATQPNYSEYSHLSHIGLIS-----ASHVKALVYVSWTHRSADRNTTIEP 504  
 Db 469 IDEIPPE--NEPLSGYSHRLSHITSYSFSKNASSPARYGNLPVPAWTHRSADVNTYVS 526  
 QY 505 NSITQIPLVKAFNLSGGAAVVRGPGFTGGDILRRNTGTGDIRVNNPFAQRYRVRIR 564  
 Db 527 DKITQIPVWKAHTLVSGTIVKPGFTGGLNLRKTSGLFAYTSVSKVSPLSQRVRAIR 586  
 QY 565 YASTTDLOFHTSINGKAINQGNFATMNRGEDLDYKTFRTVGFTTFFSFLDQVSTFTTICA 624  
 Db 587 YASTTNLRFLVTISGTRIYSINVNKTMKGGDLTENTFDLATIGTFTAFSTFSDSLTYGA 646



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QY 395 SRDVYRTESLAGLNLFLTPQVNGVPRVDFHWKVFTHPIASDNFY-----YPGYAGICTQL 449
Db 407 DRDIFEINSTVANLANYYQKAYGVPGSWFH--WVKRGTSSTAYLYSKTHLTALQGC-TQV 463
QY 450 QDSENELPEATGQPNYESYSHRLSHI-----GLISASHVKALYVSWTHRSADRNT 501
Db 464 YESDEIEPLDRT-VPVAESYSHRLSHITSHSFKNG--SAYYGSFPVFWVWTHSADLNT 520
QY 502 IEPNSITQIPLVKAENLSSGAAVRPGPGFTGGDILRRNTMTGDIRVNIINPPPAQRYRV 561
Db 521 IYSDKITQIPAVKGMILGGSVVGPGFTGGDILKRTPNPSILGTFEAVTVNGSLSQRYRV 580
QY 562 RIRYASTDLOPHTSINGKAINQGNFSATMARGEDLDYKTRTVGFTTPPSFLDVQSTFT 621
Db 581 RIRYASTTDFEP-TLYLGDITIEKNRFTKMDNGASLTVEYEFKFAFITDFQFRETQDKIL 639
QY 622 IGAWNFSNGNEVYIDRIEFPVVEVTEAEYDFEKAQEKVLTFTSTNPRGLKTDVKDYHI 681
Db 640 LSMGDFSSGQEVYIDRIEFPVDETYEAEQDLEAKKAVNALFTNTKD-GLRPGVTIYEV 698
QY 682 DQVSNLVESSLDEPYLDEKRELFIEIVKYANELHIERNM 719
Db 699 NQAANLVECLSDLLYPNEKRLIFDAVREAKRLSGARNL 736

```

Search completed: October 28, 2004, 18:41:10  
Job time : 68.6795 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 28, 2004, 17:51:02 ; Search time 86.903 Seconds  
(without alignments)  
2975.262 Million cell updates/sec

Title: US-10-019-823B-58

Perfect score: 3761

Sequence: 1 MLLKNQDKHQSFSSNAKVDK.....KRELFEIVKYANLHIERNM 719

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:\*  
1: Geneseqp1980s:\*  
2: Geneseqp1990s:\*  
3: Geneseqp2000s:\*  
4: Geneseqp2001s:\*  
5: Geneseqp2002s:\*  
6: Geneseqp2003as:\*  
7: Geneseqp2003bs:\*  
8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3736	99.3	719	4	AAB66911 Insectici
2	3736	99.3	719	6	AAE36275 B. thurin
3	3724	99.0	719	4	AAB66908 Insectici
4	3724	99.0	719	4	AAB66909 Insectici
5	3724	99.0	719	6	AAE36273 B. thurin
6	3724	99.0	719	6	AAE36272 B. thurin
7	3720	98.9	719	4	AAB66910 Insectici
8	3720	98.9	719	6	AAE36274 B. thurin
9	3715	98.8	719	4	AAU02095 Bacillus
10	3703	98.5	719	2	AAE36271 B. thurin
11	3692.5	98.2	718	6	AAE36271 B. thurin
12	3686.5	98.0	718	4	AAB66907 Insectici
13	3517	93.5	719	7	ADM74717 B. thurin
14	3484	92.6	719	4	AAB66912 Insectici
15	3484	92.6	719	6	AAE36276 B. thurin
16	3442.5	91.5	710	4	AAU02041 B. thurin
17	3363	89.4	719	3	AAW49089 Bacillus
18	3341	88.8	719	2	AAW49089 Bacillus
19	3257	86.6	1217	4	AAU02092 Bacillus
20	2705	71.9	1208	4	AAU02093 Bacillus
21	2419	64.3	1230	8	ADK98484 B. thurin
22	2419	64.3	1230	8	ADK98489 B. thurin
23	2419	64.3	1230	8	ADK98481 B. thurin
24	2419	64.3	1230	8	ADK98491 B. thurin
25	2419	64.3	1230	8	ADK98487 B. thurin

AAE54074 CryET5. 2  
AAW35259 Bacillus  
AAW17699 CryET5. 3  
AAW87633 CryET5 pr  
AAV30923 B. thurin  
ADK98479 B. thurin  
AAW44322 Bacillus  
AAB19947 Bacillus  
AAU02094 Bacillus  
AAU02094 Bacillus  
AAV31990 Chimeric  
AAW44321 Bacillus  
AAB19950 Bacillus  
AAU02046 B. thurin  
AAV16796 Amino aci  
AAU00421 B. thurin  
AAU00420 B. thurin  
AAB84628 Amino aci  
AAU02039 B. thurin  
AAV16797 Amino aci

#### ALIGNMENTS

RESULT 1  
AAB66911  
ID AAB66911 standard; protein; 719 AA.  
XX  
AC AAB66911;  
XX  
DT 12-APR-2001 (first entry)  
XX  
DE Insecticidal protein cryIIa5.  
XX  
XX Insecticide; transgenic plant; insect-resistance.  
XX  
OS Paecilomyces sp.  
XX  
PN WC200100841-A1.  
XX  
PD 04-JAN-2001.  
XX  
PF 23-JUN-2000; 2000WO-GB002457.  
XX  
PR 29-JUN-1999; 99GB-00015215.  
PR 23-DEC-1999; 99GB-00030536.  
XX  
PA (ZENE ) ZENECA LTD.  
XX  
PI Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;  
PI Vincent JL, Lee MD;  
XX  
DR WPI; 2001-123015/13.  
XX  
PT Novel insecticidal protein obtained from species of Paecilomyces for  
PT controlling insects, and for insect-resistant transgenic plant  
PT production.  
XX  
PS Claim 14; Page 62-64; 72pp; English.  
XX  
CC The present invention relates to novel insecticidal proteins obtained  
CC from Paecilomyces sp. (see AAB6699 to AAB66901 and AAB66913). The  
CC insecticidal proteins can be used to produce transgenic plants, which are  
CC insect-resistant. Also, the insecticidal proteins are useful for  
CC controlling insects by providing them at a locus where insects feed  
XX  
SQ Sequence 719 AA;

Query Match 99.3%; Score 3736; DB 4; Length 719;  
Best Local Similarity 99.7%; Pred. No. 1.1e-291;  
Matches 718; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

QY 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHNEDCLKSEYENVEPVSASTI 60  
 Db 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHNEDCLKSEYENVEPVSASTI 60  
 QY 61 QTGIGIAGKIILGTGVPFAGQVASYLSFILGELPKGNQKQWEI--PMEHVEE--INQKISTY 119  
 Db 61 QTGIGIAGKIILGTGVPFAGQVASYLSFILGELPKGNQKQWEI--PMEHVEE--INQKISTY 119  
 QY 120 ARNKALTDLKLGDALAVYHDSLESWGNRNNTARSVVRQYIALBELMFVKQLPSFAVS 179  
 Db 120 ARNKALTDLKLGDALAVYHDSLESWGNRNNTARSVVRQYIALBELMFVKQLPSFAVS 179  
 QY 180 GBEVPLLPYIAQAANLHLLLRDASIFGKENGWGLSSSEISTFYNQVERAGDYSCHVKWY 239  
 Db 180 GBEVPLLPYIAQAANLHLLLRDASIFGKENGWGLSSSEISTFYNQVERAGDYSCHVKWY 239  
 QY 240 STGLNLRGTNAESWVRYNQFRDMTLMVLDLVALFPSYDTQMPYIKTTAQLTREVTDA 299  
 Db 240 STGLNLRGTNAESWVRYNQFRDMTLMVLDLVALFPSYDTQMPYIKTTAQLTREVTDA 299  
 QY 300 IGTVPHPSPFTSTWYNNAPSFSAIEAAVVRNPHLLDFEQVTIYSLSEWSNTQYNNM 359  
 Db 300 IGTVPHPSPFTSTWYNNAPSFSAIEAAVVRNPHLLDFEQVTIYSLSEWSNTQYNNM 359  
 QY 360 WGGHKLFRFTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFLTQPVNGVP 419  
 Db 360 WGGHKLFRFTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFLTQPVNGVP 419  
 QY 420 RVDFWKVFTHPIASDNFYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLI 479  
 Db 420 RVDFWKVFTHPIASDNFYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLI 479  
 QY 480 SASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRT 539  
 Db 480 SASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRT 539  
 QY 540 NTGTGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDDLY 599  
 Db 540 NTGTGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDDLY 599  
 QY 600 KTRFTVGTFTPSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEK 659  
 Db 600 KTRFTVGTFTPSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEK 659  
 QY 660 VTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDFYLDKRELFEIVKYANELHIERNM 719  
 Db 660 VTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDFYLDKRELFEIVKYANELHIERNM 719

RESULT 2  
 AAE36275  
 ID AAE36275 standard; protein; 719 AA.

XX AAE36275;

XX AAE36275;

DT 26-JUN-2003 (first entry)

DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa5.

XX Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.

XX Bacillus thuringiensis.

XX WO200298911-A2.

XX 12-DEC-2002.

XX 30-MAY-2002; 2002WO-GB002666.

XX 07-JUN-2001; 2001GB-00013900.

XX (SYGN ) SYNGENTA LTD.

PI Vincent JL, Viner R;  
 XX WPI; 2003-175137/17.  
 XX New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.  
 PT  
 PT  
 XX  
 XX Claim 12; Page 53-56; 67pp; English.  
 XX The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects.  
 CC Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is  
 CC Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention  
 CC  
 XX Sequence 719 AA;

Query Match 99.3%; Score 3736; DB 6; Length 719;  
 Best Local Similarity 99.7%; Pred. No. 1.1e-291;  
 Matches 718; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

QY 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHNEDCLKSEYENVEPVSASTI 60  
 Db 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHNEDCLKSEYENVEPVSASTI 60  
 QY 61 QTGIGIAGKIILGTGVPFAGQVASYLSFILGELPKGNQKQWEI--PMEHVEE--INQKISTY 119  
 Db 61 QTGIGIAGKIILGTGVPFAGQVASYLSFILGELPKGNQKQWEI--PMEHVEE--INQKISTY 119  
 QY 120 ARNKALTDLKLGDALAVYHDSLESWGNRNNTARSVVRQYIALBELMFVKQLPSFAVS 179  
 Db 120 ARNKALTDLKLGDALAVYHDSLESWGNRNNTARSVVRQYIALBELMFVKQLPSFAVS 179  
 QY 180 GBEVPLLPYIAQAANLHLLLRDASIFGKENGWGLSSSEISTFYNQVERAGDYSCHVKWY 239  
 Db 180 GBEVPLLPYIAQAANLHLLLRDASIFGKENGWGLSSSEISTFYNQVERAGDYSCHVKWY 239  
 QY 240 STGLNLRGTNAESWVRYNQFRDMTLMVLDLVALFPSYDTQMPYIKTTAQLTREVTDA 299  
 Db 240 STGLNLRGTNAESWVRYNQFRDMTLMVLDLVALFPSYDTQMPYIKTTAQLTREVTDA 299  
 QY 300 IGTVPHPSPFTSTWYNNAPSFSAIEAAVVRNPHLLDFEQVTIYSLSEWSNTQYNNM 359  
 Db 300 IGTVPHPSPFTSTWYNNAPSFSAIEAAVVRNPHLLDFEQVTIYSLSEWSNTQYNNM 359  
 QY 360 WGGHKLFRFTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFLTQPVNGVP 419  
 Db 360 WGGHKLFRFTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFLTQPVNGVP 419  
 QY 420 RVDFWKVFTHPIASDNFYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLI 479  
 Db 420 RVDFWKVFTHPIASDNFYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLI 479  
 QY 480 SASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRT 539  
 Db 480 SASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRT 539  
 QY 540 NTGTGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDDLY 599  
 Db 540 NTGTGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDDLY 599  
 QY 600 KTRFTVGTFTPSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEK 659  
 Db 600 KTRFTVGTFTPSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEK 659  
 QY 660 VTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDFYLDKRELFEIVKYANELHIERNM 719  
 Db 660 VTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDFYLDKRELFEIVKYANELHIERNM 719

RESULT 3  
 ID AAB66908 standard; protein; 719 AA.  
 XX AC AAB66908;  
 XX DT 12-APR-2001 (first entry)  
 XX DE Insecticidal protein cryIIa2.  
 XX KW Insecticide; transgenic plant; insect-resistance.  
 XX OS Paecilomyces sp.  
 XX FN WO200100841-A1.  
 XX PD 04-JAN-2001.  
 XX PF 23-JUN-2000; 2000WO-GB002457.  
 XX PR 29-JUN-1999; 99GB-00015215.  
 XX PR 23-DEC-1999; 99GB-00030536.  
 XX PA (ZENE ) ZENECA LTD.  
 XX PI Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;  
 XX PI Vincent JL, Lee MD;  
 XX DR WPI; 2001-123015/13.  
 XX PT Novel insecticidal protein obtained from species of Paecilomyces for  
 XX PT controlling insects, and for insect-resistant transgenic plant  
 XX PS production.  
 XX PS Claim 14; Page 55-57; 72pp; English.  
 XX CC The present invention relates to novel insecticidal proteins obtained  
 XX CC from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The  
 XX CC insecticidal proteins can be used to produce transgenic plants, which are  
 XX CC insect-resistant. Also, the insecticidal proteins are useful for  
 XX CC controlling insects by providing them at a locus where insects feed  
 XX SQ Sequence 719 AA;  
 Query Match 99.0%; Score 3724; DB 4; Length 719;  
 Best Local Similarity 99.3%; Pred. No. 1e-290;  
 Matches 715; Conservative 2; Mismatches 1; Indels 2; Gaps 2;  
 QY 1 MCLKNQDKHQFSSNAKVDKISTDSLKNETDIELQINNHEDCLKMSYENVEPVSASTI 60  
 DB 1 MCLKNQDKHQFSSNAKVDKISTDSLKNETDIELQINNHEDCLKMSYENVEPVSASTI 60  
 QY 61 QTGIGIAGKILGTGVPAGQVASYLSPILGELMPKGNQWEILFMEHVTEE-INQKISTY 119  
 DB 61 QTGIGIAGKILGTGVPAGQVASYLSPILGELMPKGNQWEI-FMEHVTEEINQKISTY 119  
 QY 120 ARNKALTDKLGIDALAVYHDSLSWGNRNTARSVRSQYIALEIMFVKQLPSPAVS 179  
 DB 120 ARNKALTDKLGIDALAVYHDSLSWGNRNTARSVRSQYIALEIMFVKQLPSPAVS 179  
 QY 180 GEEVPLLPFYAQAANLHLLLRDASIFGKWLGLSSSEISTFYNNQVERAGDYSCHVKWY 239  
 DB 180 GEEVPLLPFYAQAANLHLLLRDASIFGKWLGLSSSEISTFYNNQVERAGDYSCHVKWY 239  
 QY 240 STGLNLLGTTVAESVRNQFRDMLMVLDLVALFPSYDTQMPYPIKTAQLTREVYVTA 299  
 DB 240 STGLNLLGTTVAESVRNQFRDMLMVLDLVALFPSYDTQMPYPIKTAQLTREVYVTA 299  
 QY 300 IGTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMMN 359  
 DB 300 IGTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMMN 359

QY 360 WGHKLEPRTIGTGLNISTQGSTNTSINPVTLPFTSRDYRTESLAGLNLFLTQPVNGVP 419  
 DB 360 WGHKLEPRTIGTGLNISTQGSTNTSINPVTLPFTSRDYRTESLAGLNLFLTQPVNGVP 419  
 QY 420 RVDFFHWKFVTHPIASDNFYYPGYAGIGTQLOQSENELPPEATGQPNYESYSHRLSHIGLI 479  
 DB 420 RVDFFHWKFVTHPIASDNFYYPGYAGIGTQLOQSENELPPEATGQPNYESYSHRLSHIGLI 479  
 QY 480 SASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSGAAVVRGFGFTGGDILRRT 539  
 DB 480 SASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSGAAVVRGFGFTGGDILRRT 539  
 QY 540 NTGTFGDIRVINPFPFAQYRVRIYASTDLOFTHSINGKAINQGNFSATWNRGDDLDY 599  
 DB 540 NTGTFGDIRVINPFPFAQYRVRIYASTDLOFTHSINGKAINQGNFSATWNRGDDLDY 599  
 QY 600 KTFRTVGTTPPSFLDVQSTFTIGAWNPFSSGNEVIDRIEFVPEVTVYEAEDYDFFKAQEK 659  
 DB 600 KTFRTVGTTPPSFLDVQSTFTIGAWNPFSSGNEVIDRIEFVPEVTVYEAEDYDFFKAQEK 659  
 QY 660 VTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKEKELFEIVKYAKQLHIERNN 719  
 DB 660 VTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKEKELFEIVKYAKQLHIERNN 719  
 RESULT 4  
 AAB66909  
 ID AAB66909 standard; protein; 719 AA.  
 XX AC AAB66909;  
 XX DT 12-APR-2001 (first entry)  
 XX DE Insecticidal protein cryIIa3.  
 XX KW Insecticide; transgenic plant; insect-resistance.  
 XX OS Paecilomyces sp.  
 XX FN WO200100841-A1.  
 XX PD 04-JAN-2001.  
 XX PF 23-JUN-2000; 2000WO-GB002457.  
 XX PR 29-JUN-1999; 99GB-00015215.  
 XX PR 23-DEC-1999; 99GB-00030536.  
 XX PA (ZENE ) ZENECA LTD.  
 XX PI Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;  
 XX PI Vincent JL, Lee MD;  
 XX DR WPI; 2001-123015/13.  
 XX PT Novel insecticidal protein obtained from species of Paecilomyces for  
 XX PT controlling insects, and for insect-resistant transgenic plant  
 XX PS production.  
 XX PS Claim 14; Page 57-59; 72pp; English.  
 XX CC The present invention relates to novel insecticidal proteins obtained  
 XX CC from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The  
 XX CC insecticidal proteins can be used to produce transgenic plants, which are  
 XX CC insect-resistant. Also, the insecticidal proteins are useful for  
 XX CC controlling insects by providing them at a locus where insects feed  
 XX SQ Sequence 719 AA;  
 Query Match 99.0%; Score 3724; DB 4; Length 719;  
 Best Local Similarity 99.4%; Pred. No. 1e-290;  
 Matches 716; Conservative 1; Mismatches 1; Indels 2; Gaps 2;

QY 1 MCLKNQDKHQSFSNAKVDKISTDSLKNETDIELQNHEDCLKMSYENVEPVSASTI 60  
 Db 1 MCLKNQDKHQSFSNAKVDKISTDSLKNETDIELQNHEDCLKMSYENVEPVSASTI 60  
 QY 61 QTGIGIAGKILGTLGVPFAGQVASYLSFILGELWPKGNQWEILFMEHVEE-INQKISTY 119  
 Db 61 QTGIGIAGKILGTLGVPFAGQVASYLSFILGELWPKGNQWEILFMEHVEE-INQKISTY 119  
 QY 120 ARNKALTDLKGGLDALAVYHDSLEWGNRNTRARSVVRVSOYIALELMFVKQLPSFAVS 179  
 Db 120 ARNKALTDLKGGLDALAVYHDSLEWGNRNTRARSVVRVSOYIALELMFVKQLPSFAVS 179  
 QY 180 GEEVPLPIYAQAANLHLLLDASIFGKEMGLSSEISTFYNRQVERAGYSYHCVKMY 239  
 Db 180 GEEVPLPIYAQAANLHLLLDASIFGKEMGLSSEISTFYNRQVERAGYSYHCVKMY 239  
 QY 240 STGLNLRGTNAESWVRVYQNRDRTMLVLDLVALFPSSYDTQMPYIKTTAQLTREVTDA 299  
 Db 240 STGLNLRGTNAESWVRVYQNRDRTMLVLDLVALFPSSYDTQMPYIKTTAQLTREVTDA 299  
 QY 300 ICTVHPHPSFTTWTWNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMM 359  
 Db 300 ICTVHPHPSFTTWTWNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMM 359  
 QY 360 WGGHKLFPRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRYSYTESLAGLNLFTQPVNGVP 419  
 Db 360 WGGHKLFPRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRYSYTESLAGLNLFTQPVNGVP 419  
 QY 420 RVDFFHWKFWTHPIASDNFYPCYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLI 479  
 Db 420 RVDFFHWKFWTHPIASDNFYPCYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLI 479  
 QY 480 SASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRT 539  
 Db 480 SASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRT 539  
 QY 540 NTGTFGDIRVNIINPPFAQRYRIRYASTTDLQPHTSINGKAINQGNFSATMNGEDLDY 599  
 Db 540 NTGTFGDIRVNIINPPFAQRYRIRYASTTDLQPHTSINGKAINQGNFSATMNGEDLDY 599  
 QY 600 KTFRTVGTFTTSPFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEK 659  
 Db 600 KTFRTVGTFTTSPFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEK 659  
 QY 660 VTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDBFYLDKRELFEIVKYANELHIERNM 719  
 Db 660 VTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDBFYLDKRELFEIVKYANELHIERNM 719

RESULT 5

AAE36273  
 ID AAE36273 standard; protein; 719 AA.  
 XX AAE36273;  
 AC AAE36273;  
 XX 26-JUN-2003 (first entry)  
 DT 26-JUN-2003 (first entry)  
 DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa3.  
 KW Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.  
 OS Bacillus thuringiensis.  
 XX WC200298911-A2.  
 PN WC200298911-A2.  
 PD 12-DEC-2002.  
 XX 30-MAY-2002; 2002WO-GB002666.  
 PF 07-JUN-2001; 2001GB-00013900.  
 XX (SYGN ) SYNGENTA LTD.  
 XX

PI Vincent JL, Viner R;  
 XX WPI; 2003-175137/17.  
 XX New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.  
 PT Claim 12; Page 47-50; 67pp; English.  
 XX The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects.  
 CC Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is CC Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This CC sequence is used in the invention  
 XX Sequence 719 AA;  
 SQ

Query Match 99.0%; Score 3724; DB 6; Length 719;  
 Best Local Similarity 99.4%; Pred. No. 1e-290;  
 Matches 716; Conservative 1; Mismatches 1; Indels 2; Gaps 2;

QY 1 MCLKNQDKHQSFSNAKVDKISTDSLKNETDIELQNHEDCLKMSYENVEPVSASTI 60  
 Db 1 MCLKNQDKHQSFSNAKVDKISTDSLKNETDIELQNHEDCLKMSYENVEPVSASTI 60  
 QY 61 QTGIGIAGKILGTLGVPFAGQVASYLSFILGELWPKGNQWEILFMEHVEE-INQKISTY 119  
 Db 61 QTGIGIAGKILGTLGVPFAGQVASYLSFILGELWPKGNQWEILFMEHVEE-INQKISTY 119  
 QY 120 ARNKALTDLKGGLDALAVYHDSLEWGNRNTRARSVVRVSOYIALELMFVKQLPSFAVS 179  
 Db 120 ARNKALTDLKGGLDALAVYHDSLEWGNRNTRARSVVRVSOYIALELMFVKQLPSFAVS 179  
 QY 180 GEEVPLPIYAQAANLHLLLDASIFGKEMGLSSEISTFYNRQVERAGYSYHCVKMY 239  
 Db 180 GEEVPLPIYAQAANLHLLLDASIFGKEMGLSSEISTFYNRQVERAGYSYHCVKMY 239  
 QY 240 STGLNLRGTNAESWVRVYQNRDRTMLVLDLVALFPSSYDTQMPYIKTTAQLTREVTDA 299  
 Db 240 STGLNLRGTNAESWVRVYQNRDRTMLVLDLVALFPSSYDTQMPYIKTTAQLTREVTDA 299  
 QY 300 ICTVHPHPSFTTWTWNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMM 359  
 Db 300 ICTVHPHPSFTTWTWNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMM 359  
 QY 360 WGGHKLFPRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRYSYTESLAGLNLFTQPVNGVP 419  
 Db 360 WGGHKLFPRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRYSYTESLAGLNLFTQPVNGVP 419  
 QY 420 RVDFFHWKFWTHPIASDNFYPCYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLI 479  
 Db 420 RVDFFHWKFWTHPIASDNFYPCYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLI 479  
 QY 480 SASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRT 539  
 Db 480 SASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRT 539  
 QY 540 NTGTFGDIRVNIINPPFAQRYRIRYASTTDLQPHTSINGKAINQGNFSATMNGEDLDY 599  
 Db 540 NTGTFGDIRVNIINPPFAQRYRIRYASTTDLQPHTSINGKAINQGNFSATMNGEDLDY 599  
 QY 600 KTFRTVGTFTTSPFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEK 659  
 Db 600 KTFRTVGTFTTSPFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEK 659  
 QY 660 VTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDBFYLDKRELFEIVKYANELHIERNM 719  
 Db 660 VTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDBFYLDKRELFEIVKYANELHIERNM 719

```

RESULT 6
AAE36272
ID AAE36272 standard; protein; 719 AA.
XX
AC AAE36272;
XX
DT 26-JUN-2003 (first entry)
XX
DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa2.
XX
KW Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.
XX
OS Bacillus thuringiensis.
XX
FN WO200298911-A2.
XX
PD 12-DEC-2002.
XX
PF 30-MAY-2002; 2002WO-GB002666.
XX
PR 07-JUN-2001; 2001GB-00013900.
XX
PA (SYGN ). SYNGENTA LTD.
XX
PI Vincent JL, Viner R;
XX
WPI; 2003-175137/17.
XX
New insecticidal protein comprising an X-glycine motif at the amino-
terminus, useful as an active ingredient of a pesticide.
XX
Claim 12; Page 44-47; 67pp; English.
XX
The invention relates to insecticidal protein comprising an X-glycine
motif at the amino-terminus. Polynucleotide or DNA constructs of the
invention are useful for producing plants or plant parts that are
resistant to insects. The protein or synergistic combination is useful as
an active ingredient of a pesticide or for controlling insects.
Antibodies raised to the insecticidal proteins can be used to identify
other proteins with insecticidal activity. The present sequence is
Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This
sequence is used in the invention
XX
Sequence 719 AA;
XX
Query Match 99.0%; Score 3724; DB 6; Length 719;
Best Local Similarity 99.3%; Pred. No. 1e-290;
Matches 715; Conservative 2; Mismatches 1; Indels 2; Gaps 2;
QY 1 MKLXQDKHQSFSSNAKVDKISTDSLKNETDIELQNIHEDCLKMSYENVEPVSASTI 60
DB 1 MKLXQDKHQSFSSNAKVDKISTDSLKNETDIELQNIHEDCLKMSYENVEPVSASTI 60
QY 61 QTGIGIAGKILGTGVPPAGOVASLYSFLIGELMPKGNOWEILFMEHVEE-INOKISTY 119
DB 61 QTGIGIAGKILGTGVPPAGOVASLYSFLIGELMPKGNOWEILFMEHVEEINOKISTY 119
QY 120 ARNKALTDKLGDALAVYHDSLSWSWGNRNNTARSVRSQYIALELMFVQKLPSFAVS 179
DB 120 ARNKALTDKLGDALAVYHDSLSWSWGNRNNTARSVRSQYIALELMFVQKLPSFAVS 179
QY 180 GEEVPLPIYAQAANLHLLLRDASIFGKENGSLSSSEISFYNNQVRAGDYSDHCVKWY 239
DB 180 GEEVPLPIYAQAANLHLLLRDASIFGKENGSLSSSEISFYNNQVRAGDYSDHCVKWY 239
QY 240 STGLNNLRGTNAESWRYNQPRRDWTLMLVDLVALFPSTYQMPYPIKTTAQLREVYVDA 299
DB 240 STGLNNLRGTNAESWRYNQPRRDWTLMLVDLVALFPSTYQMPYPIKTTAQLREVYVDA 299
QY 300 IGTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLRWSNTQMMN 359
DB 300 IGTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLRWSNTQMMN 359

RESULT 7
AAE66910
ID AAE66910 standard; protein; 719 AA.
XX
AC AAE66910;
XX
DT 12-APR-2001 (first entry)
XX
DE Insecticidal protein cryIIa4.
XX
KW Insecticide; transgenic plant; insect-resistance.
XX
OS Paecilomyces sp.
XX
PN WO200100841-A1.
XX
PD 04-JAN-2001.
XX
XX
23-JUN-2000; 2000WO-GB002457.
XX
29-JUN-1999; 99GB-00015215.
XX
23-DEC-1999; 99GB-00030536.
XX
(ZENE ) ZENECA LTD.
XX
Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;
PI Vincent JL, Lee MD;
XX
WPI; 2001-123015/13.
XX
Novel insecticidal protein obtained from species of Paecilomyces for
controlling insects, and for insect-resistant transgenic plant
production.
XX
Claim 14; Page 60-62; 72pp; English.
XX
The present invention relates to novel insecticidal proteins obtained
from Paecilomyces sp. (see AAE66910 to AAE66901 and AAE66913). The
insecticidal proteins can be used to produce transgenic plants, which are
insect-resistant. Also, the insecticidal proteins are useful for
controlling insects by providing them at a locus where insects feed
XX
Sequence 719 AA;
XX
Query Match 98.9%; Score 3720; DB 4; Length 719;
Best Local Similarity 99.2%; Pred. No. 2.2e-290;
Matches 714; Conservative 2; Mismatches 2; Indels 2; Gaps 2;
QY 360 WGGHKLFPFTICGTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGNLFLTQPVNGVP 419
DB 360 WGGHKLFPFTICGTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGNLFLTQPVNGVP 419
QY 420 RYDEHKKFVTHPIASDNFYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLI 479
DB 420 RYDEHKKFVTHPIASDNFYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLI 479
QY 480 SASHKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRT 539
DB 480 SASHKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRT 539
QY 540 NTGTGDIRVNINPBPFAQRYRVRIRYASTDLOFHTSINGKAINOGNFSATNWRGEDLDY 599
DB 540 NTGTGDIRVNINPBPFAQRYRVRIRYASTDLOFHTSINGKAINOGNFSATNWRGEDLDY 599
QY 600 KTFRTVGTFTTSPFLDVQSTFTTIGAWNFSSGNEVVIDRIEFVPEVTVYEAAYDFEKAQEK 659
DB 600 KTFRTVGTFTTSPFLDVQSTFTTIGAWNFSSGNEVVIDRIEFVPEVTVYEAAYDFEKAQEK 659
QY 660 VTALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDFYLDKRELFYKYANELHIERNM 719
DB 660 VTALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDFYLDKRELFYKYAKQLHIERNM 719

AAE66910
ID AAE66910 standard; protein; 719 AA.
XX
AC AAE66910;
XX
DT 12-APR-2001 (first entry)
XX
DE Insecticidal protein cryIIa4.
XX
KW Insecticide; transgenic plant; insect-resistance.
XX
OS Paecilomyces sp.
XX
PN WO200100841-A1.
XX
PD 04-JAN-2001.
XX
XX
23-JUN-2000; 2000WO-GB002457.
XX
29-JUN-1999; 99GB-00015215.
XX
23-DEC-1999; 99GB-00030536.
XX
(ZENE ) ZENECA LTD.
XX
Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;
PI Vincent JL, Lee MD;
XX
WPI; 2001-123015/13.
XX
Novel insecticidal protein obtained from species of Paecilomyces for
controlling insects, and for insect-resistant transgenic plant
production.
XX
Claim 14; Page 60-62; 72pp; English.
XX
The present invention relates to novel insecticidal proteins obtained
from Paecilomyces sp. (see AAE66910 to AAE66901 and AAE66913). The
insecticidal proteins can be used to produce transgenic plants, which are
insect-resistant. Also, the insecticidal proteins are useful for
controlling insects by providing them at a locus where insects feed
XX
Sequence 719 AA;
XX
Query Match 98.9%; Score 3720; DB 4; Length 719;
Best Local Similarity 99.2%; Pred. No. 2.2e-290;
Matches 714; Conservative 2; Mismatches 2; Indels 2; Gaps 2;
QY 360 WGGHKLFPFTICGTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGNLFLTQPVNGVP 419
DB 360 WGGHKLFPFTICGTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGNLFLTQPVNGVP 419
QY 420 RYDEHKKFVTHPIASDNFYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLI 479
DB 420 RYDEHKKFVTHPIASDNFYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLI 479
QY 480 SASHKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRT 539
DB 480 SASHKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRT 539
QY 540 NTGTGDIRVNINPBPFAQRYRVRIRYASTDLOFHTSINGKAINOGNFSATNWRGEDLDY 599
DB 540 NTGTGDIRVNINPBPFAQRYRVRIRYASTDLOFHTSINGKAINOGNFSATNWRGEDLDY 599
QY 600 KTFRTVGTFTTSPFLDVQSTFTTIGAWNFSSGNEVVIDRIEFVPEVTVYEAAYDFEKAQEK 659
DB 600 KTFRTVGTFTTSPFLDVQSTFTTIGAWNFSSGNEVVIDRIEFVPEVTVYEAAYDFEKAQEK 659
QY 660 VTALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDFYLDKRELFYKYANELHIERNM 719
DB 660 VTALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDFYLDKRELFYKYAKQLHIERNM 719

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RESULT 9
AAU02095
ID AAU02095 standard; protein; 719 AA.
XX
AC AAU02095;
XX
DT 07-SEP-2001 (first entry)
XX
DE Bacillus thuringiensis partial mutant CryIIa.
XX
KW Crystal protein; CryIIa; moth; butterfly; Colorado potato beetle;
KW mutant; muten.
XX
OS Bacillus thuringiensis.
XX
PH Key Location/Qualifiers
FT Peptide 1..19
FT Protein /label= Signal_peptide
FT Protein 20..719
FT Protein /label= Mature_CryIIa
XX
XX EPI099760-A1.
XX
XX 16-MAY-2001.
XX
XX 09-NOV-1999; 99EP-00203723.
XX
XX 09-NOV-1999; 99EP-00203723.
XX
XX (CPRO-) CPRO-DLO CENT PLANTENVERDEDELINGS REPROD.
XX
XX De Maagd RA, Bosch HJ;
XX
XX WPI; 2001-337141/36.
XX
XX N-PSDB; AAS04855.
XX
XX New hybrid Bacillus thuringiensis hybrid toxins comprising structural
XX domains derived from at least 2 different crystal proteins, such as
XX CryIIa and CryIIa, and having insecticidal activity, useful for combating
XX insects.
XX
XX Example; Page 30-32; 43pp; English.
XX
XX The sequence is B. thuringiensis (Bt) crystal protein CryIIa, the DNA
XX encoding which was mutated to allow cloning of domain III or domains I
XX and II, to make the hybrid protoxins of the invention. The hybrid toxins
XX of the invention, having structural domains I, II and III in this order
XX starting from the N-terminal derived from at least 2 different crystal
XX proteins, are useful for protecting plants against pest insects, e.g.
XX moths, butterflies and Colorado potato beetle or for combating insects
XX
XX Sequence 719 AA;
XX
XX Query Match 98.8%; Score 3715; DB 4; Length 719;
XX Best Local Similarity 99.2%; Pred. No. 5.4e-290;
XX Matches 714; Conservative 2; Mismatches 2; Indels 2; Gaps 2;
XX
XX 1 M L K N Q D K H Q S F S N A K V K I S T S L K N E T D I E L Q N I N H E D C L K S Y E N V E P F V S A S T I 60
XX 1 M L K N Q D K H Q S F S N A K V K I S T S L K N E T D I E L Q N I N H E D C L K S Y E N V E P F V S A S T I 60
XX
XX 61 Q T G I G A K I L G T L G V P P A G Q V A S L Y S F I L G E L M P K G N Q W E I L F M E H V E E - I N Q K I S T Y 119
XX 61 Q T G I G A K I L G T L G V P P A G Q V A S L Y S F I L G E L M P K G N Q W E I - F M E H V E E I I N Q K I S T Y 119
XX
XX 120 A R N K A L T D L K G L G A L A V H D S L S E S W G N R N T R A R S V T S Q Y I A L E I M F V Q K L P S F A V S 179
XX 120 A R N K A L T D L K G L G A L A V H D S L S E S W G N R N T R A R S V T S Q Y I A L E I M F V Q K L P S F A V S 179
XX
XX 180 G E E V P L L I P I Y A Q A A N L H L L R D A S I F G K E W G L S S E I S T F Y N R Q V E A G D Y S H C V K W Y 239

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Db 180 GEEVPLLPDYAQAANLHLLRLDASIFGKEWGLSSSEISTFYNRQVERAGDYSHCVKWKY 239
QY 240 STGLNNLGGTNAESWVRYNQFRDWTLMVLDLVALFPYSYDTQMTPIKTAQITREYVYDA 299
Db 240 STGLNNLGGTNAESWVRYNQFRDWTLMVLDLVALFPYSYDTQMTPIKTAQITREYVYDA 299
QY 300 IGTVEHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDLEQVTTIYSLSSWSNTQYNNM 359
Db 300 IGTVEHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDLEQVTTIYSLSSWSNTQYNNM 359
QY 360 WGGHKLFEFTTIGGLTNIISTOGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLOPVNGVP 419
Db 360 WGGHKLFEFTTIGGLTNIISTOGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLOPVNGVP 419
QY 420 RVDFFWKVTHPIASDNFYPGYAGIGTQLODSNELPPEATGQPNYESYSHRSLSHIGLI 479
Db 420 RVDFFWKVTHPIASDNFYPGYAGIGTQLODSNELPPEATGQPNYESYSHRSLSHIGLI 479
QY 480 SASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFLNLSGAAVVRGFGTGGDILRRT 539
Db 480 SASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFLNLSGAAVVRGFGTGGDILRRT 539
QY 540 NTGTFGDIRVINPPFAQRYRVRIRYASTTDLQHTSINGKAINQGNFSATWNRGDDLDY 599
Db 540 NTGTFGDIRVINPPFAQRYRVRIRYASTTDLQHTSINGKAINQGNFSATWNRGDDLDY 599
QY 600 KTRTVGFTTTPPSFLDVOSTFTIGAWNFSSGNEVVIDRIEFVPEVTEYAEVDFEKAQEK 659
Db 600 KTRTVGFTTTPPSFLDVOSTFTIGAWNFSSGNEVVIDRIEFVPEVTEYAEVDFEKAQEK 659
QY 660 VTALFTSNPRGLKTDVXDYHIDQVSNLVESLSDFYLDKRELFELVYKAYAKQLHIERNM 719
Db 660 VTALFTSNPRGLKTDVXDYHIDQVSNLVESLSDFYLDKRELFELVYKAYAKQLHIERNM 719

```

RESULT 10  
AAR08041  
ID AAR08041 standard; protein; 719 AA.

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XX AAR08041;
XX
XX 24-OCT-2003 (revised)
XX 25-MAR-2003 (revised)
XX 27-FEB-1991 (first entry)
XX
XX 81 kD endotoxin deduced from DNA carried on pJH12.
XX Crystal; insecticide; toxin; delta endotoxin.
XX
XX Bacillus thuringiensis; JHCC 4353 and 4835.
XX
XX WO9013651-A.
XX
XX 15-NOV-1990.
XX
XX 09-MAY-1989; 89GB-00010624.
XX
XX 09-MAY-1989; 89GB-00010624.
XX
XX (ICIL ) IMPERIAL CHEM IND PLC.
XX
XX Blenk RG, Ely S, Tailor RH, Tippet JW;
XX
XX WPI; 1990-361486/48.
XX N-PSDB; AAQ06636.
XX
XX Bacillus thuringiensis strains - used for producing an endotoxin for
XX protecting plants against insects, partic. Lepidoptera and Coleoptera.
XX
XX Claim 5; Fig 5-10; 66pp; English.
XX
XX The sequence carried on pJH12 which was isolated from B. thurin- giensis
XX strains JHCC4835 and JHCC 4353 (NCIB 40091 and 40090 resp.). The DNA can

```

CC be used to produce transformants E. coli strain MC12022/pJH12 (NCIB 40278,  
 CC or bacteriophage EMBL4 vector (NCIB 40279) or E. coli strain BL21/pJH11  
 CC (NCIB 40273). The delta-endo- toxin produced by the transformants can be  
 CC used in formulations for combatting lepidoptera and Coleoptera pests.  
 CC (Updated on 25-MAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to  
 CC standardise OS field)  
 XX  
 SQ Sequence 719 AA;

Query Match 98.5%; Score 3703; DB 2; Length 719;  
 Best Local Similarity 98.9%; Pred. No. 5e-289;  
 Matches 712; Conservative 2; Mismatches 4; Indels 2; Gaps 2;  
 QY 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQININHEDCMKSEYENVEPFSASTI 60  
 Db 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQININHEDCMKSEYENVEPFSASTI 60  
 QY 61 QTGIGIAGKILGTGVPPAGQVASYLSFILGELWPKGNQWEILFMEHVER-INOKISTY 119  
 Db 61 QTGIGIAGKILGTGVPPAGQVASYLSFILGELWPKGNQWEI-FMEHVEEIIINQKISTY 119  
 QY 120 ARNKALTDLKGGLDALAVVHDSLEWGNRNTRARSVVRSCYIALELMFVKLPSPFAVS 179  
 Db 120 ARNKALTDLKGGLDALAVVHDSLEWGNRNTRARSVVRSCYIALELMFVKLPSPFAVS 179  
 QY 180 GEEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTTFYNRQVERAGDYSDHCVKWY 239  
 Db 180 GEEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTTFYNRQVERAGDYSYHCVKWY 239  
 QY 240 STGLANLGRGTNAESVVRVYRNQFRDMLVLDLVALFPSYDTQMPYIKTTAQLTREVTDA 299  
 Db 240 STGLANLGRGTNAESVVRVYRNQFRDMLVLDLVALFPSYDTQMPYIKTTAQLTREVTDA 299  
 QY 300 IGVTHPHPSFTSTTWNNAFSSAIEAAVVRNPHLLDFLEQVTIYSLLSWSNTQYMMN 359  
 Db 300 IGVTHPHPSFTSTTWNNAFSSAIEAAVVRNPHLLDFLEQVTIYSLLSWSNTQYMMN 359  
 QY 360 WGHKLEFRTTIGTGLNISTQSTNTSINPVLPTFSRDVYTESLAGNLFLTQPVNGVP 419  
 Db 360 WGHKLEFRTTIGTGLNISTQSTNTSINPVLPTFSRDVYTESLAGNLFLTQPVNGVP 419  
 QY 420 RVDFFHWKVFTHPIASDNFYFPGYAGIGTQLODSENELPPEATGQPNYESYSHRSLHGLI 479  
 Db 420 RVDFFHWKVFTHPIASDNFYFPGYAGIGTQLODSENELPPEATGQPNYESYSHRSLHGLI 479  
 QY 480 SASHVKALVYSWTHRSADRTNTIIPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT 539  
 Db 480 SASHVKALVYSWTHRSADRTNTIIPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT 539  
 QY 540 NTGTFGDIRVINPFPFAQRVRYRYASTTDLQFHTSINGKAINQGNFSAIMNRGEDLDY 599  
 Db 540 NTGTFGDIRVINPFPFAQRVRYRYASTTDLQFHTSINGKAINQGNFSAIMNRGEDLDY 599  
 QY 600 KTFRTVGTTPFPFLDVOSTFTTIGAWNFSSGNEVYIDRIEFPVPEVTEAYEYDFEKAQEK 659  
 Db 600 KTFRTVGTTPFPFLDVOSTFTTIGAWNFSSGNEVYIDRIEFPVPEVTEAYEYDFEKAQEK 659  
 QY 660 VTALFTSTNPKGLKTDVKDHYHIDQVSNLVSLSDEFYLDKRELFEIVKYANELHIERNM 719  
 Db 660 VTALFTSTNPKGLKTDVKDHYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719

## RESULT 11

AAE36271

ID AAE36271 standard; protein; 718 AA.

XX

AC AAE36271;

XX

DT 26-JUN-2003 (first entry)

XX

DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa1.

XX

KW Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.

XX OS Bacillus thuringiensis.  
 XX PN WO200298911-A2.  
 XX PD 12-DEC-2002.  
 XX PF 30-MAY-2002; 2002WO-CB002666.  
 XX PR 07-JUN-2001; 2001GB-00013900.  
 XX PA (SYGN ) SYNGENTA LTD.  
 XX PI Vincent JL, Viner R;  
 XX WI; 2003-175137/17.  
 XX  
 PT New insecticidal protein comprising an X-glycine motif at the amino-  
 PT terminus, useful as an active ingredient of a pesticide.  
 XX  
 PS Claim 12; Page 42-44; 67pp; English.  
 XX  
 CC The invention relates to insecticidal protein comprising an X-glycine  
 CC motif at the amino-terminus. Polynucleotide or DNA constructs of the  
 CC invention are useful for producing plants or plant parts that are  
 CC resistant to insects. The protein or synergistic combination is useful as  
 CC an active ingredient of a pesticide or for controlling insects.  
 CC Antibodies raised to the insecticidal proteins can be used to identify  
 CC other proteins with insecticidal activity. The present sequence is  
 CC Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This  
 CC sequence is used in the invention  
 XX  
 SQ Sequence 718 AA;

Query Match 98.2%; Score 3692.5; DB 6; Length 718;  
 Best Local Similarity 98.9%; Pred. No. 3.5e-288;  
 Matches 712; Conservative 2; Mismatches 3; Indels 3; Gaps 3;

QY 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQININHEDCMKSEYENVEPFSASTI 60  
 Db 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQININHEDCMKSEYENVEPFSASTI 60  
 QY 61 QTGIGIAGKILGTGVPPAGQVASYLSFILGELWPKGNQWEILFMEHVER-INOKISTY 119  
 Db 61 QTGIGIAGKILGTGVPPAGQVASYLSFILGELWPKGNQWEI-FMEHVEEIIINQKISTY 119  
 QY 120 ARNKALTDLKGGLDALAVVHDSLEWGNRNTRARSVVRSCYIALELMFVKLPSPFAVS 179  
 Db 120 ARNKALTDLKGGLDALAVVHDSLEWGNRNTRARSVVRSCYIALELMFVKLPSPFAVS 179  
 QY 180 GEEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTTFYNRQVERAGDYSYHCVKWY 239  
 Db 180 GEEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTTFYNRQVERAGDYSYHCVKWY 239  
 QY 240 STGLANLGRGTNAESVVRVYRNQFRDMLVLDLVALFPSYDTQMPYIKTTAQLTREVTDA 299  
 Db 240 STGLANLGRGTNAESVVRVYRNQFRDMLVLDLVALFPSYDTQMPYIKTTAQLTREVTDA 299  
 QY 300 IGVTHPHPSFTSTTWNNAFSSAIEAAVVRNPHLLDFLEQVTIYSLLSWSNTQYMMN 359  
 Db 300 IGVTHPHPSFTSTTWNNAFSSAIEAAVVRNPHLLDFLEQVTIYSLLSWSNTQYMMN 359  
 QY 360 WGHKLEFRTTIGTGLNISTQSTNTSINPVLPTFSRDVYTESLAGNLFLTQPVNGVP 419  
 Db 360 WGHKLEFRTTIGTGLNISTQSTNTSINPVLPTFSRDVYTESLAGNLFLTQPVNGVP 419  
 QY 420 RVDFFHWKVFTHPIASDNFYFPGYAGIGTQLODSENELPPEATGQPNYESYSHRSLHGLI 479  
 Db 420 RVDFFHWKVFTHPIASDNFYFPGYAGIGTQLODSENELPPEATGQPNYESYSHRSLHGLI 479  
 QY 480 SASHVKALVYSWTHRSADRTNTIIPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT 539  
 Db 480 SASHVKALVYSWTHRSADRTNTIIPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT 539  
 QY 499 SASHVKALVYSWTHRSADRTNTIIPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT 538



QY 540 NTGTFGDIRVNINPPFAQRYVRIRYASTTDLQFHTSINGKAINQGNFSATMARGEDLDY 599  
DB 539 NTGTFGDIRVNINPPFAQRYVRIRYASTTDLQFHTSINGKAINQGNFSATMARGEDLDY 598  
QY 600 KTFRTVGTFTPFPLDQVSTFTIGAMNFSNGNEVYIDRIEFVPEVTEAEYDFEKAQEK 659  
DB 599 KTFRTVGTFTPFPLDQVSTFTIGAMNFSNGNEVYIDRIEFVPEVTEAEYDFEKAQEK 658  
QY 660 VTALFTSTNPRGLKTDVKDHYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719  
DB 659 VTALFTSTNPRGLKTDVKDHYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 718

RESULT 12  
ID AAB66907 standard; protein; 718 AA.

XX AC AAB66907;  
XX DT 12-APR-2001 (first entry)  
XX DE Insecticidal protein cryIIa1.  
XX XX Insecticide; transgenic plant; insect-resistance.  
XX KW Paecilomyces sp.  
XX OS WO200100841-A1.  
XX EN 04-JAN-2001.  
XX PD 23-JUN-2000; 2000WO-GB002457.  
XX PF 29-JUN-1999; 99GB-00015215.  
XX PR 23-DEC-1999; 99GB-00030536.  
XX XX (ZENE ) ZENECA LTD.  
XX PI Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;  
XX PI Vincent JL, Lee MD;  
XX XX WPI; 2001-123015/13.  
XX DR Novel insecticidal protein obtained from species of Paecilomyces for  
XX PT controlling insects, and for insect-resistant transgenic plant  
XX PT production.  
XX PS Claim 14; Page 53-55; 72pp; English.  
XX XX The present invention relates to novel insecticidal proteins obtained  
XX CC from Paecilomyces sp. (see AAB66907 to AAB66901 and AAB66913). The  
XX CC insecticidal proteins can be used to produce transgenic plants, which are  
XX CC insect-resistant. Also, the insecticidal proteins are useful for  
XX CC controlling insects by providing them at a locus where insects feed  
XX SQ Sequence 718 AA;

Query Match 98.0%; Score 3686.5; DB 4; Length 718;  
Best Local Similarity 98.8%; Pred. NO. 1.1e-287;  
Matches 711; Conservative 2; Mismatches 4; Indels 3; Gaps 3;  
QY 1 MKLKNQDKHQSFSSNAKDKISTSLKNETDIELQINNHEDCLKMSYENVEPVSASTI 60  
DB 1 MKLKNQDKHQSFSSNAKDKISTSLKNETDIELQINNHEDCLKMSYENVEPVSASTI 60  
QY 61 QTGIGIAGKILGTLPVAGQVASYLSFILGELWPKGNQWEILFMEHVER-INQKISTY 119  
DB 61 QTGIGIAGKILGTLPVAGQVASYLSFILGELWPKGNQWEI-FMEHVEIINQKISTY 119  
QY 120 ARNKALTDLKGIDALAYHDSLSWGNRNTRARSVRSQYTALELMFYOKLPSFAVS 179  
DB 120 ARNKALTDLKGIDALAYHDSLSWGNRNTRARSVRSQYTALELMFYOKLPSFAVS 179

QY 180 GEEVPLPIYAAQANLHLLLRDASI FGKEWGLSSSEISTFYNROVERAGDYSDHCWKY 239  
DB 180 GEEVPLPIYAAQANLHLLLRDASI FGKEWGLSSSEISTFYNROVERAGDYSDHCWKY 239  
QY 240 STGLANLRGTNAESWVRYNQFRDMTLMVLDLVALFPYDTOMYPIKTTAQLTREYVYDA 299  
DB 240 STGLANLRGTNAESWVRYNQFRDMTLMVLDLVALFPYDTOMYPIKTTAQLTREYVYDA 299  
QY 300 ICTVHPHPSFTSTTWNKNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNM 359  
DB 300 ICTVHPHPSFTSTTWNKNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNM 359  
QY 360 WGHKLEPRTIGTTLNISTQGSTNTSINPVTLPFTSRDYRTESLAGLNLFLTQPVN-VP 419  
DB 360 WGHKLEPRTIGTTLNISTQGSTNTSINPVTLPFTSRDYRTESLAGLNLFLTQPVN-VP 418  
QY 420 RVDPHWKVTHPIASDNFYPCYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLI 479  
DB 419 RVDPHWKVTHPIASDNFYPCYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLI 478  
QY 480 SASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILART 539  
DB 479 SASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILART 538  
QY 540 NTGTFGDIRVNINPPFAQRYVRIRYASTTDLQFHTSINGKAINQGNFSATMARGEDLDY 599  
DB 539 NTGTFGDIRVNINPPFAQRYVRIRYASTTDLQFHTSINGKAINQGNFSATMARGEDLDY 598  
QY 600 KTFRTVGTFTPFPLDQVSTFTIGAMNFSNGNEVYIDRIEFVPEVTEAEYDFEKAQEK 659  
DB 599 KTFRTVGTFTPFPLDQVSTFTIGAMNFSNGNEVYIDRIEFVPEVTEAEYDFEKAQEK 658  
QY 660 VTALFTSTNPRGLKTDVKDHYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719  
DB 659 VTALFTSTNPRGLKTDVKDHYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 718

RESULT 13  
ADM74717  
ID ADM74717 standard; protein; 719 AA.  
XX AC ADM74717;  
XX DT 03-JUN-2004 (first entry)  
XX DE B. thuringiensis cryIIel SEQ ID NO:2.  
XX KW cryII; toxicity; lepidoptera; cryIaB; cryIaA; coleoptera; diptera;  
XX KW cryIIel.  
XX OS Bacillus thuringiensis.  
XX PN CN1401772-A.  
XX PD 12-MAR-2003.  
XX PF 20-AUG-2001; 2001CN-00124163.  
XX PR 20-AUG-2001; 2001CN-00124163.  
XX PA (PLAN-) PLANT PROTECTION INST CHINESE ACAD AGRIC.  
XX PI Song F, Zhang J, Huang D;  
XX DR WPI; 2003-442339/42.  
XX DR N-PSDB; ADM74716.  
XX PT Bacillus thuringiensis cryI gene, expression vector, nucleotide sequence  
XX PT with high-toxicity to lepidoptera pests, encoded protein, primer  
XX PT sequences and the shuttle vector pSKY422b, useful as a pesticide.  
XX PS Example 3; SEQ ID NO 2; 29pp; Chinese.

XX CC The invention relates to a novel Bacillus thuringiensis cryI gene, gene  
 CC combination, expression vector, nucleotide sequence of the B  
 CC thuringiensis cryI gene with high-toxicity to lepidoptera pests and the  
 CC amino acid sequence of the protein encoded by it, cooperative use of the  
 CC cryI gene with the expression product of cryIaB or cryIaA, primer  
 CC sequences for expressing the genes, and the constructed shuttle vector  
 CC pSX422b. The gene in combination with the cryIaB or cryIaA genes  
 CC displays high toxicity to the lepidoptera, coleoptera and diptera pests.  
 CC The present sequence represents the cryIaI protein.  
 XX  
 SQ Sequence 719 AA;

Query Match 93.5%; Score 3517; DB 7; Length 719;  
 Best Local Similarity 93.1%; Pred. No. 4.8e-274;  
 Matches 670; Conservative 27; Mismatches 21; Indels 2; Gaps 2;  
 QY 1 MKLKNQKHQSFSNAKVDKISTDSLKNETDIELQNHEDCLKSEYENVEPFFVSASTI 60  
 DB 1 MKLKNPDKHQSLSNAKVDKIATDSLKNETDIELKNIHEDFLRSEHSIDPFFVSASTI 60  
 QY 61 QTGIGIAGKILGTGVPPAGQVASYLSFILGELWPKGNQWEILFMEHVEE-INOKISTY 119  
 DB 61 QTGIGIAGKILGTGVPPAGQVASYLSFILGELWPKGKSQWEI-FMEHVEELIDPKISTY 119  
 QY 120 ARNKALTDLKLGDALAVVHDSLESWGNRNTRARSVVRQYIALELMFVKLPSPFAVS 179  
 DB 120 ARNIALADLKLGDALAVVHDSLESWKNRNARATSVVQSYIALELLFVKLPSPFAVS 179  
 QY 180 GBEVPLPIYAQAANLHLLLRDASIFGKEMGLSSSEISTFYNNQVERAGYSYDHCVKWY 239  
 DB 180 GBEVPLPIYAQAANLHLLLRDASIFGKEMGLSSQISTFYNNQVETSYSYDHCVKWY 239  
 QY 240 STGLANLRGTNAESWVRVYQNRDQMTLMDLVALFPSYDQMPYIKTTAQLTREVYTD 299  
 DB 240 STGLANLRGTNAESWVRVYQNRKQMTLMDLVALFPSYDILVPIKTTSLTREVYTD 299  
 QY 300 IGTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNM 359  
 DB 300 IGTVHPNASFASTWYNNNAPSFAIEAGAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNM 359  
 QY 360 WGHKLEPFTIGTGLNISTQSTNTSINPVTLPFTSRDVTESLAGNLFLTPQVNGVP 419  
 DB 360 WGHKLEPFTIGGLVNTSQSTNTSINPVTLPFTSRDVTESLAGNLFLTPQVNGVP 419  
 QY 420 RVDPHKVFTHPIASDNFYFYAGIGTQLODSENELPPEATGPNVYESYSHRLSHIGLI 479  
 DB 420 RVDPHKVFATLPIASDNFYFYAGVGTQLODSENELPPEATGPNVYESYSHRLSHIGLI 479  
 QY 480 SASHVKALVYSWTHRSADRTWIEPNSITQPLKAFNLSSGAAVRGPGETGDIILRT 539  
 DB 480 SASHVKALVYSWTHRSADRTWIEPNSITQPLKAFNLSSGAAVRGPGETGDIILRT 539  
 QY 540 NTGTFGDIRVINPFPFAQRYVRIRYASTTDLPHTSINGKAINQGNFSATMNRGDLDY 599  
 DB 540 NTGTFGDIRVINPFPFAQRYVRIRYASTTDLPHTSINGKAINQGNFSATMNRGDLDY 599  
 QY 600 KTFRTVGTFTTSPFLDVOSTTIGAWNFSSGNEVYIDRIEFVPEVYEAEDPEKAQEK 659  
 DB 600 KTFRTVGTFTTSPFLDVOSTTIGAWNFSSGNEVYIDRIEFVPEVYEAEDPEKAQEK 659  
 QY 660 VTALFTSNPGLKTDVXDYHIDQVSNLVESLSDEFYLDKRELFVYKANEHLHIERNM 719  
 DB 660 VTALFTSNPGLKTDVXDYHIDQVSNLVESLSDEFYLDKRELFVYKAKQHIERNM 719

RESULT 14  
 AAB66912  
 ID AAB66912 standard; protein; 719 AA.  
 XX  
 AC AAB66912;  
 XX  
 DT 12-APR-2001 (first entry)

XX DE Insecticidal protein cryIaIb1.  
 XX KW Insecticide; transgenic plant; insect-resistance.  
 XX OS Paecilomyces sp.  
 XX EN W0200100841-A1.  
 XX PD 04-JAN-2001.  
 XX PF 23-JUN-2000; 2000WO-GB002457.  
 XX PR 29-JUN-1999; 99GB-00015215.  
 XX PR 23-DEC-1999; 99GB-00030536.  
 XX PA (ZONE ) ZENECA LTD.  
 XX PI Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;  
 XX PI Vincent JL, Lee MD;  
 XX DR WPI; 2001-123015/13.  
 XX PT Novel insecticidal protein obtained from species of Paecilomyces for  
 PT controlling insects, and for insect-resistant transgenic plant  
 PT production.  
 XX PS Claim 14; Page 64-66; 72pp; English.  
 XX CC The present invention relates to novel insecticidal proteins obtained  
 CC from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The  
 CC insecticidal proteins can be used to produce transgenic plants, which are  
 CC insect-resistant. Also, the insecticidal proteins are useful for  
 CC controlling insects by providing them at a locus where insects feed  
 XX  
 SQ Sequence 719 AA;  
 Query Match 92.6%; Score 3484; DB 4; Length 719;  
 Best Local Similarity 92.2%; Pred. No. 2.2e-271;  
 Matches 664; Conservative 33; Mismatches 21; Indels 2; Gaps 2;  
 QY 1 MKLKNQKHQSFSNAKVDKISTDSLKNETDIELQNHEDCLKSEYENVEPFFVSASTI 60  
 DB 1 MKLKNPDKHQSLSNAKVDKIATDSLKNETDIELKMNEDYLRSEHSIDPFFVSASTI 60  
 QY 61 QTGIGIAGKILGTGVPPAGQVASYLSFILGELWPKGNQWEILFMEHVEE-INOKISTY 119  
 DB 61 QTGIGIAGKILGTGVPPAGQVASYLSFILGELWPKGKSQWEI-FMEHVEEINQKILTY 119  
 QY 120 ARNKALTDLKLGDALAVVHDSLESWGNRNTRARSVVRQYIALELMFVKLPSPFAVS 179  
 DB 120 ARNKALSDLEGLDALAVVHDSLESWGNRNTRARSVVRQYIALELMFVKLPSPFAVS 179  
 QY 180 GBEVPLPIYAQAANLHLLLRDASIFGKEMGLSSSEISTFYNNQVERAGYSYDHCVKWY 239  
 DB 180 GBEVPLPIYAQAANLHLLLRDASIFGKEMGLSSSEISTFYNNQVERTRDYSCHIKWY 239  
 QY 240 STGLANLRGTNAESWVRVYQNRDQMTLMDLVALFPSYDQMPYIKTTAQLTREVYTD 299  
 DB 240 NTGLANLRGTNAESWVRVYQNRDQMTLMDLVALFPSYDILVPIKTTSLTREVYTD 299  
 QY 300 IGTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNM 359  
 DB 300 IGTVHPNQFASTWYNNNAPSFAIEAVIRSPHLLDFLEQVTIYSLLSRWSNTQYNNM 359  
 QY 360 WGHKLEPFTIGTGLNISTQSTNTSINPVTLPFTSRDVTESLAGNLFLTPQVNGVP 419  
 DB 360 WGHKLEPFTIGTGLNISTQSTNTSINPVTLPFTSRDVTESLAGNLFLTPQVNGVP 419  
 QY 420 RVDPHKVFTHPIASDNFYFYAGIGTQLODSENELPPEATGPNVYESYSHRLSHIGLI 479  
 DB 420 RVDPHKVFPTLPIASDNFYFYAGVGTQLODSENELPPEATGPNVYESYSHRLSHIGLI 479

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QY 480 SASHVKALVSWTHRSADRTNTEPNSITQIPLVKAFNLSGGAUVRGPGFTGGDILRRT 539
DB 480 SASHVKALVSWTHRSADRTNTEPNSITQIPLVKAFNLSGGAUVRGPGFTGGDILRRT 539
QY 540 NTGTFGDIRVNIINPPFAQRVVRIRYASTTDLQPHTSINGKAINQGNFSAATMRGDDLDY 599
DB 540 NTGTFGDIRVNIINPPFAQRVVRIRYASTTDLQPHTSINGKAINQGNFSAATMRGDDLDY 599
QY 600 KTFRTVGTTPFSDVQSTFTIGAMNFGSGNEVYIDRIEFVPEVTEYAEYDFEKAQEK 659
DB 600 KTFRTVGTTPFSDVQSTFTIGAMNFGSGNEVYIDRIEFVPEVTEYAEYDFEKAQEK 659
QY 660 VTALFTSTNPRGLKTDVKDHYDQVSNLVSLSDEFYLDKRELFEIVKAKQIHERNM 719
DB 660 VTALFTSTNPRGLKTDVKDHYDQVSNLVSLSDEFYLDKRELFEIVKAKQIHERNM 719

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RESULT 15

AAE36276  
ID AAE36276 standard; protein; 719 AA.

XX AAE36276;

XX 26-JUN-2003 (first entry)

XX B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIb1.  
XX Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.

XX Bacillus thuringiensis.

XX WO200298911-A2.

XX 12-DEC-2002.

XX 30-MAY-2002; 2002WO-GB002666.

XX 07-JUN-2001; 2001GB-00013900.

XX (SYGN ) SYNGENTA LTD.

XX Vincent JL, Viner R;

XX WPI; 2003-175137/17.

XX New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.

XX Claim 12; Page 56-58; 67pp; English.

XX The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects. Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention

XX Sequence 719 AA;

Query Match 92.6%; Score 3484; DB 6; Length 719;  
Best Local Similarity 92.2%; Pred. No. 2.2e-271;  
Matches 664; Conservative 33; Mismatches 21; Indels 2; Gaps 2;

```

QY 1 MKLNQDKHQSFSSNAKVDKISTDSLKNETDIELQINNHEDCLKXSEYENVEPVFSASTI 60
DB 1 MKLNQDKHQSFSSNAKVDKISTDSLKNETDIELKNNEDYLRMSEHESIDPFVSASTI 60
QY 61 QTGIGIAGKILGTGVPPAGQVASYLSFILGELWPKKNQWEILFMEHVEE-INQKISTY 119
DB 61 QTGIGIAGKILGTGVPPAGQVASYLSFILGELWPKKQWEI-FMEHVEEINQKILTY 119

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Search completed: October 28, 2004, 18:20:05  
Job time : 89.6903 secs

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QY 120 ARNKALTDLKGLDALAVYHDSLESWGNRNTRARSVVRQYIALELMFYOKLSEAVS 179
DB 120 ARNKALSDLRGLDALAVYHDSLESWGNRNTRARSVVRQYIALELMFYOKLSEAVS 179
QY 180 GBEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDRCWKY 239
DB 180 GBEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERTRDYSDRCWKY 239
QY 240 STGLNNLRGTNAESVRNQFRDNTLMDLVALFPSYDTOMYPIKTAQILTRVYIDA 299
DB 240 NTGLNNLRGTNAESVRNQFRDNTLMDLVALFPSYDTOMYPIKTAQILTRVYIDA 299
QY 300 IGTVPHPSPFTSTTWNANNAPSAIEAAVVRNPHLLDFLEQVTTYSLLSRWSNTQYMMN 359
DB 300 IGTVPHPSPFTSTTWNANNAPSAIEAAVVRNPHLLDFLEQVTTYSLLSRWSNTQYMMN 359
QY 360 WGHKLEPRTIGGTNLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGNLFLTPQVNGVP 419
DB 360 WGHKLEPRTIGGTNLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGNLFLTPQVNGVP 419
QY 420 RYDFHMKFVTHPIASDNFYPGYAGIGTQLODSENELPPEATQOPNYESYSHRLSHIGLI 479
DB 420 RYDFHMKFVTHPIASDNFYPGYAGIGTQLODSENELPPEATQOPNYESYSHRLSHIGLI 479
QY 480 SASHVKALVSWTHRSADRTNTEPNSITQIPLVKAFNLSGGAUVRGPGFTGGDILRRT 539
DB 480 SASHVKALVSWTHRSADRTNTEPNSITQIPLVKAFNLSGGAUVRGPGFTGGDILRRT 539
QY 540 NTGTFGDIRVNIINPPFAQRVVRIRYASTTDLQPHTSINGKAINQGNFSAATMRGDDLDY 599
DB 540 NTGTFGDIRVNIINPPFAQRVVRIRYASTTDLQPHTSINGKAINQGNFSAATMRGDDLDY 599
QY 600 KTFRTVGTTPFSDVQSTFTIGAMNFGSGNEVYIDRIEFVPEVTEYAEYDFEKAQEK 659
DB 600 KTFRTVGTTPFSDVQSTFTIGAMNFGSGNEVYIDRIEFVPEVTEYAEYDFEKAQEK 659
QY 660 VTALFTSTNPRGLKTDVKDHYDQVSNLVSLSDEFYLDKRELFEIVKAKQIHERNM 719
DB 660 VTALFTSTNPRGLKTDVKDHYDQVSNLVSLSDEFYLDKRELFEIVKAKQIHERNM 719

```



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 28, 2004, 18:05:43 ; Search time 19.191 Seconds  
(without alignments)  
3604.811 Million cell updates/sec

Title: US-10-019-823B-59  
Perfect score: 3742  
Sequence: 1 MKLKNPDKHQSLSSNAKVDK.....KRELPIVYKAKIHIERNM 719

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: Pir1.\*
- 2: Pir2.\*
- 3: Pir3.\*
- 4: Pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3742	100.0	719	2 140590	crvV465 protein - insecticidal prote
2	3520	94.1	719	2 139815	parasporal crystal
3	3511	93.8	719	2 S25383	parasporal crystal
4	3503	93.6	719	2 139834	insecticidal prote
5	2321.5	62.0	1228	2 S00873	parasporal crystal
6	1813	48.5	380	2 B42459	hypothetical prote
7	1507	40.3	1157	1 S49247	parasporal crystal
8	1503.5	40.2	1166	2 S32645	parasporal crystal
9	1491.5	39.9	1174	2 S32649	parasporal crystal
10	1487.5	39.8	1155	2 A26513	parasporal crystal
11	1480.5	39.6	1155	2 JD0002	parasporal crystal
12	1480.5	39.6	1156	2 A29122	parasporal crystal
13	1463.5	39.1	1155	2 S02134	parasporal crystal
14	1463.5	39.1	1181	2 A41052	parasporal crystal
15	1461.5	39.1	1155	2 139838	parasporal crystal
16	1459	39.0	934	2 A22758	parasporal crystal
17	1457	38.9	1176	2 JT0241	parasporal crystal
18	1451	38.8	1176	2 JC2219	parasporal crystal
19	1447	38.7	1176	2 A22617	parasporal crystal
20	1447	38.7	1176	2 S02215	parasporal crystal
21	1367	36.5	1174	2 A42459	parasporal crystal
22	1348	36.0	1156	2 A29838	parasporal crystal
23	1343	35.9	1138	2 A48944	parasporal crystal
24	1340.5	35.8	823	2 S04181	parasporal crystal
25	1331.5	35.6	1189	2 S00944	parasporal crystal
26	1326	35.4	1154	2 S39536	parasporal crystal
27	1292	34.5	1171	2 140572	parasporal crystal
28	1292	34.5	1171	2 A37829	parasporal crystal
29	1286	34.4	1176	2 A48970	parasporal crystal

30	1232	32.9	1160	2 S32647	parasporal crystal
31	1230.5	32.9	1165	2 S11446	parasporal crystal
32	1220.5	32.6	655	2 JC7140	protoxin - Bacilliu
33	1196.5	32.0	1172	2 S32689	parasporal crystal
34	1179	31.5	1160	2 140589	parasporal crystal
35	1178	31.5	652	2 A27323	parasporal crystal
36	1165	31.1	1178	1 USS8XH	parasporal crystal
37	1164.5	31.1	1177	2 A49785	parasporal crystal
38	1159	31.0	659	2 S10228	parasporal crystal
39	1124.5	30.1	652	2 139811	parasporal crystal
40	995	26.6	649	1 JH0261	parasporal crystal
41	938.5	25.1	618	2 S11445	parasporal crystal
42	896	23.9	1156	2 S19306	parasporal crystal
43	845	22.6	1136	1 USS881	parasporal crystal
44	662.5	17.7	934	2 B29838	parasporal crystal
45	637	17.0	1180	2 139870	parasporal crystal

ALIGNMENTS

RESULT 1

140590

crvV465 protein - Bacillus thuringiensis

C;Species: Bacillus thuringiensis

C;Date: 12-Aug-1996 #sequence revision 12-Aug-1996 #text\_change-09-Jul-2004

C;Accession: I40590

R;Shin, B.S.; Park, S.H.; Choi, S.K.; Koo, B.T.; Lee, S.T.; Kim, J.I.

Appl. Environ. Microbiol. 61: 3403-3407, 1995

A;Title: Distribution of crvV-type insecticidal protein genes in Bacillus thuringiensis s

tomocidus.

A;Reference number: I39814; MUID: 95314293; PMID: 7793960

A;Accession: I40590

A;Status: preliminary; translated from GB/EMBL/DBDJ

A;Molecule type: DNA

A;Residues: 1-719 <RES>

A;Cross-references: UNIPROT:Q45709; EMBL:U07642; NID:G467234; PIDN:AAA82114.1; PID:G46723

C;Genetics:

A;Gene: crvV465

C;Superfamily: parasporal crystal protein

Query Match 100.0%; Score 3742; DB 2; Length 719;  
Best Local Similarity 100.0%; Pred. No. 3.1e-258;  
Matches 719; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLKNPDKHQSLSSNAKVDKIATDSLKNETDIELKNMNNEDYLRMSEHSDPFFVSASTI 60

Db 1 MKLKNPDKHQSLSSNAKVDKIATDSLKNETDIELKNMNNEDYLRMSEHSDPFFVSASTI 60

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Db 61 QTGIGTAGKILGTGVPPFAGQIASIYSPILGELWPKGKSQWEIFMEHVVEEIIQKILTYA 120

QY 121 RNKALSDLEGLGDALAVVHSESVENNRNTRASVVKNOVIALELMFVKLPSPFVSG 180

Db 121 RNKALSDLEGLGDALAVVHSESVENNRNTRASVVKNOVIALELMFVKLPSPFVSG 180

QY 181 EEVPLLPPIYAQAANLELLLRDASIFGKEWGLSASEISTFYNRQVTRTRDYSDHCIKWYN 240

Db 181 EEVPLLPPIYAQAANLELLLRDASIFGKEWGLSASEISTFYNRQVTRTRDYSDHCIKWYN 240

QY 241 TGINLRGNNAKSWRYNQCFKQDMTLMVLDAVALPSPVDTLVYPIKTTTSQLTREYVTDAT 300

Db 241 TGINLRGNNAKSWRYNQCFKQDMTLMVLDAVALPSPVDTLVYPIKTTTSQLTREYVTDAT 300

QY 301 GTVHFNQAFASITWYNNNAPPSAIEAAVIRSPHLLDLEKVTIYSLLSRWNTQYMMNW 360

Db 301 GTVHFNQAFASITWYNNNAPPSAIEAAVIRSPHLLDLEKVTIYSLLSRWNTQYMMNW 360

QY 361 GGRHLESPIGALNTSTQGSTNTSINPVTLOFTQDRDYRTESLAGLNLFTQPVNGVPR 420

Db 361 GGRHLESPIGALNTSTQGSTNTSINPVTLOFTQDRDYRTESLAGLNLFTQPVNGVPR 420

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 DB 421 VDFHKKFPTLPASDNFYVLGYAGVGTQLODSENELPPTTGPQNYESYSHRLSHIGLIS 480  
 QY 481 ASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILARTN 540  
 DB 481 ASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILARTN 540  
 QY 541 TGTGDIRVNWNPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATNRGDDLDYK 600  
 DB 541 TGTGDIRVNWNPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATNRGDDLDYK 600  
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 DB 601 TPTTIGFTTPPSFSDVQSTFTIGANFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEKV 660  
 QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQIHIERNM 719  
 DB 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQIHIERNM 719

## RESULT 2

I39815  
 insecticidal protein cryv - Bacillus thuringiensis  
 C:Species: Bacillus thuringiensis  
 C:Date: 19-Jul-1996 #sequence\_revision 19-Jul-1996 #text\_change 09-Jul-2004  
 C:Accession: I39815  
 R:Gleave, A.P.; Williams, R.; Hedges, R.J.  
 Appl. Environ. Microbiol. 59, 1683-1687, 1993  
 A:Title: Screening by polymerase chain reaction of Bacillus thuringiensis serotypes for  
 iensis subsp. kurstaki.  
 A:Reference number: I39815; MUID:93298009; PMID:8517758  
 A:Accession: I39815  
 A:Status: preliminary; translated from GE/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-719 <RES>  
 A:Cross-references: UNIPROT:Q45752; GB:M98544; NID:g142767; PIDN:AAA22354.1; PID:g142768  
 C:Gene: cryv  
 C:Superfamily: parasporal crystal protein

Query Match 94.1%; Score 3520; DB 2; Length 719;  
 Best Local Similarity 92.9%; Pred. No. 2e-242;  
 Matches 668; Conservative 31; Mismatches 20; Indels 0; Gaps 0;  
 QY 1 MKLKNPDKHQSLSNAKVDKIATDSLKNETDIELKNMNNEDYLRMSEHESIDPFVSASTI 60  
 DB 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNIHEDCLKNSEYENVEPVSASTI 60  
 QY 61 QTGIGIAGKILGTGVPPAGQIASLYSFLGELWPKGKSOWEIFMEHVVEEIIINQKILTYA 120  
 DB 61 QTGIGIAGKILGTGVPPAGQVASLYSFLGELWPKGKNQWEIFMEHVVEEIIINQKISYA 120  
 QY 121 RNKALSDLRGLDALAVYHESLESVWENNRNTRARSVVKNQYIALELMFVKLPSFAVSG 180  
 DB 121 RNKALTDLKGLDALAVYHDSLESWVGNNRNRARSVVKSQYIALELMFVKLPSFAVSG 180  
 QY 181 BEVPLLPYIAQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVTRDYSDHCIKWYN 240  
 DB 181 BEVPLLPYIAQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVTRDYSDHCVKWYS 240  
 QY 241 TGLNLRGTNAKSWRVYRNFQKDMTLMVLDLVALPSPYDTLWYPIKTTTSQLTREYVYDAI 300  
 DB 241 TGLNLRGTNAESWRYRNFQFRDMLTLMVLDLVALPSPYDTQWYPIKTTAQLTREYVYDAI 300  
 QY 301 GTVHPNQAFASFTWNNNAPSFAEAAVIRSPHLLDFLEKVTIYSLSRWSNTQYMMW 360  
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 QY 361 GGHRLSREPIGGALNTSTQGSTNTSINPVTLOFTSRDYRTESLAGLNLFLTQPVNGVPR 420  
 DB 361 GGHKLEFRTIGTLNISTQGSTNTSINPVTLPFTSRDYRTESLAGLNLFLTQPVNGVPR 420

QY 421 VDFHKKFPTLPASDNFYVLGYAGVGTQLODSENELPPTTGPQNYESYSHRLSHIGLIS 480  
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 DB 601 TPTTIGFTTPPSFSDVQSTFTIGANFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEKV 660  
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 DB 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQIHIERNM 719

## RESULT 3

S25383  
 parasporal crystal protein cryIIaI - Bacillus thuringiensis  
 N:Alternate names: delta-endotoxin; parasporal crystal protein cryV  
 C:Species: Bacillus thuringiensis  
 C:Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 09-Jul-2004  
 C:Accession: S25383  
 R:Tailor, R.; Tippet, J.; Gibb, G.; Pells, S.; Pike, D.; Jordan, L.; Ely, S.  
 Mol. Microbiol. 6, 1211-1217, 1992  
 A:Title: Identification and characterization of a novel Bacillus thuringiensis delta-end  
 A:Reference number: S25383; MUID:92269582; PMID:1588820  
 A:Accession: S25383  
 A:Molecule type: DNA  
 A:Residues: 1-719 <TAI>  
 A:Cross-references: UNIPROT:Q45752; EMBL:X62821; NID:g40289; PIDN:CAA44633.1; PID:g40290  
 C:Gene: cryv  
 C:Superfamily: parasporal crystal protein  
 C:Keywords: delta-endotoxin

Query Match 93.8%; Score 3511; DB 2; Length 719;  
 Best Local Similarity 92.8%; Pred. No. 8.7e-242;  
 Matches 667; Conservative 31; Mismatches 21; Indels 0; Gaps 0;  
 QY 1 MKLKNPDKHQSLSNAKVDKIATDSLKNETDIELKNMNNEDYLRMSEHESIDPFVSASTI 60  
 DB 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNIHEDCLKNSEYENVEPVSASTI 60  
 QY 61 QTGIGIAGKILGTGVPPAGQIASLYSFLGELWPKGKSOWEIFMEHVVEEIIINQKILTYA 120  
 DB 61 QTGIGIAGKILGTGVPPAGQVASLYSFLGELWPKGKNQWEIFMEHVVEEIIINQKISYA 120  
 QY 121 RNKALSDLRGLDALAVYHESLESVWENNRNTRARSVVKNQYIALELMFVKLPSFAVSG 180  
 DB 121 RNKALTDLKGLDALAVYHDSLESWVGNNRNRARSVVKSQYIALELMFVKLPSFAVSG 180  
 QY 181 BEVPLLPYIAQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVTRDYSDHCIKWYN 240  
 DB 181 BEVPLLPYIAQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVTRDYSDHCVKWYS 240  
 QY 241 TGLNLRGTNAKSWRVYRNFQKDMTLMVLDLVALPSPYDTLWYPIKTTTSQLTREYVYDAI 300  
 DB 241 TGLNLRGTNAESWRYRNFQFRDMLTLMVLDLVALPSPYDTQWYPIKTTAQLTREYVYDAI 300  
 QY 301 GTVHPNQAFASFTWNNNAPSFAEAAVIRSPHLLDFLEKVTIYSLSRWSNTQYMMW 360  
 DB 301 GTVHPHPSFTSTWNNNAPSFAEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMMW 360  
 QY 361 GGHRLSREPIGGALNTSTQGSTNTSINPVTLOFTSRDYRTESLAGLNLFLTQPVNGVPR 420  
 DB 361 GGHKLEFRTIGTLNISTQGSTNTSINPVTLPFTSRDYRTESLAGLNLFLTQPVNGVPR 420

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DB 421 VDFHWKFTPLPIASDNFYLYGAGVGTQLQDSNELPPTTGPQNVESYSHRLSHIGLIS 480  
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DB 481 ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAENLSSGAAVVRGPGFTGGDILRRTN 540  
QY 541 TGTFGDIRVNNPFPFAQRVVRIRYASTTDLQPHSTINGKAINQGNFSAATMRGEDLDYK 600  
DB 541 TGTFGDIRVNNPFPFAQRVVRIRYASTTDLQPHSTINGKAINQGNFSAATMRGEDLDYK 600  
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DB 601 TPTTIGFTTTPFSFSDVQSTFTTIGAWNFSSGNEVYIDRIEFVFPVEVYEAEDFEKAQEKV 660  
QY 661 TALFTSTNPRGLKTDVKDHYDQVSNLVESLSDEFYLDKRELFVIVKAKQIHIERNM 719  
DB 661 TALFTSTNPRGLKTDVKDHYDQVSNLVESLSDEFYLDKRELFVIVKAKQIHIERNM 719

## RESULT 4

I39814  
insecticidal protein cryV1 - Bacillus thuringiensis  
C:Species: Bacillus thuringiensis  
C:Date: 19-Jul-1996 #sequence\_revision 19-Jul-1996 #text\_change 26-Aug-1999  
C:Accession: I39814  
R:Shin, B.S.; Park, S.H.; Choi, S.K.; Koo, B.T.; Lee, S.T.; Kim, J.I.  
Appl. Environ. Microbiol. 61, 2402-2407, 1995  
A:Title: Distribution of cryV-type insecticidal protein genes in Bacillus thuringiensis  
tomocidus.  
A:Reference number: I39814; MUID:95314293; PMID:7793960  
A:Accession: I39814  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-719 <RES>  
A:CROSS-references: GB:I36338; NID:G540281; PIDN:AAC36999.1; PID:G540282  
C:Genetics:  
A:Gene: cryV1  
C:Superfamily: parasporal crystal protein

Query Match 93.6%; Score 3503; DB 2; Length 719;  
Best Local Similarity 92.5%; Pred. No. 3.2e-241;  
Matches 665; Conservative 32; Mismatches 22; Indels 0; Gaps 0;

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QY 61 QTGIGIAGKILGTGVFPAGQIASLYSFIIGELWPKGKSQWEIFMEHVHEIINQKILTYA 120  
DB 61 QTGIGIAGKILGTGVFPAGQIASLYSFIIGELWPKGKNQWEIFMEHVHEIINQKISTYA 120  
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QY 241 TGLNLRGTAESVWRVYQNFQDRTMLVLDLVALFPSSYDTQMPYIKTAQTLREVTYDAI 300  
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DB 301 GTVHPNPFSTTWNNNAPFSAIEAAVIRSPHLLDFLEQVTIYSLLSRWSNTQYNNMW 360  
QY 361 GGHLESRPICGALNTSQGSTNTSINPVTLOFTSRDVRTTESLAGNLFLTPQVNGVPR 420  
DB 361 GGKLEPFTIGTGLNISQGSTNTSINPVTLPFTSRDVRTTESLAGNLFLTPQVNGVPR 420

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DB 421 VDFHWKFTPLPIASDNFYLYGAGVGTQLQDSNELPPTTGPQNVESYSHRLSHIGLIS 480  
QY 481 ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAENLSSGAAVVRGPGFTGGDILRRTN 540  
DB 481 ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAENLSSGAAVVRGPGFTGGDILRRTN 540  
QY 541 TGTFGDIRVNNPFPFAQRVVRIRYASTTDLQPHSTINGKAINQGNFSAATMRGEDLDYK 600  
DB 541 TGTFGDIRVNNPFPFAQRVVRIRYASTTDLQPHSTINGKAINQGNFSAATMRGEDLDYK 600  
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DB 601 TPTTIGFTTTPFSFSDVQSTFTTIGAWNFSSGNEVYIDRIEFVFPVEVYEAEDFEKAQEKV 660  
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DB 661 TALFTSTNPRGLKTDVKDHYDQVSNLVESLSDEFYLDKRELFVIVKAKQIHIERNM 719

## RESULT 5

S00873  
parasporal crystal protein cryBa1 - Bacillus thuringiensis subsp. thuringiensis  
N:Alternate names: parasporal crystal protein cryA4  
C:Species: Bacillus thuringiensis subsp. thuringiensis  
C:Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 09-Jul-2004  
C:Accession: S00873  
R:Brizard, B.L.; Whiteley, H.R.  
Nucleic Acids Res. 16, 2723-2724, 1988  
A:Title: Nucleotide sequence of an additional crystal protein gene cloned from Bacillus t  
A:Reference number: S00873; MUID:88203216; PMID:3362680  
A:Accession: S00873  
A:Molecule type: DNA  
A:Residues: 1-1228 <BRI>  
A:CROSS-references: UNIPROT:P05517; EMBL:X06711; NID:G40264; PIDN:CAA29898.1; PID:G580945  
C:Genetics:  
A:Gene: cryA4  
A:Start codon: TTG  
C:Superfamily: parasporal crystal protein  
C:Keywords: delta-endotoxin

Query Match 62.0%; Score 2321.5; DB 2; Length 1228;  
Best Local Similarity 63.6%; Pred. No. 1e-156;  
Matches 453; Conservative 80; Mismatches 162; Indels 17; Gaps 4;

QY 23 TDSLKNKNETDI-----ELKNNMNNEDYLRMSHESIDPFVSASTIQTGIGIAGKI 70  
DB 2 TSNRKNNEIINAVSNHSAQMDLLDPARIEDSLCIAEGNNIDPFVSASTVQTGINIAGRI 61  
QY 71 LGTLGVFPAGQIASLYSFIIGELWPKGKSQWEIFMEHVHEIINQKILTYARNKALSDLRG 130  
DB 62 LGVLGVFPAGQIASLYSFIIGELWPRGRDQWEIFLEHVEQLNQOITENARNALTARLQG 121  
QY 131 LGDALAVYHSESLESVENNRNTRARSVVKNQYIALELMFVKLPSPAVSGEVPLLPIYA 190  
DB 122 LGDSFPAVQOQSLIEDMLENRDDARTSVLYQVIALELOFLNAMPFLAIRNQEVPLLMVYA 181  
QY 191 QAANLHLLLRDASIIFGKEWGLSASEISTFYNRQVTRDYSIDHCIRKYNLTGNLRGYN 250  
DB 182 QAANLHLLLRDASLFGSEFGLTSQEIORYERQVTRDYSIDYCEVWYNTGNSLRGN 241  
QY 251 AKSWRYNQFRKDMTLMVLDLVALFPSSYDTLVYPIKTSQTLREVTYDAIGTVHPNOAFA 310  
DB 242 AASWRYNQFRDRLTLGVLDLVALFPSSYDTRYPINTSAQLREVYTDIGATGVN--VA 299  
QY 311 STTWYNNAPFSAIEAAVIRSPHLLDFLEKVTIYSLLSRWSNTQYNNMWGHRLESRP 370  
DB 300 SMWYNNAPFSAIEAAVIRSPHLLDFLEQVTIYSLLSRWSNTRHMTYRGHTIQSRPI 359  
QY 371 GGALNTSQGSTNTSINPVTLOFTSRDVRTTESLAGNLFLTPQVNGVPRVDFHWKPE 428  
DB 360 GGGLNTSTGATNTSINPVTLPFASRDVYRTESAGVLLWGILYLPFHGVPTVRFNFTNP 419

QY 429 -TLPIASDNFYVLGYAGVCTQLQDSNELPPTTQOPNYESYSHRLSHIGHLSHVKAL 487  
Db 420 QNISDRGTANYSQPYESPOLQKDSLETLPPTTERPNYESYSHRLSHIGHLSHVKAL 479  
QY 488 VYSWTHRSADRNTNTPNSITQIPLVKAFNLSSGAAGVVRGPGFTGGDILRLTNTGTGDI 547  
Db 480 VYSWTHRSADRNTNTPNRIQIPVKASSELPGFTVVRGPGFTGGDILRLTNTGGGPI 539  
QY 548 RVNINPPFAQVRVIRVASTTDLQFHSINGKAINQGNFATMWRGSDLYKTFRTIGF 607  
Db 540 RVTAGELQRYRIGFRYASTVDFPFVSRGTTVNNFRFLRTMNSGDELKYGNFVRAF 599  
QY 608 TTPFSDVQSFTTICAMNFSNGEVIYDRIEFVVEVYEAEDFEKAQKVTALTTST 667  
Db 600 TTPFTTQIOLIRTSIQGLSNGEVIYDKIEIIVTATFAEVDLEKRAQAVNALTNT 659  
QY 668 NPGRLKTDVKYHIDQVSNLVESLSEFYLDEKRELFEIVKYAKQIHIERNM 719  
Db 660 NPRELKTVDYHIDQVSNLVACLSEFCLDEKRELLEKVKYAKRLSDERNL 711

RESULT 6  
B42459  
Hypothetical protein 2 (cryIF 3' region) - Bacillus thuringiensis (strain aizawai) (frag  
C:Species: Bacillus thuringiensis  
C:Date: 10-Jul-1992 #sequence\_revision 10-Jul-1992 #text\_change 09-Jul-2004  
C:Accession: B42459  
R:Chambers, J.A.; Jelen, A.; Gilbert, M.P.; Jany, C.S.; Johnson, T.B.; Gawron-Burke, C.  
J. Bacteriol. 173, 3966-3976, 1991  
A:Title: Isolation and characterization of a novel insecticidal crystal protein gene fr  
A:Reference number: A42459; MUID:91286178; PMID:2061280  
A:Accession: B42459  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-380 <CHA>  
A:Cross-references: UNIPROT:O8KY61; UNIPROT:Q45740; GB:M63897  
C:Superfamily: parasporal crystal protein

Query Match 48.5%; Score 1813; DB 2; Length 380;  
Best Local Similarity 90.3%; Pred. No. 2.5e-121;  
Matches 343; Conservative 24; Mismatches 13; Indels 0; Gaps 0;

QY 1 MKLNPKDKHQSLSNAKVDKIATDSLKNETDIELKNNEDYLRMSHESIDPFVSATI 60  
Db 1 MKLNPKDKHQSLSNAKVDKIATDSLKNETDIELKNNEDYLRMSHESIDPFVSATI 60  
QY 61 QTGIGIAGKILGTGVPAGQIASLYSIFLGELWPKGKQWEIEMHVEEIIINQKILTYA 120  
Db 61 QTGIGIAGKILGTGVPAGQIASLYSIFLGELWPKGKQWEIEMHVEEIIINQKILTYA 120  
QY 121 RNKALSDLRGLDALAVYHESLESWENNRNTRARVVKQYIALELMFVKQLPSFAVSG 180  
Db 121 RNKALTDLKGGLDALAVYHESLESWGNRNKTRARVVKQYIALELMFVKQLPSFAVSG 180  
QY 181 BEVPLLPYAAANLHLLLDASIFGKEWGLSASEISTFYNROVERTDYSDHCIKWYN 240  
Db 181 BEVPLLPYAAANLHLLLDASIFGKEWGLSASEISTFYNROVERTDYSDHCIKWYN 240  
QY 241 TGLNLRGNTAKSWRYNQPKMTLMVLVLPSPYDILVPIKTTSLTREVYTDI 300  
Db 241 TGLNLRGNTAKSWRYNQPKMTLMVLVLPSPYDILVPIKTTSLTREVYTDI 300  
QY 301 GTVHPNOAFSTTWNNAFSAEIAEAVIRSPHLLDFLEKVTIYSLLSRWNSNTQYNNW 360  
Db 301 GTVHPNOAFSTTWNNAFSAEIAEAVIRSPHLLDFLEKVTIYSLLSRWNSNTQYNNW 360  
QY 361 GGHRLSRPIGALNTSTQ 380  
Db 361 GGHRLSRPIGALNTSTQ 380

RESULT 7

S49247  
parasporal crystal protein cry9Cai [validated] - Bacillus thuringiensis  
N:Alternate names: parasporal crystal protein cryIH  
C:Species: Bacillus thuringiensis  
C:Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 09-Jul-2004  
C:Accession: A59350; S49247  
R:Lambert, B.; Buysse, L.; Decock, C.; Janssens, S.; Piens, C.; Saey, B.; Seurinck, J.; V  
Appl. Environ. Microbiol. 62, 80-86, 1996  
A:Title: A Bacillus thuringiensis insecticidal crystal protein with a high activity agai  
A:Reference number: A59350; MUID:96141404; PMID:8572715  
A:Accession: A59350  
A:Molecule type: DNA  
A:Residues: 1-1157 <LAM>  
A:Cross-references: UNIPROT:Q45733; EMBL:Z37527; NID:G547554; PIDN:CAA85764.1; PID:G5475  
A:Experimental source: serovar tolworthi  
C:Comment: This parasporal crystal protein, active against corn borer and other insects,  
C:Superfamily: parasporal crystal protein  
C:Keywords: delta-endotoxin

Query Match 40.3%; Score 1507; DB 1; Length 1157;  
Best Local Similarity 44.1%; Pred. No. 9e-99;  
Matches 326; Conservative 116; Mismatches 217; Indels 80; Gaps 15;

QY 26 LKNETDIELKNNEDYLRMSHESIDPFVSAS-----TIQTGIGIAGKILGTGLVVPF 78  
Db 29 LASDPNALQNNYKDYLMQTDDEYDTSYINPSLSISGRDAVQTALTVVGRILGALGVFP 88  
QY 79 AGCIASLYSPILGELWPKGKQ-WEIEMHVEEIIINQKILTYARNKALSDLRGLDALAV 137  
Db 89 SQGIVSYFYLNTLWPNVDIAWAFMRQVDELVNOQTEFARNQALRQGLGDSFNV 148  
QY 138 YHESLESWENNRNTRARVVKQYIALELMFVKQLPSFAVSGEVPPLPIYAQANLHL 197  
Db 149 YQSLQNLWADRNTNLSVRAQFIALDLDFVNAIPLFAVNGQQVPLLSVYAQANLHL 208  
QY 198 LILRLASIFGKEWGLSASEISTFYNROVERTDYSDHCIKWYNKLNKRNKAKSVRY 257  
Db 209 LLKQASLFGEGWGFTQGEISTYIDRQLELTAKYNYCETWNTYDGLRLRGTNTESWLY 268  
QY 258 NQFRKMTLMVLVLPSPYDILVPIKTTSLTREVYTDIAGTVHPNOAFSTTWN 317  
Db 269 HQFRREMLVLVDVVALFPYDVRVLYPTGSPQLTREVYTDIPIVFNPNANVCLCRWGTN 328  
QY 318 NAPSATBAAVIRSPHLLDFLEKVTIYSLLSRWNS-NTQYNNMGCHRLSRPIG-GALN 375  
Db 329 PYNTFSELENAFIRPPHLLDFRLNLSLTSS--NRFPVSNFMDYNSGHTLRSLYNSAVQ 386  
QY 376 TSTQG---STNTSINP---VTLQFTSRDVRVATESLAGL-----NLF--LTQPVN 416  
Db 387 EDSYGLITTRATINPGVDGNRIESTAVDFRSALIGIVGNRASFPVPGFLNGTTSAN 446  
QY 417 GVRVDFHKKFTLPFASDNFYLYGAGVCTQLQDSNELPP-ETTQPNYESYSHRLSH 475  
Db 447 GGCR-----DLYTDNELPDEBETG-----SSTHRLSH 474  
QY 476 IGLIS-----ASHVKALVSWTHRSADRNTIENSTIQLPVKAFNLSSGAAVR 526  
Db 475 VTFFSFQINQAGSIANAGSVTYVWRDVLNIIITPNRIITQLPLVKASAPVSGTTVLK 534  
QY 527 GSGFTGGDILRNTGTGDIRVININPPFAQVRVIRVASTTDLQFHSINGKAINQGN 586  
Db 535 GSGFTGGGILRNTGTGTLRVTVNSPLTQQYRLRVRAFASTGNFSLRVLRGGVSIQDVR 594  
QY 587 FSATMNRGCDLYKTFRTIGTT-----PFSFSDVQSTFTIGANWSSGNEVYIDREF 640  
Db 595 LGSTWNRQCEIYESFFTRFTTTGPNPPTFTTQAQAILTVNAEGVSTGEYIDRIEI 654  
QY 641 VPVEVTYEAEYDFEKAQKVTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDRYLDEK 700  
Db 655 VPVNPAREAEEDLEAKKAVASLFTTRTD-GLQVNVTDYQVDQAANLVSCLSDDSOYGHDK 713  
QY 701 RELFEIVKYAKQIHIERNM 719



Db 714 KWLLEAVRAAKRLSRNL 732

## RESULT 8

S32645  
parasporal crystal protein cryiGal - Bacillus thuringiensis  
C:Species: Bacillus thuringiensis  
C>Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
C:Accession: S32645  
R:Lambert, B.  
submitted to the EMBL Data Library, April 1993  
A:Reference number: S32645  
A:Accession: S32645  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1166 <LAW>  
A:Cross-references: UNIPROT:Q45746; EMBL:Z22510; NID:9295861; PIDN:CAA80233.1; PID:g29586  
C:Superfamily: parasporal crystal protein  
C:Keywords: delta-endotoxin

Query Match 40.2%; Score 1503.5; DB 2; Length 1166;  
Best Local Similarity 46.6%; Pred. No. 1.6e-98;  
Matches 330; Conservative 97; Mismatches 210; Indels 71; Gaps 15;  
Qy 28 NETDIEKNNEDYLRMSHESIDPFVSASTIGTIGIAGKILGTGLGVFPAGQIASLYS 87  
Db 16 NPPESEIFNARNSN-----EGLVSQVSSGL---TRFLEAAVPEAGFALGLFD 60  
Qy 88 FILGELMPKGSQWEIFMEHVEEIIQKILTYARNKALSRLGLGDALAVYHESLSWVE 147  
Db 61 IIWGAL---GVDQSLFLRQIEQLRQIEITELERNRATALTGLSSSYNYVLEALREWE 117  
Qy 148 NNNTRARSVKNQYIALELMFVKLPSPFVSGVEVPLFIYQAANLHLLLRDSIFG 207  
Db 118 DPNNPASQERVRTRFLTDIAIVTGLPTLAIRNLEVNLSVYTOAANLHLLLRDAVYFG 177  
Qy 208 KEMGLSASEISTFVNRQVTRDYSKCIKWNTGLNLRGTAQNAKSWRVYRQNRKQWTL 267  
Db 178 ERWGLTQANIEDLTRUTSNQIEYSDHCARWYNOGLNEIGISR---RYLDFQRLDTIS 233  
Qy 268 VLDLVALFPSTLVPIKTSQLTREVYTDAL--GVVHPNQAPASTWYNNAPSFSAI 325  
Db 234 VLDLVALFPNYDIPTQSLTRITSPVAGNI-----NFGLS 276  
Qy 326 EAAVIRPHLLDFLEKVTIYSLRSWNTQYMNWGGHRLSRPI-----GGALNTSTQGS 381  
Db 277 IANVLRAPHLMDFIDRIVIVTNSVR--STPY---WAGHEVISRTGGQGNRIFPLVGV 331  
Qy 382 TNSINPVTLO---FT--SRDVYRTESLAGLNLFLTQPVNGVPRVDFHWKFFTLPIASDN 436  
Db 332 AANAEPVPIPTGFTDEQWYRARSRVVSFRSSGQDFSLVAVGLTIPSASVYRNG 391  
Qy 437 FYIYGYAGVGTQLODSNELPPETTGQPNVESYSHRLSHIGLISAS-----HYKALVYSW 491  
Db 392 F-----GFNT---DTIDEIPIE--GTDPTGYSHRLCHVGLASSPFIQYARAPIFSW 440  
Qy 492 THRSADRTNTEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRNTGTGDIRVNI 551  
Db 441 THRSATNTIAPVITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRNTGTGDIRVNI 500  
Qy 552 NPPFAQYRVRIRYASTDQLQFTSINGKAINQGNFSAVMNNGEDLDYKTRTIGTTPP 611  
Db 501 TAPLSQYRVRIRYASTDQLQFTYNTINGTTINIGNFSSTWDSGDDLDYGRFRVAGFTTP 560  
Qy 612 SFSDVQSTFTIGANNFSGNEVYIDRIEFVPEVVEYAEVDFEKAQEKVTALTSINPRG 671  
Db 561 TFSANSTFTIGAGFGSPNNEVYIDRIEFVPEVVEYAEVDFEKAQEKVTALTSINPRG 620  
Qy 672 LKTDVQYHIDQVSNLVESLSDEFYLDKEKRELFIYKAKQIHIERNM 719  
Db 621 LKTDVTDYHIDQVSNLVESLSDEFYLDKEKRELSEKVKHAKRLSDERNL 668

## RESULT 9

S32649  
parasporal crystal protein cryiPa3 - Bacillus thuringiensis  
C:Species: Bacillus thuringiensis  
C>Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
C:Accession: S32649  
R:Lambert, B.  
submitted to the EMBL Data Library, April 1993  
A:Reference number: S32645  
A:Accession: S32649  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1174 <LAW>  
A:Cross-references: UNIPROT:Q45749; EMBL:Z22512; NID:g295865; PIDN:CAA80235.1; PID:g29586  
C:Superfamily: parasporal crystal protein  
C:Keywords: delta-endotoxin

Query Match 39.9%; Score 1491.5; DB 2; Length 1174;  
Best Local Similarity 47.4%; Pred. No. 1.2e-97;  
Matches 323; Conservative 88; Mismatches 179; Indels 91; Gaps 14;

Qy 76 VFPAGQIASLYSIFILGELMPKGSQWEIFMEHVEEIIQKILTYARNKALSRLGLGDAL 135  
Db 49 VFGVGVAFLGLDINGFITP---SEWSLFLQIEQLRQIEITELERNRATITLIRGLADSY 105  
Qy 136 AYTHESLESWENNRNTRARSVKNQYIALELMFVKLPSPFVSGVEVPLFIYQAANL 195  
Db 106 EYVLEALREWEENPNNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANL 165  
Qy 196 HLLLRDASIFCKEGLSASEISTFVNRQVTRDYSKCIKWNTGLNLRGTAQNAKSW 255  
Db 166 HLLLRDASVFCQGGWGLDIATVNNHYNLINLIHRYTEHCLDTYNOGLENLRTNRQWS 225  
Qy 256 RYNQFRKQMTLVLDLVALFPSTLVPIKTSQLTREVYTDALGVVHPNQAPASTWY 315  
Db 226 RENQFRRELTVLVDLVALFPNYDARAYPIQTSQLTREIYTSVIEDSPVSA----- 278  
Qy 316 NNWAPS-PSAIAAVIRSPHLLDFLEKVTIYSLRSWNTQYMNWGGHRLSRPIGGAL 374  
Db 279 --NIPNGFNRAEFGV-RPEHLMDFVN-----SLFVTAETVRSQTWGGHLYSSR----- 324  
Qy 375 NTSQGSTNTSINPVTLOF-----TSRDVYRTESLAGLNLFLTQPVNGVP 419  
Db 325 -----NTAGNPINFIYGIFFGGAIWIADEDPFPFYI-----LSDPV--FV 365  
Qy 420 RVDHFKKPTLPDASDNFYIYGYAGVGTQLO-----DSNELPPETTGQPN 465  
Db 366 RGGF-----GNPHYVLGLRGVAFQQTGTNHTRTFRNSGTIDSLSDEIPQDNSGAP 415  
Qy 466 YESYSHRLSHI-----GLISASHV-KALVYSWTHRSADRTNTEPNSITQIPLVKAFL 518  
Db 416 WNDYSHVLNHTVFWPFWPGEIAGSDSWRAPMFSWTHRSADRTNINPNIITQIPAKAHL 475  
Qy 519 SSGAAVVRGPGFTGGDILRRNTGTGDIRVINPFPFAQYRVRIRYASTDQLQFTSIN 578  
Db 476 HSGSTVVRGPGFTGGDILRRNTGTGDIRVINPFPFAQYRVRIRYASTDQLQFTSIN 535  
Qy 579 GKAINQGNFSAVMNNGEDLDYKTRTIGTTPFSSDVSQSTETIGANNFSGNEVYIDRI 638  
Db 536 GTSVNGQNFQRTMNRKGNLESNFRTAGFTSTPFSNQAQSTFTLTGTQAFSN--QEVYIDRI 594  
Qy 639 EFVPEVVEYAEVDFEKAQEKVTALFTSNPRLKTDYKDHIDQVSNLVESLSDEFYLD 698  
Db 595 EFVPAEVEFEASDLEAQAQKAVNALFTSTSQLKLTNVTGYHIDQVSNLVACLSDDEFCLD 654  
Qy 699 EKRELFEIVKYAKQIHIERNM 719  
Db 655 EKRELSEKVKHAKRLSDERNL 675

## RESULT 10

A26513  
parasporal crystal protein - Bacillus thuringiensis (strain aizawai)



Db	228	RYNQFRRUTLVLDIVSLFPNDYBRTVPIRTVQSLTREIYTNPV-----L 273
Qy	316	NNNAPGF---SAIEAAVIRSPHLLDFLEKVTIYSLSRWSNTQYMMWGCHRESRPIC 371
Db	274	ENPDGSRGSAQIGEGS-IRSPHLMJILNSTIITYTDAHR---GEY--YWSGHQIVASPVG 327
Qy	372	-----GAL-NTSQSGTNTSINPVTLQFTSRDVTRESLAGNLFLTPQVNGVP 419
Db	328	PSGPETFPFLYGTMGNAPOQRIVAQLQGQVYRLSTLVRPNFNGIN--NQULSV 384
Qy	420	RVDFWKFTPLPIASDNFYLYGAGVGTQLODSNELPPETTGOPNVYESYHRLSHIGI 479
Db	385	GTEFAYG-----TSSNLPASVYRKSGT--VDSLDEIIPPQNNVPPRQGFSHRLSHVSMF 436
Qy	480	-----SASHVKALVYSWTHRSADRTWTIEPNISITQIPLVKAPNLSSGAAVRGPGFTG 532
Db	437	RSGFNSSVSYIIRAPFMFSWIHSABFNIIIPSSQITQIPLTKSTNLGSGYVVKGPGFTG 496
Qy	533	GDLIRRTVGTGDRVNVNPPFAQRYVRTRYASTTDLQPHTSINGKALNQGNFSAITN 592
Db	497	GDLIRRTSPQISTURVNITAPLSQRYEVRTRYASTTNLQPHTSIDGRPINQGNFSAITS 556
Qy	593	RGBDLKYKTRIGETTPPFSFDVGSTFTIGAMFFSGNEVYIDRIEFVEVETVYBAED 652
Db	557	SGSNLQSGSFRTVGTTPPFTNSNGSSVFTLSAHVFNSGNEVYIDRIEFVPAETPEAYD 616
Qy	653	FEKAQEKVIALTSTNPGLKTDUKDVHIDQVSNLVSLSDEFVLDEKRLFLVYKAKO 712
Db	617	LERAQKAVNELFTSSNQGLKTDVDYHDIDQVSNLVECLDSEPCLDKESLSEKVHAKR 676
Qy	713	IHIERN 719
Db	677	LSDERNL 683

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RESULT 12
A29125
parasporal crystal protein Bt2 - Bacillus thuringiensis subsp. kurstaki (strain HD-1)
C:Species: Bacillus thuringiensis subsp. kurstaki
C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 09-Jul-2004
C:Accession: A29125
R:Rischhoff, D.A.; Bowdish, K.S.; Perlak, F.J.; Marrone, P.G.; McCormick, S.M.; Niedermeyer,
Bio/Technology 5, 807-813, 1987
A:Title: Insect Tolerant transgenic tomato plants.
A:Reference number: A29125
A:Accession: A29125
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-1156 <FIS>
A:Cross-references: UNIPROT:Q9P296; UNIPROT:Q93T21
C:Superfamily: parasporal crystal protein
C:Keywords: delta-endotoxin

Query Match 39.6%; Score 1480.5; DB 2; Length 1156;
Best Local Similarity 46.5%; Pred. No. 6.9e-97;
Matches 310; Conservative 105; Mismatches 195; Indels 57; Gaps 12;

Qy 76 VPGAQIASLYSFYLGELWPKGSQSEIPEWHEVEIINOKILTYARNKALSDLEGIGDAL 135
Db 51 VPGAQFVLGLVDIWGIF---GPSQDAFLVQIEQLINQRIEFARNQALSRLEGSLNY 107

Qy 136 AVYHESLESWVENRNNTRASVYKNQYIALELMFVQKLPSPFVSGEEVPLPIYAQAANL 195
Db 108 QIVAESPREWEADPTNPALREEMRIQENDMNSALTTAIPLFAVQNYQVPLLSVYVQAANL 167

Qy 196 HLLLLRDASTFGKEWGLSAGEISFTFYNRQVETRDYSDHCGIKMYNTGLNNLRGNAKSW 255
Db 168 HLSVLRDVSVFGGWGPDATINRSYNDLITGLNYTDHVRVNTGLERWGPDSRDWI 227

Qy 256 RYNQFRKDMTLMVLDLVALPSPYDITLYPIKTTSQLPREVYITDAIGTWENQAFASTTW 315
Db 228 RYNQFRRELFTLVLIDVLSLPENDSDRYPRTVTSQLTREIYTPV-----L 273

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Qy	316	NNNADSF-----SAIEAAVIRSFHLLDFLEKVTIYSLLSRMSNTQYMMWCGHRLSRPIG	371
Db	274	ENFDGSRGSAQIEGS-IRSFHLMILNLSITIVTDAHR--GEY--YMSGHQIMASPGV	327
Qy	372	-----GAL-NTSTQSTNTSINPVTLOFTSRDVIYRTSLAGLNLFLTQPVNGVP	419
Db	328	FSGPEFTPLYGTWGNAAPOQRIVAQLCGQGVYRTLSSTLYRRPFNIGIN--NQQLSVLD	384
Qy	420	RVDFFHWKFTPLIADNPFYIYGAGVGTQLODSNELPPETTCQPNVYESVHRLSHGLI	479
Db	385	GTEFAYG-----TSGNLPASVYKSGT--VDSUDEIPQNNNVNPRQGSFHLSHVSMF	436
Qy	480	-----SASHYKALVYSWTHRSADRTNTIPENSITQIPLVKAFNLSSGAAVVRGPGFTG	532
Db	437	RSGFNSSVSIIRAPMFWIHKRSAEFNMIIPSSQITQIPLTKSTNLGSGTSVVKGPGFTG	496
Qy	533	GDILARTNTGTGDIRVNNINPPFAORVYRIRVASTTDLQFHTSINGKAINOCNPSATNN	592
Db	497	GDILRTSPQGISURLVNITAPLSQRTKRVIRVASTTNLQFHTSIDGRPINQGNFSATMS	556
Qy	593	RGEDLDYKTRTIGFTTTFPSFSDVQSTFTIGAMFFSSGNEVYIDRIEFVPVEVYEAED	652
Db	557	SGSNLQSGSFRTVGTFTTFFNFSNGSSVFTLSAHVFNESGNEVYIDRIEFVPAEVTFEAED	616
Qy	653	FKAQEKYTAFTSNPNGLKTDYKHIDOVSNLYESLDEFLVDEKELFEIVKYAKO	712
Db	617	LERAQKAVNELFTSSNQIGLTKDVTYHIDQVSNLVCLSDFCLEKELSEKVAHAKR	676
Qy	713	IHIERNM 719	
Db	677	LSDERNL 683	
RESULT 13			
S02134			
parasporal crystal protein cryIC1 - Bacillus thuringiensis (strain aizawai ICI			
N;Alternate names: delta-endotoxin ICI; entomocidal crystal protein			
C;Species: Bacillus thuringiensis			
A;Variety: strain aizawai ICI			
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004			
C;Accession: S02134; S04994			
R;Haider, M.Z.; Ellar, D.J.			
Nucleic Acids Res. 16, 10927, 1988			
A;Title: Nucleotide sequence of a Bacillus thuringiensis aizawai ICI entomocid			
A;Reference number: S02134; MUID:89083518; PMID:3205732			
A;Accession: S02134			
A;Status: translation not shown			
A;Molecule type: DNA			
A;Residues: 1-1155 <HAI>			
A;Cross-references: UNIPROT:P06578; EMBL:X13233; NID:g40277; PIDN:CAA31620.1; I			
A;Experimental source: Strain aizawai ICI			
R;Haider, M.Z.; Ellar, D.J.			
J. Mol. Biol. 208, 183-194, 1989			
A;Title: Functional mapping of an entomocidal delta-endotoxin. Single amino ac			
A;Reference number: S04994; MUID:89362455; PMID:2769751			
A;Accession: S04994			
A;Molecule type: DNA			
A;Residues: 429-449, 'A', 451-724 <HAW>			
A;Cross-references: EMBL:X16315			
A;Experimental source: strain aizawai ICI			
C;Comment: This toxin is lethal to the larvae of lepidopterans and dipterans.			
C;Superfamily: parasporal crystal protein			
C;Keywords: delta-endotoxin			
Query Match 39.1%; Score 1463.5; DB 2; Length 1155;			
Best Local Similarity 46.0%; Pred. No. 1 ie-95;			
Matches 307; Conservative 105; Mismatches 198; Indels 57; Gaps 12			
Qy	76	VFPAGIASLYSFILGEIWPKGQSWEIFWEHVEEINQKILTYARNKALSDLRGLGDAL	135
Db	51	VFGAGFVLGLVDITWGIF--GPSQDAFLVQIEQLINQRIEFARNOAISRLGLSNLY	107

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Query Match      39.1%; Score 1463.5; DB 2; Length 1155;
Best Local Similarity 46.0%; Pred.No. 1.1e-98;
Matches 307; Conservative 105; Mismatches 195; Indels 57; Gaps 12

Qy       76 VFFAQIASLVSFILGELWPKGSQWFIFMEHVEEINIKLTYYANKALSRLRGLDAL 135
          ||| | | | | | : | : | : | : | : | : | : | : | : | : | : |
Db       51 VPAGFVLGVLDITWGIF--GPSQDAFLVQLQEIQINRIEFARQAQSIRLEGISLNLY 107
```

QY 136 AVYHESLESWENRNTRARSVVKNQYIALELMFVQKLPSPFAVSGEEVPLLPYIAQAANL 195  
Db 108 QIYAESFREWEADPTNPALREEMRIQFNDMSALTATPLFAVQNYQVPLLSVVYQAANL 167  
QY 196 HLLLRDASIFKWKGLSASEISTFYNQVERTRDYSCHICKWNTGLNNLRGNNAKSW 255  
Db 168 HLLSVLRDVSFQORWGLDVATINSRYNDLTRIGITYTDYAVRWYNTGLERWVGPSDRDW 227  
QY 256 RYNQFRKDMTLMVLDAVALFSPYDVLVPIKTTSQLREVYTDALGTVHPNQAFASITWY 315  
Db 228 RYNQFRRELTALVLDIVSLFPNYSRTYPIRTVSQLTREIYNPV-----L 273  
QY 316 NNNAPSF-----SAIBAAVIRSPHLLDFLEKVTIYSLSRWNTQYMMNGHRLSRPIG 371  
Db 274 ENFDGSRGSAQIGBS-IRSPHLLDILNSITIVTDAHR---GEV--YWSGHQIMASPVG 327  
QY 372 -----GAL-NTSTQGSTNTSINPVLTQFTSRDVRVYTESLAGNLFLTOPVNGVP 419  
Db 328 FSGPEFTPLYGTMGNAAAPQORIVAOLGQGVYRTLSSTLYRRPFIIGIN---NQQLSVLD 384  
QY 420 RYDHPKFTPLPIASDNFYLGYAGVGTQLODSNELPPTTQOPNYESYSHRLSHICLI 479  
Db 386 GTEFAYG-----TSNLPMSAVYKSGT--VDSLDEIPQNNVPVPRQGFHRLSHVSMF 436  
QY 480 -----SASHVKALVYSWTHRSADRTNTEIPNSITQIPLVKAFNLSSGAAVVRGPGFTG 532  
Db 437 RSGFNSVSIIRPMPFMSWIRHSAEFNNIIPSSQITQIPLTKSTNLGSGTSVVKGPFTG 496  
QY 533 GDLARTNTGFGDIRVNIINPPFAQRYVRIRYASTTDQPHTSINGKAINQGNFSATMN 592  
Db 497 GDLARTSPQISTLRVNIITAPLSQRYVRIRYASTNLQHTSIDGRPINQGNFSATMS 556  
QY 593 RGEDLDYKFTRTIGTTPFSDVOSTFTIGAMFSSGNEVYIDRIEFVPEVYTYAEYD 652  
Db 557 SGNLSQSGFRIVGTTPFNSGSSVFTLSAHVFNSGNEVYIDRIEFVPAEVTFEAYD 616  
QY 653 EKAQEKVTALFTSTNPRGLTKDVKYHIDQVSNLVESLSDPYLDEKRELFEIVYAKQI 713  
Db 617 ERAQEAVALFTSPNQIGLKTVDYHIDQVSNLVESLSDPYLDEKRELFEIVYAKQI 677  
QY 713 IHIERNM 719  
Db 677 LSDEENL 683  
RESULT 14  
A41052  
Parasporal crystal protein cryAel - Bacillus thuringiensis (strain alesti)  
C/Species: Bacillus thuringiensis  
C/Date: 03-Apr-1992 #sequence\_revision 03-Apr-1992 #text\_change 09-Jul-2004  
C/Accession: A41052  
R/Lee, C.S.; Aronson, A.I.  
J. Bacteriol. 173, 6635-6638, 1991  
A/Title: Cloning and analysis of delta-endotoxin genes from Bacillus thuringiensis subsp  
A/Reference number: A41052; PMID:92011442; PMID:1655719  
A/Accession: A41052  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-1181 <LSE>  
A/Cross-references: UNIPROT:Q03748; GB:M65252; NID:g142874; PIDN:AAA22410.1; PID:g142875  
C/Superfamily: parasporal crystal protein  
C/Keywords: delta-endotoxin  
Query Match 39.1%; Score 1463.5; DB 2; Length 1181;  
Best Local Similarity 45.9%; Pred. No. 1.2e-95;  
Matches 306; Conservative 104; Mismatches 201; Indels 55; Gaps 11;  
QY 76 VFPAGQIASLYSIFLIGELWPKGQWEIEMHEVEIINQKILTYARNKALSGLGLDAL 135  
Db 51 VPCAGFVLGLIDLIWGFV---GPSQWDAFLVQIEQLISQRIEFPARNQAIISRLGLSNLY 107  
QY 136 AVYHESLESWENRNTRARSVVKNQYIALELMFVQKLPSPFAVSGEEVPLLPYIAQAANL 195

Db 108 QIYAEAFREWEADPTNPALREEMRIQFNDMSALTATPLFTVQNYQVPLLSVVYQAANL 167  
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Db 168 HLLSVLRDVSFQORWGLDVATINSRYNDLTRIGITYTDYAVRWYNTGLERWVGPSDRDW 227  
QY 256 RYNQFRKDMTLMVLDAVALFSPYDVLVPIKTTSQLREVYTDALGTVHPNQAFASITWY 315  
Db 228 RYNQFRRELTALVLDIVSLFPNYSRTYPIRTVSQLTREIYNPV-----L 273  
QY 316 NNNAPSFASIAEAV---IRSPHLLDFLEKVTIYSLSRWNTQYMMNGHRLSRPIG- 371  
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QY 372 -----GAL-NTSTQGSTNTSINPVLTQFTSRDVRVYTESLAGNLFLTOPVNGVP 420  
Db 329 SGPEFTPLYGTMGNAAAPQORIVAOLGQGVYRTLSSTFYRNPFIIIGIN---NQQLSVLDG 385  
QY 421 VDPHMKFTPLPTASDNFYLGYAGVGTQLODSNELPPTTQOPNYESYSHRLSHICLI- 479  
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QY 480 -----SASHVKALVYSWTHRSADRTNTEIPNSITQIPLVKAFNLSSGAAVVRGPGFTG 533  
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QY 534 DILRTNTGFGDIRVNIINPPFAQRYVRIRYASTTDQPHTSINGKAINQGNFSATMN 593  
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QY 594 GEDLDYKFTRTIGTTPFSDVOSTFTIGAMFSSGNEVYIDRIEFVPEVYTYAEYD 653  
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QY 654 EKAQEKVTALFTSTNPRGLTKDVKYHIDQVSNLVESLSDPYLDEKRELFEIVYAKQI 713  
Db 618 ERAQEAVALFTSPNQIGLKTVDYHIDQVSNLVESLSDPYLDEKRELFEIVYAKQI 677  
QY 714 IHIERNM 719  
Db 678 SDERNL 683  
RESULT 15  
I39838  
Parasporal crystal protein - Bacillus thuringiensis  
C/Species: Bacillus thuringiensis  
C/Date: 19-Jul-1996 #sequence\_revision 19-Jul-1996 #text\_change 09-Jul-2004  
C/Accession: I39838  
R/Hefford, M.A.; Brousseau, R.; Prefontaine, G.; Hanna, Z.; Condie, J.A.; Lau, P.C.K.  
J. Biotechnol. 6, 307-322, 1987  
A/Title: Sequence of a lepidopteran toxin gene of Bacillus thuringiensis subsp kurstaki  
A/Reference number: I39838  
A/Accession: I39838  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-1155 <RES>  
A/Cross-references: UNIPROT:P06578; GB:M37263; NID:g142885; PIDN:AAA22420.1; PID:g142886  
C/Superfamily: parasporal crystal protein  
C/Keywords: delta-endotoxin  
Query Match 39.1%; Score 1461.5; DB 2; Length 1155;  
Best Local Similarity 46.2%; Pred. No. 1.6e-95;  
Matches 308; Conservative 103; Mismatches 199; Indels 57; Gaps 12;  
QY 76 VFPAGQIASLYSIFLIGELWPKGQWEIEMHEVEIINQKILTYARNKALSGLGLDAL 135  
Db 51 VPCAGFVLGLIDLIWGFV---GPSQWDAFLVQIEQLINQRIEFPARNQAIISRLGLSNLY 107  
QY 136 AVYHESLESWENRNTRARSVVKNQYIALELMFVQKLPSPFAVSGEEVPLLPYIAQAANL 195  
Db 108 QIYAEFREWEADPTNPALREEMRIQFNDMSALTATPLFAVQNYQVPLLSVVYQAANL 167

QY 196 HLLLRDASIFGKSWGLSASEISTFYNRQVERTDYSCHICKWYNTGLNNLRGTNAKSWV 255  
 D5 168 HSLVLRDVSVFQWQAGDAATINSYNDLTELIGNYTDHAVRWYNTGLERWGPDSWDWI 227  
 QY 256 RYNQFRKMDLMLVDLVALPPSYDTLVPYIKTTSQLTREYVYTDAGTGVHPNQAFSTWY 315  
 D5 228 RYNQFRRELTLVLDIVSLFNYDSRTYPIRTVSQLTREYVTFV-----L 273  
 QY 316 NNNAPSF-----SATEAAVIRSPHLDLEKVTIYSLLSRWSNTQYMMWGGHRLSPIG 371  
 D5 274 ENFGSPRGSQGIIEGS-IRSPHLMIDILNSITIYTDHR--GEY--YWSGHQIMASPVG 327  
 QY 372 -----GAL-NTSTQGSTNTSINPVTLOFTSRDVTYRTESLAGLNLELTQPVNGVP 419  
 D5 328 FSGPEFTFPLXGTMGNAAPQORIWAQLGQGVYRTLSSTLYRRPENIGIN--NQQLSVLD 384  
 QY 420 RVDPHWKEFTPLIASDNFYLYGAGVGTQLODSNELPPETTGQPNYESYSHRLSHIGLI 479  
 D5 385 GTEFAYG-----TSSNLPASVYRKSGT--VDSLDEIPQNNNVPPQGFHRLSHVSMF 436  
 QY 480 -----SASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSGGAUVVPGGFTG 532  
 D5 437 RSGFNSSVSITIRAPMFSWTHRSANFNNIIPSSQITQIPLTKSTNLGSGTVVKGPGFTG 496  
 QY 533 GDILRTNTGFGDIRVNIINPPFAQRYRVRIRYASTTDLOFHTSINGKAINQGNFSATMN 592  
 D5 497 GDILRTSPQGISTRVNIITAPLSQRYRVRIRYASTTNLOFHTSIHGRPINQGNFSATMS 556  
 QY 593 RGEDLDYKFTGTGFTTFFGFSVDQSTFTIGAMNPFSSGNEVYIDRIEFVPEVTEAEYD 652  
 D5 557 SGNLQSGSFHGLGFTTFFNFSNGSVFTLSAHVFNSGNEVYIDRIEFVPAEVTFEAEYD 616  
 QY 653 PEKAEKVLTALFTSTNPRGLKTDVKYHIDQVSNLVESSLDEFYLDKRELFEIVKYAKQ 712  
 D5 617 LERAKAVNELFTSSNOIGLKTVDYHIDQVSNLVECLSEFCLDEKELSEKVKHANG 676  
 QY 713 IHIERNM 719  
 D5 677 LSDERNL 693

Search completed: October 28, 2004, 18:32:04  
 Job time : 26.191 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 28, 2004, 17:52:12 ; Search time 98.4365 Seconds  
(without alignments)  
4202.652 Million cell updates/sec

Title: US-10-019-823B-59

Perfect score: 3742

Sequence: 1 MKLKNPDKQSLSSNAKVDK.....KRELFEIVKYAKQIHIRMN 719

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 segs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt 02.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query Match %	Score	Length	DB ID	Description
1	3742	100.0	719	1	CLIB_BACTE
2	3598	96.2	719	2	Q9F0P8
3	3546	94.8	719	1	CLIB_BACTU
4	3520	94.1	719	1	CLIB_BACTK
5	3520	94.1	719	2	Q6X181
6	3520	94.1	719	2	AAP86782
7	3515	93.9	719	2	Q93N75
8	3514	93.9	719	2	Q85796
9	3512	93.9	719	2	CAC85964
10	3510	93.8	719	2	Q8K161
11	3311	88.5	719	1	CLIB_BACTU
12	2459	65.7	1229	1	CLIB_BACTU
13	2459	65.7	1233	1	CLIB_BACTM
14	2322.5	62.1	1228	2	Q93775
15	2321.5	62.0	1228	1	CLIB_BACTK
16	2313.5	61.8	1228	2	Q93NM5
17	2243	59.9	849	2	Q6PYW8
18	2243	59.9	849	2	AAS93797
19	2243	59.9	1227	1	CLIB_BACTU
20	2129	56.9	1231	2	Q8KNY2
21	2116	56.5	1231	1	CLIB_BACTV
22	1863	52.5	1215	1	CLIB_BACTM
23	1817	48.6	381	2	Q45740
24	1670	44.6	1144	2	Q8KZL7
25	1657.5	44.3	1157	1	C8AA_BACUK
26	1507	40.3	1157	1	C9CA_BACTO
27	1503.5	40.2	1166	1	CLIB_BACTU
28	1491.5	40.0	1169	1	CLIB_BACTM
29	1481.5	39.9	1174	2	Q45749
30	1484.5	39.7	1169	1	C8BA_BACUK
31	1480.5	39.6	1155	1	CLIB_BACTK

32 1480.5 39.6 1155 2 Q7BE98 Q7be98 bacillus th  
33 1480.5 39.6 1155 2 Q9F296 Q9f296 bacillus th  
34 1480.5 39.6 1155 2 AAN76494 AAN76494 bacillus  
35 1480.5 39.6 1155 2 AAO13302 AAO13302 bacillus  
36 1475.5 39.4 1156 2 Q6GJA7 Q6gja7 bacillus th  
37 1473.5 39.4 1118 2 Q9AM83 Q9am83 bacillus th  
38 1470.5 39.3 793 2 Q6PYW7 Q6pyw7 bacillus th  
39 1470.5 39.3 793 2 AAS93798 AAS93798 bacillus th  
40 1470.5 39.3 793 2 Q6EIX3 Q6eix3 bacillus th  
41 1468.5 39.2 1155 2 Q93T21 Q93t21 bacillus th  
42 1468 39.2 1167 1 CLIB\_BACTU CLIB\_BACTU  
43 1463.5 39.1 1181 1 CLIB\_BACTL CLIB\_BACTL  
44 1459 39.0 1180 2 Q9S5V8 Q9s5v8 bacillus th  
45 1457 38.9 1176 2 Q7WZT9 Q7wzt9 bacillus th

#### ALIGNMENTS

#### RESULT 1

CLIB\_BACTE  
ID CLIB\_BACTE STANDARD; PRT; 719 AA.  
AC Q45709;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DE Pesticidal crystal protein cryIIb (insecticidal delta-endotoxin  
GN Name=cryIIb; Synonyms=cryII(b), cryV, cryV465;  
OS Bacillus thuringiensis (subsp. entomocidus).  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=1436;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BP465;  
RX MEDLINE=95314293; PubMed=7793960;  
RA Shin B.-S., Park S.-H., Choi S.-K., Koo B.-T., Lee S.-T., Kim J.-I.;  
RT "Distribution of cryV-type insecticidal protein genes in Bacillus  
RT thuringiensis and cloning of cryV-type genes from Bacillus  
RT thuringiensis subsp. kurstaki and Bacillus thuringiensis subsp.  
RT entomocidus";  
RL Appl. Environ. Microbiol. 61:2402-2407 (1995).  
CC FUNCTION: Promotes colitodermotic lysis by binding to the midgut  
CC epithelial cells of certain coleopteran and lepidopteran species.  
CC Active on Plutella xylostella but not on Bombyx mori  
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during  
CC sporulation and is accumulated both as an inclusion and as part of  
CC the spore coat.  
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-  
CC terminus.  
CC -!- SIMILARITY: Belongs to the delta endotoxin family.  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/  
CC or send an email to license@isb-sib.ch).  
CC  
CC EMBL; U07642; AAA82114.1; -.  
CC PIR; I40590; I40590.  
CC HSSP; P02965; 1CIY.  
CC InterPro; IPR001178; Endotoxin.  
CC InterPro; IPR005638; endotoxin\_C.  
CC InterPro; IPR005639; endotoxin\_N.  
CC Pfam; PF03944; Endotoxin\_C; 1.  
CC Pfam; PF00555; Endotoxin\_M; 1.  
CC Pfam; PF03945; Endotoxin\_N; 1.  
KW Sporulation; Toxin.  
SQ SEQUENCE 719 AA; 81295 MW; E8210ABEAE97688E CRC64;

Query Match 100.0%; Score 3742; DB 1; Length 719;  
 Best Local Similarity 100.0%; Pred. No. 5,4e-250;  
 Matches 719; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLKNPKDQHSLSNAKVDKIATDSLKNETDIELKMNEDYLRMSHESIDPVSASTI 60  
 DB 1 MKLKNPKDQHSLSNAKVDKIATDSLKNETDIELKMNEDYLRMSHESIDPVSASTI 60

QY 61 QTGIGIAGKILGTGVPFAGQIASLYSIFLGELMPKGSQWEIFMEHVEEIIINOKILTYA 120  
 DB 61 QTGIGIAGKILGTGVPFAGQIASLYSIFLGELMPKGSQWEIFMEHVEEIIINOKILTYA 120

QY 121 RNKALSDRLGDLAVVHSHESLVENNRNTRASVVKQYIALELMFVKLSPFAVSG 180  
 DB 121 RNKALSDRLGDLAVVHSHESLVENNRNTRASVVKQYIALELMFVKLSPFAVSG 180

QY 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVTRDYSDHCIKWYN 240  
 DB 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVTRDYSDHCIKWYN 240

QY 241 TGLNLRGTNAKSWRYNQFRKDMTLMVLDLVALPSPSYDTLVYPIKTTQSOLTREVYTDI 300  
 DB 241 TGLNLRGTNAKSWRYNQFRKDMTLMVLDLVALPSPSYDTLVYPIKTTQSOLTREVYTDI 300

QY 301 GTVHPNQAFSTTWNNAAPSFAIEAAVIRSPHLLDFLEKVTIYSLSRWSNTQYNNMW 360  
 DB 301 GTVHPNQAFSTTWNNAAPSFAIEAAVIRSPHLLDFLEKVTIYSLSRWSNTQYNNMW 360

QY 361 GGHRLSPIGALNTSTQGSTNTSINPVTLOFTSRDVRVRESLAGNLFLOTPVNGVPR 420  
 DB 361 GGHRLSPIGALNTSTQGSTNTSINPVTLOFTSRDVRVRESLAGNLFLOTPVNGVPR 420

QY 421 VDFHMKFPTLPASDNFYVLGAGVGTQLODSENELPETTGQPNYESYSHRLSHIGLIS 480  
 DB 421 VDFHMKFPTLPASDNFYVLGAGVGTQLODSENELPETTGQPNYESYSHRLSHIGLIS 480

QY 481 ASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 540  
 DB 481 ASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 540

QY 541 TGTFGDIRVNPFPQAQRYRIRYASTTDLOFTSINGKAINQGNFSATWNGEDLDYK 600  
 DB 541 TGTFGDIRVNPFPQAQRYRIRYASTTDLOFTSINGKAINQGNFSATWNGEDLDYK 600

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 DB 601 TFRITGFTTSPFSQVSTFTIGAWNFSSGNEVYIDRIEFVPVETVYEAEDFEKAQEKV 660

QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQIHIERNM 719  
 DB 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQIHIERNM 719

RESULT 2  
 Q9F0P8 PRELIMINARY; PRT; 719 AA.

AC Q9F0P8;  
 DT 01-MAR-2001 (TREMELrel. 16, Created)  
 DT 01-MAR-2001 (TREMELrel. 16, Last sequence update)  
 DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)  
 DE Cryll.

GN Name=Cryll;  
 OS Bacillus thuringiensis.  
 OG Plasmid pBrc19.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1428;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BT007;  
 RX MEDLINE=22837682; PubMed=12957903;  
 RA Song F., Zhang J., Gu A., Wu Y., Han L., He K., Chen Z., Yao J.,  
 Hu Y., Li G., Huang D.;  
 RA "Identification of cryII-type genes from Bacillus thuringiensis

strains and characterization of a novel cryII-type gene.";  
 Appl. Environ. Microbiol. 69:5207-5211(2003).  
 DR EMBL; AF211190; AAG43526.1; -;  
 DR HSSP; P02965; 1C1Y.  
 DR GO:0005102; F:receptor binding; IEA.  
 DR GO:0006952; P:defense response; IEA.  
 DR GO:0009405; P:pathogenesis; IEA.  
 DR InterPro; IPR001178; Endotoxin.  
 DR InterPro; IPR005638; endotoxin\_C.  
 DR InterPro; IPR005639; endotoxin\_N.  
 DR InterPro; IPR008979; Gal bind like.  
 DR Pfam; PF03944; Endotoxin\_C; 1.  
 DR Pfam; PF00555; Endotoxin\_M; 1.  
 DR Pfam; PF03945; Endotoxin\_N; 1.  
 KW Plasmid.  
 SQ SEQUENCE 719 AA; 81024 MW; 7E174B1922C435E6 CRC64;

Query Match 96.2%; Score 3598; DB 2; Length 719;  
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 Matches 684; Conservative 23; Mismatches 12; Indels 0; Gaps 0;

QY 1 MKLKNPKDQHSLSNAKVDKIATDSLKNETDIELKMNEDYLRMSHESIDPVSASTI 60  
 DB 1 MKLKNPKDQHSLSNAKVDKIATDSLKNETDIELKMNEDYLRMSHESIDPVSASTI 60

QY 61 QTGIGIAGKILGTGVPFAGQIASLYSIFLGELMPKGSQWEIFMEHVEEIIINOKILTYA 120  
 DB 61 QTGIGIAGKILGTGVPFAGQIASLYSIFLGELMPKGSQWEIFMEHVEEIIINOKILTYA 120

QY 121 RNKALSDRLGDLAVVHSHESLVENNRNTRASVVKQYIALELMFVKLSPFAVSG 180  
 DB 121 RNKALSDRLGDLAVVHSHESLVENNRNTRASVVKQYIALELMFVKLSPFAVSG 180

QY 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVTRDYSDHCIKWYN 240  
 DB 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVTRDYSDHCIKWYN 240

QY 241 TGLNLRGTNAKSWRYNQFRKDMTLMVLDLVALPSPSYDTLVYPIKTTQSOLTREVYTDI 300  
 DB 241 TGLNLRGTNAKSWRYNQFRKDMTLMVLDLVALPSPSYDTLVYPIKTTQSOLTREVYTDI 300

QY 301 GTVHPNQAFSTTWNNAAPSFAIEAAVIRSPHLLDFLEKVTIYSLSRWSNTQYNNMW 360  
 DB 301 GTVHPNQAFSTTWNNAAPSFAIEAAVIRSPHLLDFLEKVTIYSLSRWSNTQYNNMW 360

QY 361 GGHRLSPIGALNTSTQGSTNTSINPVTLOFTSRDVRVRESLAGNLFLOTPVNGVPR 420  
 DB 361 GGHRLSPIGALNTSTQGSTNTSINPVTLOFTSRDVRVRESLAGNLFLOTPVNGVPR 420

QY 421 VDFHMKFPTLPASDNFYVLGAGVGTQLODSENELPETTGQPNYESYSHRLSHIGLIS 480  
 DB 421 VDFHMKFPTLPASDNFYVLGAGVGTQLODSENELPETTGQPNYESYSHRLSHIGLIS 480

QY 481 ASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 540  
 DB 481 ASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 540

QY 541 TGTFGDIRVNPFPQAQRYRIRYASTTDLOFTSINGKAINQGNFSATWNGEDLDYK 600  
 DB 541 TGTFGDIRVNPFPQAQRYRIRYASTTDLOFTSINGKAINQGNFSATWNGEDLDYK 600

QY 601 TFRITGFTTSPFSQVSTFTIGAWNFSSGNEVYIDRIEFVPVETVYEAEDFEKAQEKV 660  
 DB 601 TFRITGFTTSPFSQVSTFTIGAWNFSSGNEVYIDRIEFVPVETVYEAEDFEKAQEKV 660

QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQIHIERNM 719  
 DB 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQIHIERNM 719

RESULT 3  
 CLIC\_BACTU  
 ID CLIC\_BACTU STANDARD; PRT; 719 AA.



AC O87404;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 08-JUL-2004 (Rel. 44, Last annotation update)  
 DE Pesticidal crystal protein cryIIc (insecticidal delta-endotoxin)  
 DE CryII(c) (Crystalline entomocidal protoxin) (81 kDa crystal protein).  
 GN Name=cryIIc; Synonyms=cryII(c);  
 OS Bacillus thuringiensis.  
 OG Plasmid.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1428;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C18 / Egypt;  
 RA Osmay Y.A., Madkour M.A., Bulla L.A. Jr.;  
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: Promotes colloidosmotic lysis by binding to the midgut  
 CC epithelial cells of insects.  
 CC -1- DEVELOPMENTAL STAGE: The crystal protein is produced during  
 CC sporulation and is accumulated both as an inclusion and as part of  
 CC the spore coat.  
 CC -1- MISCELLANEOUS: Toxic segment of the protein is located in the N-  
 CC terminus.  
 CC -1- SIMILARITY: Belongs to the delta endotoxin family.  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC -----  
 CC DE EMBL; AF056933; AAC62933.1; .  
 DR HSP; P02965; IC1Y.  
 DR InterPro; IPR001178; Endotoxin.  
 DR InterPro; IPR005638; endotoxin\_C.  
 DR InterPro; IPR005638; endotoxin\_N.  
 DR InterPro; IPR008979; Gal\_Bind\_Like.  
 DR Pfam; PF03944; Endotoxin\_C; 1.  
 DR Pfam; PF00555; Endotoxin\_M; 1.  
 DR Pfam; PF03945; Endotoxin\_N; 1.  
 KW Plasmid; Sporulation; Toxin.  
 SQ SEQUENCE 719 AA; 81210 MW; 8370B3F06B905DFF CRC64;  
 Query Match 94.8%; Score 3546; DB 1; Length 719;  
 Best Local Similarity 95.0%; Pred. No. 1.9e-236;  
 Matches 683; Conservative 11; Mismatches 25; Indels 0; Gaps 0;  
 QY 1 MKLNPKHOSLSNAKVDAIATDSLKNETDIELKNNNEDYLRMGHEHSIDPFVSASTI 60  
 DB 1 MKLNPKKHOTLSNAKVDAIATDSLKNETDIELKNNNEDYLRMGHEHSIDPFVSASTI 60  
 QY 61 QTGIGIAGKTLGTGVFPAGQIASLVSFILGELWPKGKQWEIFMBHVEIINQKILTVA 120  
 DB 61 QTGIGIAGKTLGTGVFPAGQIASLVSFILGELWPKGKQWEIFMBHVEIINQKILTVA 120  
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 DB 121 RNKALDRLGIGDALAVYHESLSQWENRNTARSVKNQYATALELMFVKLPSPAVSG 180  
 QY 181 EEVPLLPYQAANHLHLLLRDASIFGKEWGLSASEISTFYNQVTRDRDYSRCHIKWYN 240  
 DB 181 EEVPLLPYQAANHLHLLLRDASIFGKEWGLSASEISTFYNQVTRDRDYSRCHIKWYN 240  
 QY 241 TGLNLEGTKAKWVRNQKQDWTIMVLVDVALFSDYTLVYPIKTSQLTREYVTDAL 300  
 DB 241 TGLNLEGTKAKWVRNQKQDWTIMVLVDVALFSDYTLVYPIKTSQLTREYVTDAL 300  
 QY 301 GTVHPNQAFASTTWNNNAPSFSAIEAAVIRSPHLLDFLEKVTIYSLLSRWSNTQYMNW 360  
 DB 301 GTVHPNQAFASTTWNNNAPSFSAIEAAVIRSPHLLDFLEKVTIYSLLSRWSNTQYMNW 360

## RESULT 4

C11A\_BACTK  
 ID C11A\_BACTK STANDARD; PRT; 719 AA.  
 AC Q45752; P11092; Q45750; Q45751; Q45756;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Pesticidal crystal protein cryIIa (Insecticidal delta-endotoxin)  
 DE CryII(a) (Crystalline entomocidal protoxin) (81 kDa crystal protein).  
 GN Name=cryIIa; Synonyms=cryII(a), cryV, cryVI, CGCryV;  
 OS Bacillus thuringiensis (subsp. kurstaki).  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=29339;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=DSIR732;  
 RX MEDLINE=93298009; PubMed=8517758;  
 RA Gleave A.P., Williams R., Hedges R.J.;  
 RT "Screening by polymerase chain reaction of Bacillus thuringiensis  
 RT serotypes for the presence of cryV-like insecticidal protein genes and  
 RT characterization of a cryV gene cloned from B. thuringiensis subsp.  
 RT kurstaki.";  
 RL Appl. Environ. Microbiol. 59:1683-1687(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=JHCC4835;  
 RX MEDLINE=92269582; PubMed=1588820;  
 RA Taylor R., Tippet J., Gibb G., Bells S., Pike D., Jordan L., Ely S.;  
 RT "Identification and characterization of a novel Bacillus thuringiensis  
 RT delta-endotoxin entomocidal to coleopteran and lepidopteran larvae."  
 RL Mol. Microbiol. 6:1211-1217(1992).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SD-1.  
 RX MEDLINE=95314293; PubMed=7793960;  
 RA Shin B.-S., Park S.-H., Choi S.-K., Koo B.T., Lee S.T., Kim J.I.;  
 RT "Distribution of cryV-type insecticidal protein genes in Bacillus  
 RT thuringiensis and cloning of cryV-type genes from Bacillus  
 RT thuringiensis subsp. kurstaki and Bacillus thuringiensis subsp.  
 RT entomocidus.";  
 RL Appl. Environ. Microbiol. 61:2402-2407(1995).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=AB88;  
 RX MEDLINE=96178985; PubMed=8606196;  
 RA Kostichka K., Warren G.W., Mullins M., Mullins A.D., Palekar N.V.,  
 RA Craig J.A., Koziel M.G., Estruch J.J.;  
 RT "Cloning of a cryV-type insecticidal protein gene from Bacillus

QY 361 GCHRLSRPIGALNTSTQSGTNTSINPVTLOFTSRDYRTESLAGNLFQTQPVNGVPR 420  
 DB 361 GCHRLSRPIGALNTSTQSGTNTSINPVTLOFTSRDYRTESLAGNLFQTQPVNGVPR 420  
 QY 421 VDFHWKFTLPIASDNFYLYGAGVGTQLODSENELPPTTGPQNYESYSHRLSHIGLIS 480  
 DB 421 VDFHWKFTLPIASDNFYLYGAGVGTQLODSENELPPTTGPQNYESYSHRLSHIGLIS 480  
 QY 481 ASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSSGAAVVRGFGTGGDILRETN 540  
 DB 481 GSHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSSGAAVVRGFGTGGHILRETK 540  
 QY 541 TGTGDIRVNNPPPAQRYRVRIRYASTTDLQFHTSINGKAINQCNFSATWNGEDLDYK 600  
 DB 541 SGTFGHVRVNNPPPAQRYRVRMSYASTTDLQFHTSINGKAINQCNFSATWNGEDLDYK 600  
 QY 601 TFRITGFTTPSFSDVQSTFTTIGAWNFSSGNEVVIDRIEFPVVEVTEAEYDFEKAQEKV 660  
 DB 601 TFRITGFTTPSFSDVQSTFTTIGAWNFSSGNEVVIDRIEFPVVEVTEAEYDFEKAQEKV 660  
 QY 661 TALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDFYLDKRELFEIVYAKQIHIERNM 719  
 DB 661 TALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDELVDKRELFEIVYAKQIHIERNM 719

thuringiensis: the cryV-encoded protein is expressed early in stationary phase.";  
 RL J. Bacteriol. 178:2141-2144(1996).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=61;  
 RA Selvapandian A., Bhatnagar R.K.;  
 RT "Isolation, cloning and expression of cryV gene;"  
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
 CC !- FUNCTION: Promotes colloidosmotic lysis by binding to the midgut  
 CC epithelial cells of certain coleopteran and lepidopteran species.  
 CC Active on Plutella xylostella and Bombyx mori.  
 CC !- DEVELOPMENTAL STAGE: The crystal protein is produced during  
 CC sporulation and is accumulated both as an inclusion and as part of  
 CC the spore coat.  
 CC !- MISCELLANEOUS: Toxic segment of the protein is located in the N-terminus.  
 CC !- SIMILARITY: Belongs to the delta endotoxin family.  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC -----  
 CC EMBL; M98544; AAA22354.1; -;  
 CC EMBL; X62821; CAA44633.1; -;  
 CC EMBL; L36338; AAC36999.1; -;  
 CC EMBL; L49391; AAB00958.1; -;  
 CC EMBL; Y08920; CAA70124.1; -;  
 CC PIR; I39845; I39845;  
 CC PIR; S25383; S25383;  
 CC HSSP; P02965; IC1Y.  
 CC InterPro; IPR001178; Endotoxin.  
 CC InterPro; IPR005638; endotoxin C.  
 CC InterPro; IPR005639; endotoxin N.  
 CC InterPro; IPR008979; Gal bind like.  
 CC Pfam; PF03944; Endotoxin\_C; 1.  
 CC Pfam; PF00555; Endotoxin\_M; 1.  
 CC Pfam; PF03945; Endotoxin\_N; 1.  
 CC Sporulation; Toxin.  
 FT VARIANT 159 159 K -> R (in strain 61).  
 FT VARIANT 233 233 D -> Y (in strain JHCC4835 and strain HD-1).  
 FT VARIANT 443 443 A -> V (in strain AB88).  
 FT VARIANT 711 712 KQ -> NE (in strain HD-1 and strain 61).  
 SQ SEQUENCE 719 AA; 81216 MW; 3627ESA6C25DAFF5 CRC64;  
 Query Match 94.1%; Score 3520; DB 1; Length 719;  
 Best Local Similarity 92.9%; Pred. No. 1.2e-234;  
 Matches 668; Conservative 31; Mismatches 20; Indels 0; Gaps 0;  
 QY 1 MKLNKPDHQSSNAKVDKATDSLKNETDIELKNMNNEDYLRMSHESIDPFVSASTI 60  
 DB 1 MKLNKQDKHQSSNAKVDKISTDSLKNETDIELQNHEDCLKMSBYENVEPFVSASTI 60  
 QY 61 QTGIGIAGKILGTGVFPAGQIASLYSPILGELMPKGSQWEIFMEHVEEIIINOKILTYA 120  
 DB 61 QTGIGIAGKILGTGVFPAGQVASLYSPILGELMPKGNQWEIFMEHVEEIIINOKISTYA 120  
 QY 121 RNKALSDRLGIGDALAVYHESLSEWENNRNTRARSVVKNQYIALELMFVQKLPSPFVSG 180  
 DB 121 RNKALTDLKGIGDALAVYHDSLESWGNRNTRARSVVKSQYIALELMFVQKLPSPFVSG 180  
 QY 181 BEVPLLPYQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVTRDYSDHCIKWYN 240  
 DB 181 BEVPLLPYQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVTRDYSDHCIKWYN 240  
 QY 241 TGLNNLRGTNAESWVRVYVQFQKDMTLMVLVLPSPYDTLVYPIKTTQSUTREVYTDI 300  
 DB 241 TGLNNLRGTNAESWVRVYVQFQKDMTLMVLVLPSPYDTLVYPIKTTQSUTREVYTDI 300

QY 301 GTVHPNQAFSTWYNNNAPSFAIAEAAVIRSPHLLDFLEKVTIYSLSRWSNTQYMNW 360  
 DB 301 GTVHPNPSTWYNNNAPSFAIAEAAVIRSPHLLDFLEKVTIYSLSRWSNTQYMNW 360  
 QY 361 GGHRLSPRIGGALNTSGSTNTSINPVTLQFTSRDYVYRTESLAGNLFLTPQVNGVPR 420  
 DB 361 GGHKLEFRTIGTGLNISTGSTNTSINPVTLQFTSRDYVYRTESLAGNLFLTPQVNGVPR 420  
 QY 421 VDFHMKFPTLPASDNFFYVLGAGVGTQLQDSSENLPPETTPQPNYESYSHRLSHIGLIS 480  
 DB 421 VDFHMKFVTHPIASDNFFYVLGAGVGTQLQDSSENLPPETTPQPNYESYSHRLSHIGLIS 480  
 QY 481 ASHVKALVYSWTHRSADRNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRET 540  
 DB 481 ASHVKALVYSWTHRSADRNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRET 540  
 QY 541 TGTFGDIRVNPPEAQRVVRIRVASTTDLQFHTSINGKAINQGNFSATMNRGDLDYK 600  
 DB 541 TGTFGDIRVNPPEAQRVVRIRVASTTDLQFHTSINGKAINQGNFSATMNRGDLDYK 600  
 QY 601 TPTTIGTTPFSFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVYVTEAEYDFEKAQEKV 660  
 DB 601 TPTTIGTTPFSFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVYVTEAEYDFEKAQEKV 660  
 QY 661 TALFTSTPRGLKTDVKDHYIDQVSNLVESLSDRYLDEKRELFELFVYKQIHIERNM 719  
 DB 661 TALFTSTPRGLKTDVKDHYIDQVSNLVESLSDRYLDEKRELFELFVYKQIHIERNM 719  
 RESULT 5  
 G6X181 PRELIMINARY; PRT; 719 AA.  
 ID G6X181  
 AC G6X181;  
 DT 05-JUL-2004 (TREMBLrel. 27, Created)  
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
 DE CryII.  
 GN Name=cryII;  
 OS Bacillus thuringiensis.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1428;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Espindola R., Lemos M.V.F., Lemos E.G.M., Sena J.A.D.;  
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY262167; AAP86782.1; -;  
 DR InterPro; IPR001178; Endotoxin.  
 DR InterPro; IPR005639; endotoxin C.  
 DR InterPro; IPR008979; endotoxin N.  
 DR Pfam; PF03944; Endotoxin\_C; 1.  
 DR Pfam; PF00555; Endotoxin\_M; 1.  
 DR Pfam; PF03945; Endotoxin\_N; 1.  
 SQ SEQUENCE 719 AA; 81216 MW; 3627ESA6C25DAFF5 CRC64;  
 Query Match 94.1%; Score 3520; DB 2; Length 719;  
 Best Local Similarity 92.9%; Pred. No. 1.2e-234;  
 Matches 668; Conservative 31; Mismatches 20; Indels 0; Gaps 0;  
 QY 1 MKLNKPDHQSSNAKVDKATDSLKNETDIELKNMNNEDYLRMSHESIDPFVSASTI 60  
 DB 1 MKLNKQDKHQSSNAKVDKISTDSLKNETDIELQNHEDCLKMSBYENVEPFVSASTI 60  
 QY 61 QTGIGIAGKILGTGVFPAGQIASLYSPILGELMPKGSQWEIFMEHVEEIIINOKILTYA 120  
 DB 61 QTGIGIAGKILGTGVFPAGQVASLYSPILGELMPKGNQWEIFMEHVEEIIINOKISTYA 120  
 QY 121 RNKALSDRLGIGDALAVYHESLSEWENNRNTRARSVVKNQYIALELMFVQKLPSPFVSG 180  
 DB 121 RNKALTDLKGIGDALAVYHDSLESWGNRNTRARSVVKSQYIALELMFVQKLPSPFVSG 180  
 QY 181 BEVPLLPYQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVTRDYSDHCIKWYN 240

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Db 181 EEEVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWYS 240
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Db 241 TGLNNLRGTNAKSWRYNQPRKDMTLMVLDLVALFSDYDTLVYPIKTTTSQLTREVVYTDI 300
QY 301 GTVHPNQAFASFTWYNNNAPSFAIAAARVRSRPHLLDFLEKVTIYSLLSRWNTQYMMNM 360
Db 301 GTVHPNPSFTSTWYNNNAPSFAIAAARVRSRPHLLDFLEKVTIYSLLSRWNTQYMMNM 360
QY 361 GGHRLSRPPTGGALNTSTQSTNTSINPVTLOFTSDVYRTESLAGLNLFLTQPVNGVPR 420
Db 361 GGHKLEFRTIGGLNLTSTQSTNTSINPVTLOFTSDVYRTESLAGLNLFLTQPVNGVPR 420
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Db 421 VDFHWKFPVTHPIASDNFYLYGAGVGTQLODSENELPPTTGPQNYESYSHRLSHIGLIS 480
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Db 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
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Db 601 TPTRTGFTTPTPSFSDVQSTFTIGAMFSSGNEVYIDRIEFVPEVYEAEDYFEKAQEKV 660
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Db 661 TALFTSTNPRGLTKDVKDHYDQVSNLVESLSEDEFYLDKRELFVYKAKQIHIERNM 719

RESULT 6
AAP86782 PRELIMINARY; PRT; 719 AA.
AC AAP86782;
DT 02-MAR-2004 (TREMREL. 27, Created)
DT 02-MAR-2004 (TREMREL. 27, Last sequence update)
DT 02-MAR-2004 (TREMREL. 27, Last annotation update)
DE CryII.
GN CryII.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=T01 328;
RA Espindola R., Lemos M.V.F., Lemos E.G.M., Sena J.A.D.;
RT "Complete sequence of cryII gene of isolate T01 328 from Bacillus
RT thuringiensis from Cubatao (SP - Brazil) soil."
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY262167; AAP86782.1; -.
SQ SEQUENCE 719 AA; 81216 MW; 3627E5A6C25DAFF5 CRC64;

Query Match 94.1%; Score 3520; DB 2; Length 719;
Best Local Similarity 92.9%; Pred. No. 1.2e-234;
Matches 668; Conservative 31; Mismatches 20; Indels 0; Gaps 0;

QY 1 MMLKNDPKHQSLSNAKVDKIATDSLKNETDIELKNNEDYLRMGESIDPFVSASTI 60
Db 1 MMLKNDPKHQSLSNAKVDKIATDSLKNETDIELKNNEDYLRMGESIDPFVSASTI 60
QY 61 OTGIGIAGKLTGTCVPAQGIASIFILGELWPKGSOWEIMFMEHVEIINOKILTYA 120
Db 61 OTGIGIAGKLTGTCVPAQGIASIFILGELWPKGSOWEIMFMEHVEIINOKILTYA 120
QY 121 RNKALSLRGLGDALAVYHDSLSWVNNRNNTRARSVVKVQYIALELMFVKQLPSFAVSG 180
Db 121 RNKALSLRGLGDALAVYHDSLSWVNNRNNTRARSVVKVQYIALELMFVKQLPSFAVSG 180
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Db 181 EEEVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWYS 240
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Db 241 TGLNNLRGTNAKSWRYNQPRKDMTLMVLDLVALFSDYDTLVYPIKTTTSQLTREVVYTDI 300
QY 301 GTVHPNQAFASFTWYNNNAPSFAIAAARVRSRPHLLDFLEKVTIYSLLSRWNTQYMMNM 360
Db 301 GTVHPNPSFTSTWYNNNAPSFAIAAARVRSRPHLLDFLEKVTIYSLLSRWNTQYMMNM 360
QY 361 GGHRLSRPPTGGALNTSTQSTNTSINPVTLOFTSDVYRTESLAGLNLFLTQPVNGVPR 420
Db 361 GGHKLEFRTIGGLNLTSTQSTNTSINPVTLOFTSDVYRTESLAGLNLFLTQPVNGVPR 420
QY 421 VDFHWKFPPTPIASDNFYLYGAGVGTQLODSENELPPTTGPQNYESYSHRLSHIGLIS 480
Db 421 VDFHWKFPVTHPIASDNFYLYGAGVGTQLODSENELPPTTGPQNYESYSHRLSHIGLIS 480
QY 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
Db 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
QY 541 TGTGFGDIRVNNPFPQAQRVRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
Db 541 TGTGFGDIRVNNPFPQAQRVRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
QY 601 TPTRTGFTTPTPSFSDVQSTFTIGAMFSSGNEVYIDRIEFVPEVYEAEDYFEKAQEKV 660
Db 601 TPTRTGFTTPTPSFSDVQSTFTIGAMFSSGNEVYIDRIEFVPEVYEAEDYFEKAQEKV 660
QY 661 TALFTSTNPRGLTKDVKDHYDQVSNLVESLSEDEFYLDKRELFVYKAKQIHIERNM 719
Db 661 TALFTSTNPRGLTKDVKDHYDQVSNLVESLSEDEFYLDKRELFVYKAKQIHIERNM 719

RESULT 7
Q93NJ5 PRELIMINARY; PRT; 719 AA.
AC Q93NJ5;
DT 01-DEC-2001 (TREMREL. 19, Created)
DT 01-DEC-2001 (TREMREL. 19, Last sequence update)
DT 01-MAR-2004 (TREMREL. 26, Last annotation update)
DE CryIIa.
GN Name=CryIIa;
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RA Song F., Zhang J., Gu A., Huang D., Li G.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF732207; AAK66742.1; -.
DR HSSP; P02965; 1CIY.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR008979; Gal_bind_Like.
DR Pfam; PF03944; Endotoxin C; 1.
DR Pfam; PF00555; Endotoxin M; 1.
DR Pfam; PF03945; Endotoxin N; 1.
SQ SEQUENCE 719 AA; 81225 MW; C629DF2C44827241 CRC64;

Query Match 93.9%; Score 3515; DB 2; Length 719;
Best Local Similarity 92.8%; Pred. No. 2.7e-234;
Matches 667; Conservative 31; Mismatches 21; Indels 0; Gaps 0;
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QY 1 MKLKNDPDKHQSSNAKVDKIATDSLKNETDIELKNMNNEDYLRMSHESIDPVSASTI 60
DB 1 MKLKNDKQHQSSNAKVDKISTLSKNETDIELQNINHEDECLKSNYENVEPVSASTI 60
QY 61 QTGIGIAGKILGTGVPFAGQIASLYSFI LGELWPKGKOWEIPMEHVBEIINQKILTYA 120
DB 61 QTGIGIAGKILGTGVPFAGQIASLYSFI LGELWPKGKOWEIPMEHVBEIINQKISTYA 120
QY 121 RNKALSDLRGLGDALAVVHESLESWENNRNTRARSVVKNOVIALELMFVQKLPFAVSG 180
DB 121 RNKALTDLRGLGDALAVVHDSLESWGNRNTRARSVVKQIYIALELMFVQKLPFAVSG 180
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DB 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVTRDYSDHCVKWYS 240
QY 241 TGLNNLRGTNAKSWRYNQFRKDMTLVLDLVALFPSYDILVPIKTSQLTREVTDAI 300
DB 241 TGLNNLRGTNAESWRYNQFRDMTLVLDLVALFPSYDITQMPYIKTAQLTREVTDAI 300
QY 301 GTVHPNQAFSTTWYNNNAPSFAIEAAVIRSPHLLDFLEKVTIYSLLSRWSNTQYNNMW 360
DB 301 GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMW 360
QY 361 GGHRLSPRIGGALNTSTQGSTNTSINPVTLOFTSRDVRTESLAGNLFITOPVNGVPR 420
DB 361 GGHKLEFRITGTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGNLFITPVGNGVPR 420
QY 421 VDFHKKFPTLPASDNFYLYGAGVGTQLODSENELPETTGQPNYESYSHRLSHIGLIS 480
DB 421 VDFHKKFVTHFIASDNFYLYGAGVGTQLODSENELPETTGQPNYESYSHRLSHIGLIS 480
QY 481 ASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSSGAAVVRPGFTGGDILRTN 540
DB 481 ASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSSGAAVVRPGFTGGDILRTN 540
QY 541 TGTGDIRVNIAPPFAQRYRIRYASTDLOFTSINGKAINQGNFSATMNRGEDLDYK 600
DB 541 TGTGDIRVNIAPPFAQRYRIRYASTDLOFTSINGKAINQGNFSATMNRGEDLDYK 600
QY 601 TFRITGFTTSPFSDVOSTFTTIGAMNFSNGNEVYIDRIEFVVPVEVYEAEDFEKAQEKV 660
DB 601 TFRITGFTTSPFSDVOSTFTTIGAMNFSNGNEVYIDRIEFVVPVEVYEAEDFEKAQEKV 660
QY 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVESLSDFFYLDEKRELFEIVKYAKQHIERNM 719
DB 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVESLSDFFYLDEKRELFEIVKYAKQHIERNM 719

RESULT 8
ID O85796 PRELIMINARY; PRT; 719 AA.
AC O85796;
DT 01-NOV-1998 (TRENBLrel. 08, Created)
DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)
DE 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Insecticidal protein.
GN Name=crv101;
OS Bacillus thuringiensis (subsp. kurstaki).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OC NCBI_TaxID=29339;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S101;
EA Zhong Q., Deng R., Long Q., Yuan M., Pang Y., Wang X.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF076953; AAC26910.1; -.
DR HSSP; P02965; 1CIY.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.

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DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal_bind_Like.
DR Pfam; PF03944; Endotoxin_C_1.
DR Pfam; PF00555; Endotoxin_M_1.
DR Pfam; PF03945; Endotoxin_N_1.
DR Plasmid.
SQ SEQUENCE 719 AA; 81230 MW; 42746D478359BBA7 CRC64;

Query Match 93.9%; Score 3514; DB 2; Length 719;
Best Local Similarity 92.8%; Pred. No. 3.2e-234;
Matches 667; Conservative 31; Mismatches 21; Indels 0; Gaps 0;

QY 1 MKLKNDPDKHQSSNAKVDKIATDSLKNETDIELKNMNNEDYLRMSHESIDPVSASTI 60
DB 1 MKLKNDKQHQSSNAKVDKISTLSKNETDIELQNINHEDECLKSNYENVEPVSASTI 60
QY 61 QTGIGIAGKILGTGVPFAGQIASLYSFI LGELWPKGKOWEIPMEHVBEIINQKILTYA 120
DB 61 QTGIGIAGKILGTGVPFAGQIASLYSFI LGELWPKGKOWEIPMEHVBEIINQKISTYA 120
QY 121 RNKALSDLRGLGDALAVVHESLESWENNRNTRARSVVKNOVIALELMFVQKLPFAVSG 180
DB 121 RNKALTDLRGLGDALAVVHDSLESWGNRNTRARSVVKQIYIALELMFVQKLPFAVSG 180
QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVTRDYSDHCIRKYN 240
DB 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVTRDYSDHCVKWYS 240
QY 241 TGLNNLRGTNAKSWRYNQFRKDMTLVLDLVALFPSYDILVPIKTSQLTREVTDAI 300
DB 241 TGLNNLRGTNAESWRYNQFRDMTLVLDLVALFPSYDITQMPYIKTAQLTREVTDAI 300
QY 301 GTVHPNQAFSTTWYNNNAPSFAIEAAVIRSPHLLDFLEKVTIYSLLSRWSNTQYNNMW 360
DB 301 GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMW 360
QY 361 GGHRLSPRIGGALNTSTQGSTNTSINPVTLOFTSRDVRTESLAGNLFITOPVNGVPR 420
DB 361 GGHKLEFRITGTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGNLFITPVGNGVPR 420
QY 421 VDFHKKFPTLPASDNFYLYGAGVGTQLODSENELPETTGQPNYESYSHRLSHIGLIS 480
DB 421 VDFHKKFVTHFIASDNFYLYGAGVGTQLODSENELPETTGQPNYESYSHRLSHIGLIS 480
QY 481 ASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSSGAAVVRPGFTGGDILRTN 540
DB 481 ASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSSGAAVVRPGFTGGDILRTN 540
QY 541 TGTGDIRVNIAPPFAQRYRIRYASTDLOFTSINGKAINQGNFSATMNRGEDLDYK 600
DB 541 TGTGDIRVNIAPPFAQRYRIRYASTDLOFTSINGKAINQGNFSATMNRGEDLDYK 600
QY 601 TFRITGFTTSPFSDVOSTFTTIGAMNFSNGNEVYIDRIEFVVPVEVYEAEDFEKAQEKV 660
DB 601 TFRITGFTTSPFSDVOSTFTTIGAMNFSNGNEVYIDRIEFVVPVEVYEAEDFEKAQEKV 660
QY 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVESLSDFFYLDEKRELFEIVKYAKQHIERNM 719
DB 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVESLSDFFYLDEKRELFEIVKYAKQHIERNM 719

RESULT 9
CAC85964 PRELIMINARY; PRT; 719 AA.
ID CAC85964
AC CAC85964;
DT 02-MAR-2004 (TRENBLrel. 27, Created)
DT 02-MAR-2004 (TRENBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TRENBLrel. 27, Last annotation update)
DE Delta-endotoxin.
GN CRyIIA.
OS Bacillus thuringiensis (subsp. kurstaki).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

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RESULT 11
C1ID BACTU STANDARD; PRT; 719 AA.
AC Q9XDL1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pesticidal crystal protein cryII (insecticidal delta-endotoxin)
DE CryII(d) (Crystalline entomocidal protoxin) (81 kDa crystal protein).
GN Name=cryIId; Synonyms=cryII(d), NRCryV;
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=BR30;
RX MEDLINE=20374042; PubMed=10919402;
RA Choi S.-K., Shin B.-S., Kong E.-M., Rho H.M., Park S.-H.;
RT "Cloning of a new Bacillus thuringiensis cryII-type crystal protein
gene."
RL Curr. Microbiol. 41:65-69(2000).
CC -!- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut
epithelial cells of many lepidopteran larvae. Active on Plutella
xylostella and on Bombyx mori.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
sporulation and is accumulated both as an inclusion and as part of
the spore coat.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
terminus.
CC -!- SIMILARITY: Belongs to the delta endotoxin family.
CC
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or send an email to license@isb-sib.ch).
CC
DR HSPB; AP047579; AAD44366.1; -.
DR HSPB; P02965; 1CIY.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin C.
DR InterPro; IPR005639; endotoxin N.
DR InterPro; IPR008979; Gal_bind_like.
DR Pfam; PF03944; Endotoxin C; 1.
DR Pfam; PF00555; Endotoxin M; 1.
DR Pfam; PF03945; Endotoxin N; 1.
KW Sporulation; Toxin.
SQ SEQUENCE 719 AA; 81403 MW; F335F5689D3B0C45 CRC64;
Query Match 88.5%; Score 3311; DB 1; Length 719;
Best Local Similarity 87.2%; Pred. No. 3.5e-220;
Matches 627; Conservative 50; Mismatches 42; Indels 0; Gaps 0;
QY 1 MKLKNPDKHSLSSNAKVDKATSLKNETDIELKNNWEDYLMWSHESIDPVSASTI 60
DB 1 MKSRQNNYRFSNNATVDKSTDPLEHTNMLQNGNHDCLKMSYESVEFVSVSTI 60
QY 61 QTGIGIAGKILGTGVPAGQIASLYSPILGELPKGKQSWEIFMEHVEELINQILTYA 120
DB 61 QTGIGIAGKILGNLGVPPAGQVASLYSPILGELPKGKQSWEIFMEHVEELINQISTYA 120
QY 121 RNKALSDRLGLDALAVTHESLESWVENNTRASVVKQYIALELMFVKQLPSPAVSG 180
DB 121 RNKALADLKGGLDALAVTHESLESWVENNTRASVVKQYIALELMFVKQLPSPAVSG 180
QY 181 BEVPLLPYAAQANLHLLLDASIFGKWLGSASEISTFVNRQVTRDYSCHIKWYN 240
DB 181 BEVPLLPYAAQANLHLLLDASIFGKWLGSASEISTFVNRQVTRDYSCHIKWYN 240

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QY 241 TGLNNLRGTNAKSWRYNQFRKDMTLMVLDLVALPSPYDTLVYPIKTTTSOLTREYTTDAI 300
DB 241 TGLNRLRGINAESWRYNQFRDMTLMVLDLVALPSPYDTLVYPIKTTTSOLTREYTTDAI 300
QY 301 GTVHPNQAFASFTWYNNNAPSFAIEAAVIRSPHLLDFLEKVTIYSLLSRWSTNTQYNNW 360
DB 301 GTVHPNAPASFTWYNNNAPSFTIEAAVVRNPHLLDFLEQVTIYSLLSRWSTNTQYNNW 360
QY 361 GGRHLESRPDGGALANTSTGTSNTSINPVTLQFTSRDVTYTESLAGLNLFTQPVNGVPR 420
DB 361 GGRHLEFRIGTLNTSTGTSNTSINPVTLQFTSRDVTYTESLAGLNLFTQPVNGVPR 420
QY 421 VDFHMKFPTLPFIASDNFFYVLGAGVGTQLQDSNELPPTTQPNYESYSHRLSHIGLIS 480
DB 421 VDFHMKFVTHPIASDNFFYVYAGIGTQLQDSNELPPTTQPNYESYSHRLSHIGLIS 480
QY 481 ASHVKALVYSWTHRSADRTNTEPNSTIQIPLVKAFNLSSGNAVVRGPGFTGGDILRTN 540
DB 481 ASHVKALVYSWTHRSADRTNTEPNSTIQIPLVKAFNLSSGNAVVRGPGFTGGDILRTN 540
QY 541 TGTFGDIRVNNPFPFAQRYRVRIRYASTDQLQFHTSINGKALNQGNSATVNRGDLDYK 600
DB 541 TGTFGDIRVNNPFPFAQRYRVRIRYASTDQLQFHTSINGKALNQGNSATVNRGDLDYK 600
QY 601 TTRTGTFTTTPSPFSDVQSTFTTIGAWNPSGNEVYIDRIEFVFPVEVYEAEDFEXAQEKV 660
DB 601 AFRTVGTFTTTPSPFSDVQSTFTTIGAWNPSGNEVYIDRIEFVFPVEVYEAEDFEXAQEKV 660
QY 661 TALFTSTNPRGLKTDVQVHIDQVNLVSLSDRYLDEKRELPFIKVAQIHERNM 719
DB 661 TAWFISTNLRKLTNVTCHIDQVNLVSLSDRYLDEKRELPFIKVAQIHERNM 719

RESULT 12
C1BB BACTU STANDARD; PRT; 1229 AA.
ID C1BB BACTU STANDARD; PRT; 1229 AA.
AC Q45739;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pesticidal crystal protein cryIbB (insecticidal delta-endotoxin)
DE CryIb(b) (Crystalline entomocidal protoxin) (140 kDa crystal protein).
GN Name=cryIbB; Synonyms=cryIb(b), cryET5;
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=NRRL B-21110 / EG5847;
RA Donovan W.P., Tan Y., Jany C.S., Gonzalez J.M. Jr.;
RT "Bacillus thuringiensis cryet4 and cryet5 toxin genes and proteins
toxic to lepidopteran insects."; 1994.
RL Patent number US5322687, 21-JUN-1994.
CC -!- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut
epithelial cells of many lepidopteran larvae.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
sporulation and is accumulated both as an inclusion and as part of
the spore coat.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
terminus.
CC -!- SIMILARITY: Belongs to the delta endotoxin family.
CC
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or send an email to license@isb-sib.ch).
CC
DR EMBL; L32020; AAA22344.1; -.
DR HSSP; P02965; 1CIY.
DR InterPro; IPR001178; Endotoxin.

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DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal_bind_Like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
KW Sporulation; Toxin.
SQ SEQUENCE 1229 AA; 139769 MW; A4C949DB675C3269 CRC64;

Query Match 65.7%; Score 2459; DB 1; Length 1229;
Best Local Similarity 64.8%; Pred. No. 6.8e-161;
Matches 470; Conservative 91; Mismatches 128; Indels 36; Gaps 5;

QY 3 LKNPKDQHSLSNAKVQKIATDSLKNETDIELKMNNDYLRMSHESIDPFVSASTQT 62
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
20 VSNPSTQWNLSPDARI-----EDSLCAEVNNDIPFVSASTVQT 58

QY 63 GIGIAGKILGTGVFPAGQIASYSLFGLBWPKGSKQWEIFMEHVEEIIINQILTYARN 122
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
59 GINIAGRILGVLPFAGQIASYSLFGLBWPKGSKQWEIFMEHVEEIIINQILTYARN 118

QY 123 KALSDRLGLGDALAVYHESLESWVENNTRASVVKVQYIALELMFVKQLPSFAVS 182
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
119 TAIARLEGGRGYSYQQALETWLDNRDARSIIILERYVALELDITTAIPLRIRNEE 178

QY 183 VPLLPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNQVETRDYSDHCIKWYNTG 242
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
179 VPLLPIYAQAANLHLLLRDASIFGSEWGLSASSVQYIQIRYTESYSHCVQWYNTG 238

QY 243 LNNLRGTNAKSVRYNQFRKDMTLMVLVDLVALFPSSYDTLVYPIKTTSQLREVTDAIGT 302
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
239 LNNLRGTNAESWLRYNQFRDRLTLGVLDLVALFPSSYDTRTYPINTSAQLTRBIYTDPIGR 298

QY 303 VHPNQAPASTWYNNNAPSFSAIEAAVRSRPHLLDFLEKVIYISLLSRNSQYNNMGG 362
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
299 TNAPSGFASTWYNNNAPSFSAIEAAVRSRPHLLDFLEKVIYISLLSRNSQYNNMGG 358

QY 363 HRLSRPRTGGALNTSTQGST-NTSINPVTLQFTSRDVRTESLAGNLFLTPQVNGVPRV 421
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
359 HRLNFRPIGGTLNTSTQGLTNTSINPVTLQFTSRDVRTESNAGTNILFLTPVNGVPA 418

QY 422 DFHWKFTPLFIASDNFYILG-----YAGVGTQLQDSENELPPTTCQPNYESYSHRLS 474

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DE InterPro; IPR005638; endotoxin_C.
DE Name-crylBc; Synonyms-crylB(C), crylBc;
OS Bacillus thuringiensis (subsp. morrisoni).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1441;
RN [1]
RP SEQUENCE FROM N.A.
RA Bishop A.H., Bone E.J., Ellar D.J.;
RT "Cloning of novel Bacillus thuringiensis delta-endotoxin.";
RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Promotes colloid osmotic lysis by binding to the midgut
CC epithelial cells of insects.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat. Toxic segment of the protein is located in the N-
CC -!- MISCELLANEOUS: Belongs to the delta endotoxin family.
CC -!- SIMILARITY:
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; Z46442; CAA86568.1; -
DR HSSP; P02965; LC1Y.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal_bind_Like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
KW Sporulation; Toxin.
SQ SEQUENCE 1233 AA; 140451 MW; 7318382413529F21 CRC64;

Query Match 65.7%; Score 2459; DB 1; Length 1233;
Best Local Similarity 64.8%; Pred. No. 6.8e-161;
Matches 470; Conservative 91; Mismatches 128; Indels 36; Gaps 5;

QY 3 LKNPKDQHSLSNAKVQKIATDSLKNETDIELKMNNDYLRMSHESIDPFVSASTQT 62
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
20 VSNPSTQWNLSPDARI-----EDSLCAEVNNDIPFVSASTVQT 58

QY 63 GIGIAGKILGTGVFPAGQIASYSLFGLBWPKGSKQWEIFMEHVEEIIINQILTYARN 122
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
59 GINIAGRILGVLPFAGQIASYSLFGLBWPKGSKQWEIFMEHVEEIIINQILTYARN 118

QY 123 KALSDRLGLGDALAVYHESLESWVENNTRASVVKVQYIALELMFVKQLPSFAVS 182
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
119 TAIARLEGGRGYSYQQALETWLDNRDARSIIILERYVALELDITTAIPLRIRNEE 178

QY 183 VPLLPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNQVETRDYSDHCIKWYNTG 242
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
179 VPLLPIYAQAANLHLLLRDASIFGSEWGLSASSVQYIQIRYTESYSHCVQWYNTG 238

QY 243 LNNLRGTNAKSVRYNQFRKDMTLMVLVDLVALFPSSYDTLVYPIKTTSQLREVTDAIGT 302
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
239 LNNLRGTNAESWLRYNQFRDRLTLGVLDLVALFPSSYDTRTYPINTSAQLTRBIYTDPIGR 298

QY 303 VHPNQAPASTWYNNNAPSFSAIEAAVRSRPHLLDFLEKVIYISLLSRNSQYNNMGG 362
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
299 TNAPSGFASTWYNNNAPSFSAIEAAVRSRPHLLDFLEKVIYISLLSRNSQYNNMGG 358

QY 363 HRLSRPRTGGALNTSTQGST-NTSINPVTLQFTSRDVRTESLAGNLFLTPQVNGVPRV 421
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
359 HRLNFRPIGGTLNTSTQGLTNTSINPVTLQFTSRDVRTESNAGTNILFLTPVNGVPA 418

QY 422 DFHWKFTPLFIASDNFYILG-----YAGVGTQLQDSENELPPTTCQPNYESYSHRLS 474

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RESULT 13

C1BC\_BACTM

ID\_C1BC\_BACTM

AC 045774;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

STANDARD;

PRT;

1233 AA.

712 DERNL 716

715 IERNM 719

652 RAQKAVNALFTSTNPRELKTVDYHIDQVSNMVACLSDFCLEKRELFKRYAKRLS 711

655 KAQKVYALTSTNPRGLKTDYHIDQVSNLVESLSDFFYDKEKRELFKRYAKQIH 714

593 DNLEYSFRAGSTPNFLNAQSTFTLGAQSFN-QEVIDRVEFVPAEVEAEVDLE 651

595 EDIDYKTFRTIGFTTFPSFSDVOSTFTIGAWNFSSGNEVIDRIEFVPEVTVAEADFE 654

533 ILRRNTGTGDIRLNINVLQSQRVRIYASTDLOQFTRINGTIVNIGNFSRTMNRG 592

535 ILRRNTGTGDIRVNINPFAQRYRIYASTDLOFTSINGKAINQGNFSATMNRG 594

473 HIGLIIGNTLRAPVYSWTHSADRTNTIGNRITQIPLVKALNLHSGTVVGGPGFTGGD 532

475 HIGLISHVKALVYSWTHSADRTNTIENSTQIPLVKAFNLSSGAAVVRGPGFTGGD 534

419 RFNP-----INPQIVRGATVYQYQGVGLQFDSSETLPPETTERPNYESYSHRLS 472

422 DFHWKFTPLFIASDNFYILG-----YAGVGTQLQDSENELPPTTCQPNYESYSHRLS 474

359 HRLNFRPIGGTLNTSTQGLTNTSINPVTLQFTSRDVRTESNAGTNILFTTPVNGVPA 418

363 HRLSRPRTGGALNTSTQGST-NTSINPVTLQFTSRDVRTESLAGNLFLTPQVNGVPRV 421

299 TNAPSGFASTWYNNNAPSFSAIEAAVRSRPHLLDFLEKVIYISLLSRNSQYNNMGG 362

239 LNNLRGTNAESWLRYNQFRDRLTLGVLDLVALFPSSYDTRTYPINTSAQLTRBIYTDPIGR 298

243 LNNLRGTNAKSVRYNQFRKDMTLMVLVDLVALFPSSYDTLVYPIKTTSQLREVTDAIGT 302

179 VPLLPIYAQAANLHLLLRDASIFGSEWGLSASSVQYIQIRYTESYSHCVQWYNTG 238

183 VPLLPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNQVETRDYSDHCIKWYNTG 242

119 TAIARLEGGRGYSYQQALETWLDNRDARSIIILERYVALELDITTAIPLRIRNEE 178

123 KALSDRLGLGDALAVYHESLESWVENNTRASVVKVQYIALELMFVKQLPSFAVS 182

59 GINIAGRILGVLPFAGQIASYSLFGLBWPKGSKQWEIFMEHVEEIIINQILTYARN 118

63 GIGIAGKILGTGVFPAGQIASYSLFGLBWPKGSKQWEIFMEHVEEIIINQILTYARN 122

20 VSNPSTQWNLSPDARI-----EDSLCAEVNNDIPFVSASTVQT 58

3 LKNPKDQHSLSNAKVQKIATDSLKNETDIELKMNNDYLRMSHESIDPFVSASTQT 62

Matches 470; Conservative 91; Mismatches 128; Indels 36; Gaps 5;

Best Local Similarity 64.8%; Pred. No. 6.7e-161;

Query Match 65.7%; Score 2459; DB 1; Length 1229;

SQ SEQUENCE 1229 AA; 139769 MW; A4C949DB675C3269 CRC64;

KW Sporulation; Toxin.

DR Pfam; PF03945; Endotoxin\_N; 1.

DR Pfam; PF00555; Endotoxin\_M; 1.

DR Pfam; PF03944; Endotoxin\_C; 1.

DR InterPro; IPR008979; Gal\_bind\_Like.

DR InterPro; IPR005639; endotoxin\_N.

DR InterPro; IPR005638; endotoxin\_C.



```

Db 419 RPNF-----INPNYIERGATTYSQPGVGIGLQFSETELPETTERPNYESYSHRLS 472
QY 475 HIGLISASHVKALVYSWTHRSADRTNTEPNISITQIPLVKAFNLSSGAAVVRGPGFTGGD 534
Db 473 HIGLIIGNTLRAPVYVSWTHRSADRTNIGPNRIQIPLVKALNLHSGVTVVGGPGFTGGD 532
QY 535 ILRRTNTGFGDIRVNNPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATNRG 594
Db 533 ILRRTNTGFGDIRLNNINPLSQRYRVRIRYASTTDLQFFTRINGTNNIGNFSRTNRG 592
QY 595 EDLDYKTRTIGFTTPPFSVQSTFTIGAMNFFSGNEVYIDRIEFVFPVEVYEAEDFE 654
Db 593 DNLEVRSPRTAGSTPFPFLNAQSTFLGAQSFEN-QEVIDRVEFPFAEVTFAEYDLE 651
QY 655 KAEQKVTALFTSTNPRGLKTDVKDQVHIDQVNLVESLSDEPYLDEKRELFEIVKYAKOIH 714
Db 652 RAQKAVNALFTSTNPRRLKTDVTDHIDQVSNMVACLSDFCLEKRELFEKVKYAKRLS 711
QY 715 IERNM 719
Db 712 DERNL 716

RESULT 14
Q93T75 PRELIMINARY; PRT; 1228 AA.
AC Q93T75;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Delta-endotoxin CryIa2.
GN Name=CryIa2;
OS Bacillus thuringiensis (subsp. entomocidus).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1436;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HD-9;
RA Mat Isa M.N., Abdullah M.A.F., Mahadi N.M.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF363025; AKS1084.1; -.
DR HSSP; P07130; 1DLC.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal_bind_Like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
SQ SEQUENCE 1228 AA; 139620 MW; 3DA2A4DBF59C95C3 CRC64;

Query Match 62.1%; Score 2322.5; DB 2; Length 1228;
Best Local Similarity 63.6%; Pred. No. 1.9e-151;
Matches 453; Conservative 80; Mismatches 162; Indels 17; Gaps 4;

QY 23 TDSLAKNETDI-----ELKNMNEEDYLRMSHESIDPFVSASTTQTGTGIGAKGI 70
Db 2 TSNRKNENEIINAVSNHSAQMDLLPDARIEDSLCTAEGNIDPFVSASTVQTGTGINAGRI 61
QY 71 LGTIGVPPAGIASLYSILGELPWPXKSWEIFMEHVEEIIINQILTYARNKALSIRG 130
Db 62 LGVLGVPPAGLASFYSLVGELPWRGRDQWEIFLEHVEQLINQIITENARNTALARLQ 121
QY 131 LGDALAVHESLESVENNRNTRSVVKNOYIALALEMFVKLPSPFAVSVEEVLPIYA 190
Db 122 LGDSFRAVQQLSLEDWLENRDDARTSVLHTQYIALELDFLNAMPFLFAIRNCEVPLMYA 181
QY 191 QAAUNHLLLRDASLFGSEFGTSGEIQRYERYEQVERTSDYCYVWYNTGLNLRGTN 241
Db 182 QAAUNHLLLRDASLFGSEFGTSGEIQRYERYEQVERTSDYCYVWYNTGLNLRGTN 241
QY 251 AKSWRYNQFRKMTLMVLDLVALFSPVDLTVPIKTSQLTREYVTAIGTVHQNQAF 310
Db 242 AASWRYNQFRDLTLGLVDLVALFSPVDTRTPYINTSAQLTREYVTAIGATGVN--MA 299
QY 311 SITWYNNAPSAEAAVIRSPHLLDLEKVTIYSLSRWSNTQYMMWGHRLSRLPI 370
Db 300 SMWYNNAPSAEAAVIRSPHLLDLEKVTIYSLSRWSNTQYMMWGHRLSRLPI 359
QY 371 GGALNTSTQGSTNTSINPVTLQFTSRDYRTESLAGLNLF--LTQPVNGVPRVDFHWKEP 428
Db 360 GGLNTSTEGATNTSINPVTLQFTSRDYRTESLAGLNLF--LTQPVNGVPRVDFHWKEP 419
QY 429 -TLPTASDNFYLVGAGVTQLQDSNELPPTTQGNVYESYSHRLSHIGLISASHVKAL 487
Db 420 QNISDRGTANYSQPYESPGLQKDSLETLPPTTERPNYESYSHRLSHIGLISASHVKAL 479
QY 488 VYSWTHRSADRTNTEPNISITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTNTGFGDI 547
Db 480 VYSWTHRSADRTNTEPNISITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTNTGFGDI 539
QY 548 RVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATNRGDLKYKTRTIGF 607
Db 540 RVTANGPLTQRYRIGFRYASTVDFDFVSRGGTTVNNFRFRTMNSGDELKYGNEVRRAF 599
QY 608 TTPPFSVQSTFTIGAMNFFSGNEVYIDRIEFVFPVEVYEAEDFEKAEQKVTALFTST 667
Db 600 TTPPFTQIQDIIRTSIQGLSGNGEYIDKIEIIPVTATFAEYDLERAQAVNALFTNT 659
QY 668 NPRGLKTDVKDQVHIDQVNLVESLSDEPYLDEKRELFEIVKYAKOIHIERNM 719
Db 660 NPRELKTVDVTDHIDQVSNMVACLSDFCLEKRELFEKVKYAKELSDERNL 711

RESULT 15
CIBA_BACTK STANDARD; PRT; 1228 AA.
AC P05517; Q45731;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pesticidal crystal protein cryIa (Insecticidal delta-endotoxin CryIb(a)) (Crystalline entomocidal protoxin) (140 kDa crystal protein).
GN Name=cryIa; Synonyms=cryIb(a), cryA4;
OS Bacillus thuringiensis (subsp. kurstaki), and
OS Bacillus thuringiensis (subsp. entomocidus).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=29339; 1436;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.kurstaki; STRAIN=HD-2;
RX MEDLINE=88203216; PubMed=3362680;
RA Brizzard B.L., Whiteley H.R.;
RT "Nucleotide sequence of an additional crystal protein gene cloned from Bacillus thuringiensis subsp. thuringiensis.";
RL Nucleic Acids Res. 16:2723-2723(1988).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.entomocidus; STRAIN=HD-110;
RA Soetaert P.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut epithelial cells of insects.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of the spore coat.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-terminus.
CC -!- SIMILARITY: Belongs to the delta endotoxin family.
CC This SWISS-PROT entry is copyright.. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -

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CC use by non-profit institutions as long as its content is in no way  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----

DR EMBL; X06711; CAA29898.1; -;  
DR EMBL; X95704; CAA55003.1; -;  
DR PIR; S00873; S00873.  
DR HSPP; P07130; 1DLC.  
DR InterPro; IPR001178; Endotoxin.  
DR InterPro; IPR005638; endotoxin\_C.  
DR InterPro; IPR005639; endotoxin\_N.  
DR InterPro; IPR008979; Gal\_bind\_Like.  
DR Pfam; PF03944; Endotoxin\_C; 1.  
DR Pfam; PF00555; Endotoxin\_M; 1.  
DR Pfam; PF03945; Endotoxin\_N; 1.  
KW Sporulation; Toxin.  
FT VARIANT 150 150 Y -> H (in strain HD-110).  
SQ SEQUENCE 1228 AA; 139647 MW; C8E3A19FB5D98575 CRC64;

Query Match 62.0%; Score 2321.5; DB 1; Length 1228;  
Best Local Similarity 63.6%; Pred.No. 2.2e-151;  
Matches 453; Conservative 80; Mismatches 162; Indels 17; Gaps 4;

QY	23	TDSLKNETDI-----ELKNNNEDYLRMSEHESIDPFVSASTTQTGTGIGIAGKI	70
DB	2	TSNEKNEEINAVSNHSAQMDLLPDARIEDSLCIAEGNNIDPFVSASTVQTGTINIAGRI	61
QY	71	LGTLGVFPAGQIASLYFILGELWPKGSQWEIPMEHVEIINQKILTYARNKALSDLRG	130
DB	62	LGVLGVFPAGQLASFYSFLVGLWPRGRDQWEIFLEHVEQLINQOITENARNATALARLQ	121
QY	131	LGDAVAVYHESLESWENRNTARSVVKQYIALELMFVOKLPSPAVSGEEVPLPIYA	190
DB	122	LGDSFRAYQGSLEDWLENRDDARTSRVLYQYIALELDFLNAMPLFAIRNCEVPLIMVYA	181
QY	191	QAANLHLLLRDASIFGKRWGLSASEISTFYNQOVERDYSDHCIKWYNTGLNLRGTN	250
DB	182	QAANLHLLLRDASLFGSEGLTSQEIQRVYRQVERTRDYSDYCVIEWYNTGLNLRGTN	241
QY	251	AKSVRYNQRKMTLVLDLVALFSPYDVLVPIKTTLSQLTREVYTDALGTVHPNCPA	310
DB	242	AASWRYNQRFRDUTLGLVLDLVALFSPYDRTPTINTSAQLTREVYTDALGATGVN--MA	299
QY	311	STTWYNNAPSFSAIEAAVIRSPHLLDFLEKVTIYSLLSRWSNTQYNNMGGHRLSRPI	370
DB	300	SMWYNNAPSFSAIEAAVIRSPHLLDFLEKVTIYSLLSRWSNTQYNNMGGHRLSRPI	359
QY	371	GGALNTSQGSTNTSINPVLQFTSRDYRTESLAGNLP--LTQPVNGYPRVDHFKPP	428
DB	360	GGGLNTSTHGATNTSINPVLRFASRDVYRTESYAGVLLMGVLEPIHGVTVRFNFTNP	419
QY	429	-TLPIASDNFYLGAGVGTQLODSENELPETTGPQNPYESYSHRLSHIGLISASHVKAL	487
DB	420	QNISDRGTANYSQYESFGQLKDSFETELPETTERPNYESYSHRLSHIGLILQSRVNP	479
QY	488	VYSWTHRSADRTNIENSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTNIGTGGDI	547
DB	480	VYSWTHRSADRTNIGNRITQIPMWKASELPQGTTVVRGPGFTGGDILRRTNIGTGGPI	539
QY	548	RVNINPPFACRYRIRYASTDLQFHTSINGKAINQGNFSATMNRGCDLDYKTERIGF	607
DB	540	RVTVNGDLTQYRIGFRYASTVDFDFVSRGGTIVNNFRFRTMNSGDELKYNFVRRAF	599
QY	608	TTPEFSQVQSTFTIGAMNFSNGNEVYIDRIEFVPEVETVEAEYDFEKAQEKVTAFTST	667
DB	600	TTPTFTQIQDIIRTSIQGLSGNGEVYIDKIEIIPVTATPEAEYDLERAQEAVALFTNT	659
QY	668	NPRGLKTDVDKDYHDVSNLVESLDEFPYLDKEELFEIVKYAKQIHIERNM	719
DB	660	NPRELKTVDVTDHYHDQVSNLVACLSDSEFCULDEKLELKVYAKRLSDERNL	711

Search completed: October 28, 2004, 18:30:12  
Job time : 101.579 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 28, 2004, 18:10:58 ; Search time 65.6795 Seconds  
(without alignments)  
3549.224 Million cell updates/sec

Title: US-10-019-823b-59

Perfect score: 3742

Sequence: 1 MLLKNPKHQSLSSNAKVDK.....KRELFYIKVAKQIHIERNM 719

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1370721 seqs, 324215800 residues

Total number of hits satisfying chosen parameters: 1370721

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*
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- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep.\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
- 20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3520	94.1	719	17	US-10-782-020-10
2	3520	94.1	719	17	US-10-782-141-8
3	3520	94.1	719	17	US-10-782-096-10
4	3520	94.1	719	17	US-10-782-570-7
5	3368.5	90.0	710	14	US-10-428-961-42
6	2324.5	62.1	1228	16	US-10-809-953-10
7	2314.5	61.9	1207	10	US-09-988-462-7
8	2234	59.7	1227	14	US-10-428-961-63
9	2219	59.3	1186	9	US-09-826-660-23
10	2170.5	58.0	1228	14	US-10-428-961-38
11	2170.5	58.0	1228	15	US-10-614-524-2
12	1982	53.0	643	9	US-09-826-660-25
13	1734.5	46.4	1167	14	US-10-089-678-1
					Sequence 10, Appl
					Sequence 8, Appl
					Sequence 10, Appl
					Sequence 7, Appl
					Sequence 42, Appl
					Sequence 10, Appl
					Sequence 7, Appl
					Sequence 63, Appl
					Sequence 23, Appl
					Sequence 38, Appl
					Sequence 2, Appl
					Sequence 25, Appl
					Sequence 1, Appl

#### ALIGNMENTS

##### RESULT 1

US-10-782-020-10

; Sequence 10, Application US/10782020  
; Publication No. US20040197916A1  
; GENERAL INFORMATION:  
; APPLICANT: Carozzi, Nadine  
; APPLICANT: Hargiss, Tracy  
; APPLICANT: Koziel, Michael G.  
; APPLICANT: Duck, Nicholas B.  
; APPLICANT: Carr, Brian  
; TITLE OF INVENTION: AXMI-004, A Delta-Endotoxin Gene and  
; FILE REFERENCE: 045600/274139  
; CURRENT APPLICATION NUMBER: US/10/782,020  
; PRIOR FILING DATE: 2004-02-19  
; PRIOR FILING DATE: 2003-02-20  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 719  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
US-10-782-020-10

Query Match 94.1%; Score 3520; DB 17; Length 719;  
Best Local Similarity 92.9%; Pred. No. 1.4e-286;  
Matches 668; Conservative 31; Mismatches 20; Indels 0; Gaps 0;

QY 1 MLLKNPKHQSLSSNAKVDKATDSIKNETDTELKNNMEDYLRKSEHSIDPFVSASTI 60  
Db 1 MLLKNPKHQSFSSNAKVDKISTDSUKNETDLELNINHEDCIKMSEYENFFVSASTI 60  
QY 61 QTGIGIAGKILGTGLGVFPFAGQIASLYSFTLGBLWPKGKQSQWEIFMHEVBEIINQKILTYA 120  
Db 61 QTGIGIAGKILGTGLGVFPFAGQIASLYSFTLGBLWPKGKQSQWEIFMHEVBEIINQKILTYA 120

Sequence 6, Appli  
Sequence 16, Appl  
Sequence 17, Appl  
Sequence 13, Appl  
Sequence 2, Appli  
Sequence 2, Appli  
Sequence 2, Appli  
Sequence 72, Appl  
Sequence 28, Appl  
Sequence 4, Appli  
Sequence 4, Appli  
Sequence 4, Appli  
Sequence 2, Appli  
Sequence 9, Appli  
Sequence 2, Appli  
Sequence 11, Appl  
Sequence 13, Appl  
Sequence 17, Appl  
Sequence 28, Appl  
Sequence 8, Appli  
Sequence 10, Appl  
Sequence 12, Appl  
Sequence 6, Appli  
Sequence 24, Appl  
Sequence 2, Appli  
Sequence 8, Appli  
Sequence 6, Appli  
Sequence 7, Appli

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QY 121 RNKALSDRLGLDGLDALAVHSHESLESWEVNRNTRASVNVNQYIALELMFVKQLSPFAVSG 180
DB 121 RNKALTDLGLDGLDALAVHSHESLESWEVNRNTRASVNVKSQYIALELMFVKQLSPFAVSG 180
QY 181 BEVPLPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVVERTRDYSDHCIKWYN 240
DB 181 BEVPLPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVVERAGDYSDHCVKWYS 240
QY 241 TGLNLRGNAKSWRYNQFRKDMTLMVLDLVALPSPYDTLVPIKTTSQLTRVYTDI 300
DB 241 TGLNLRGNAESWRYNQFRKDMTLMVLDLVALPSPYDTLVPIKTTSQLTRVYTDI 300
QY 301 GTVHPNQAFSTTWYNNAPSPSAEAAVIRSPHLLDFLEKVTIYSLSRWSNTQYNNMW 360
DB 301 GTVHPSPSTTWYNNAPSPSAEAAVIRSPHLLDFLEKVTIYSLSRWSNTQYNNMW 360
QY 361 GGHRLSRPIGGALNTSTOGSTNTSINPVTLOFTSRDVYRTESLAGLNLFTQPVNGVPR 420
DB 361 GGHLEFRTIGTGLNLTSTOGSTNTSINPVTLOFTSRDVYRTESLAGLNLFTQPVNGVPR 420
QY 421 VDFHMKFPTLPASDNFYVYLGAGVGTQLODSENELPPEATTGQPNYESYSHLSHIGLIS 480
DB 421 VDFHMKFVTHPIASDNFYVYLGAGVGTQLODSENELPPEATTGQPNYESYSHLSHIGLIS 480
QY 481 ASHVKALVYSWTHRSADRNTNTEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 540
DB 481 ASHVKALVYSWTHRSADRNTNTEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 540
QY 541 TGTFGDIRVNIAPPFAQRYVRIRVASTTDLQFHTSINGKAINQGNFSATMNRGDDLDYK 600
DB 541 TGTFGDIRVNIAPPFAQRYVRIRVASTTDLQFHTSINGKAINQGNFSATMNRGDDLDYK 600
QY 601 TPTTGTFTFPFSDVQSTFTIGANFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 660
DB 601 TPTTGTFTFPFSDVQSTFTIGANFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 660
QY 661 TALFTSTNPRGLKTDVKYHIDQVSNLVSLSDEFYLDKRELFELFVYKAKQIHIERNM 719
DB 661 TALFTSTNPRGLKTDVKYHIDQVSNLVSLSDEFYLDKRELFELFVYKAKQIHIERNM 719

RESULT 2
US-10-782-141-8
; Sequence 8, Application US/10782141
; Publication No. US20040197917A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and
; TITLE OF INVENTION: Methods for Its Use
; FILE REFERENCE: 045600/274143
; CURRENT APPLICATION NUMBER: US/10/782,141
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: 60/448,632
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 719
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-782-141-8

Query Match 94.1%; Score 3520; DB 17; Length 719;
Best Local Similarity 92.9%; Pred. No. 1.4e-286;
Matches 668; Conservative 31; Mismatches 20; Indels 0; Gaps 0;

QY 1 MKLKNQDKHQSSNAKVDKIATDSLKNETDIELQNHEDCLKMSYEYENVEFPFVSASTI 60

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DB 1 MKLKNQDKHQSSNAKVDKIATDSLKNETDIELQNHEDCLKMSYEYENVEFPFVSASTI 60
QY 61 QTGIGTAGKILCTGLVPPFAGQIASLYSFTLGLWPKGKSOWEIPMEHVEEIIINQKILTYA 120
DB 61 QTGIGTAGKILCTGLVPPFAGQIASLYSFTLGLWPKGKSOWEIPMEHVEEIIINQKILTYA 120
QY 121 RNKALSDRLGLDGLDALAVHSHESLESWEVNRNTRASVNVNQYIALELMFVKQLSPFAVSG 180
DB 121 RNKALTDLGLDGLDALAVHSHESLESWEVNRNTRASVNVKSQYIALELMFVKQLSPFAVSG 180
QY 181 BEVPLPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVVERTRDYSDHCIKWYN 240
DB 181 BEVPLPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVVERAGDYSDHCVKWYS 240
QY 241 TGLNLRGNAKSWRYNQFRKDMTLMVLDLVALPSPYDTLVPIKTTSQLTRVYTDI 300
DB 241 TGLNLRGNAESWRYNQFRKDMTLMVLDLVALPSPYDTLVPIKTTSQLTRVYTDI 300
QY 301 GTVHPNQAFSTTWYNNAPSPSAEAAVIRSPHLLDFLEKVTIYSLSRWSNTQYNNMW 360
DB 301 GTVHPSPSTTWYNNAPSPSAEAAVIRSPHLLDFLEKVTIYSLSRWSNTQYNNMW 360
QY 361 GGHRLSRPIGGALNTSTOGSTNTSINPVTLOFTSRDVYRTESLAGLNLFTQPVNGVPR 420
DB 361 GGHLEFRTIGTGLNLTSTOGSTNTSINPVTLOFTSRDVYRTESLAGLNLFTQPVNGVPR 420
QY 421 VDFHMKFPTLPASDNFYVYLGAGVGTQLODSENELPPEATTGQPNYESYSHLSHIGLIS 480
DB 421 VDFHMKFVTHPIASDNFYVYLGAGVGTQLODSENELPPEATTGQPNYESYSHLSHIGLIS 480
QY 481 ASHVKALVYSWTHRSADRNTNTEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 540
DB 481 ASHVKALVYSWTHRSADRNTNTEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 540
QY 541 TGTFGDIRVNIAPPFAQRYVRIRVASTTDLQFHTSINGKAINQGNFSATMNRGDDLDYK 600
DB 541 TGTFGDIRVNIAPPFAQRYVRIRVASTTDLQFHTSINGKAINQGNFSATMNRGDDLDYK 600
QY 601 TPTTGTFTFPFSDVQSTFTIGANFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 660
DB 601 TPTTGTFTFPFSDVQSTFTIGANFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 660
QY 661 TALFTSTNPRGLKTDVKYHIDQVSNLVSLSDEFYLDKRELFELFVYKAKQIHIERNM 719
DB 661 TALFTSTNPRGLKTDVKYHIDQVSNLVSLSDEFYLDKRELFELFVYKAKQIHIERNM 719

RESULT 3
US-10-782-096-10
; Sequence 10, Application US/10782096
; Publication No. US20040210964A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-009, A Delta-Endotoxin Gene and
; TITLE OF INVENTION: Methods for Its Use
; FILE REFERENCE: 045600/274148
; CURRENT APPLICATION NUMBER: US/10/782,096
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: 60/448,633
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 719
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-782-096-10

Query Match 94.1%; Score 3520; DB 17; Length 719;

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; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-782-570-7

Query Match 94.1%; Score 3520; DB 17; Length 719;
Best Local Similarity 92.9%; Pred. No. 1.4e-286;
Matches 668; Conservative 31; Mismatches 20; Indels 0; Gaps 0;

QY 1 M K L N P D K H Q S L S S N A K V D K I A T D S L K N E T D I E L K M N N E D Y L R M S H E S I D P F V S A S T I 60
DB 1 M K L N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y E N V P F V S A S T I 60

QY 61 Q T G I G I A G K I L G T L G V P P A G Q V A S I L S F I L G E L M P K G K Q W E I F M E H V E E I I N O K I L T Y A 120
DB 61 Q T G I G I A G K I L G T L G V P P A G Q V A S I L S F I L G E L M P K G K Q W E I F M E H V E E I I N O K I L T Y A 120

QY 121 R N K A L S D L R G L G D A L A V Y H S L E S V E N R N T R A S V V K N O Y I A L E M F V Q K L P S F A V S G 180
DB 121 R N K A L T D L K G L G D A L A V Y H S L E S V E N R N T R A S V V K S O Y I A L E M F V Q K L P S F A V S G 180

QY 181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S A S E I S T F Y N Q V E R T R D Y S D H C I K W N 240
DB 181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S A S E I S T F Y N Q V E R A G D Y S D H C V K W Y S 240

QY 241 T G L N N R L G T N A K S W R Y N Q F R K D M T L M V L D L V A L P S Y D T L V P I K T T S O L T R E V Y T D A I 300
DB 241 T G L N N R L G T N A E S W R Y N Q F R D M T L M V L D L V A L P S Y D T Q W Y P I K T T A Q L T R E V Y T D A I 300

QY 301 G T V H P N Q A F A S T T W Y N N N A P S F A I E A A V I R S P H L L D F L E K V T I Y S L L S R W S N T Q Y M N W 360
DB 301 G T V H P H P S F T T T W Y N N N A P S F A I E A A V V N P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N W 360

QY 361 G G H R L E S R P I G G A L N T S T G S T N T S I N P V T L Q T S R D V Y T E S I A G L N L F L T O P V N G V P R 420
DB 361 G G H K L E F R T I G G T L N I S T G S T N T S I N P V T L P F T S R D V Y T E S L A G L N L F L T O P V N G V P R 420

QY 421 V D F H W K E P T L P I A S D N F Y Y L G A G V G T Q L O D S E N L P P E T T G Q P N Y E S Y S H R L S H I G L I S 480
DB 421 V D F H W K F V T H P I A S D N F Y P G Y A G I G T Q L O D S E N L P P E A T G Q P N Y E S Y S H E L S H I G L I S 480

QY 481 A S H V K A L Y S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G G D I L R R T N 540
DB 481 A S H V K A L Y S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G G D I L R R T N 540

QY 541 T G T F G D I R V N I N P P A Q R Y R V I R Y A S T T D L Q F H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 600
DB 541 T G T F G D I R V N I N P P A Q R Y R V I R Y A S T T D L Q F H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 600

QY 601 T F R T G T T P P S F S D V Q S T F T I G A W N F S S G N E V Y I D R I E F V P V E V T Y E A S Y D F E K A Q E K V 660
DB 601 T F R T V G T T P P S F L D V Q S T F T I G A W N F S S G N E V Y I D R I E F V P V E V T Y E A S Y D F E K A Q E K V 660

QY 661 T A L F T S T N P R G L K T D V K D Y H I D Q V N L V E S I S D F Y L D E K R E L F E I V K Y A K O I H I E R N M 719
DB 661 T A L F T S T N P R G L K T D V K D Y H I D Q V N L V E S L S D F Y L D E K R E L F E I V K Y A K O L H I E R N M 719

RESULT 4
US-10-782-570-7
; Sequence 7, Application US/10782570
; Publication No. US20040210965A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Carozzi, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-007, A Delta-Endotoxin Gene and
; TITLE OF INVENTION: Methods for Its Use
; FILE REFERENCE: 045600/274144
; CURRENT APPLICATION NUMBER: US/10/782,570
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: 60/448,812
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 719

```

```

; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-782-570-7

Query Match 94.1%; Score 3520; DB 17; Length 719;
Best Local Similarity 92.9%; Pred. No. 1.4e-286;
Matches 668; Conservative 31; Mismatches 20; Indels 0; Gaps 0;

QY 1 M K L N P D K H Q S L S S N A K V D K I A T D S L K N E T D I E L K M N N E D Y L R M S H E S I D P F V S A S T I 60
DB 1 M K L N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y E N V P F V S A S T I 60

QY 61 Q T G I G I A G K I L G T L G V P P A G Q V A S I L S F I L G E L M P K G K Q W E I F M E H V E E I I N O K I L T Y A 120
DB 61 Q T G I G I A G K I L G T L G V P P A G Q V A S I L S F I L G E L M P K G K Q W E I F M E H V E E I I N O K I S T Y A 120

QY 121 R N K A L S D L R G L G D A L A V Y H S L E S V E N R N T R A S V V K N O Y I A L E M F V Q K L P S F A V S G 180
DB 121 R N K A U T D L K G L G D A L A V Y H S L E S V G N R N T R A S V V K S O Y I A L E M F V Q K L P S F A V S G 180

QY 181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S A S E I S T F Y N Q V E R T R D Y S D H C I K W N 240
DB 181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S E I S T F Y N Q V E R A G D Y S D H C V K W Y S 240

QY 241 T G L N N R L G T N A K S W R Y N Q F R K D M T L M V L D L V A L P S Y D T L V P I K T T S O L T R E V Y T D A I 300
DB 241 T G L N N R L G T N A E S W R Y N Q F R D M T L M V L D L V A L P S Y D T Q W Y P I K T T A Q L T R E V Y T D A I 300

QY 301 G T V H P N Q A F A S T T W Y N N N A P S F A I E A A V I R S P H L L D F L E K V T I Y S L L S R W S N T Q Y M N W 360
DB 301 G T V H P H P S F T T T W Y N N N A P S F A I E A A V V N P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N W 360

QY 361 G G H R L E S R P I G G A L N T S T G S T N T S I N P V T L Q T S R D V Y T E S I A G L N L F L T O P V N G V P R 420
DB 361 G G H K L E F R T I G G T L N I S T G S T N T S I N P V T L P F T S R D V Y T E S L A G L N L F L T O P V N G V P R 420

QY 421 V D F H W K E P T L P I A S D N F Y Y L G A G V G T Q L O D S E N L P P E T T G Q P N Y E S Y S H R L S H I G L I S 480
DB 421 V D F H W K F V T H P I A S D N F Y P G Y A G I G T Q L O D S E N L P P E A T G Q P N Y E S Y S H E L S H I G L I S 480

QY 481 A S H V K A L Y S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G G D I L R R T N 540
DB 481 A S H V K A L Y S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G G D I L R R T N 540

QY 541 T G T F G D I R V N I N P P A Q R Y R V I R Y A S T T D L Q F H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 600
DB 541 T G T F G D I R V N I N P P A Q R Y R V I R Y A S T T D L Q F H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 600

QY 601 T F R T G T T P P S F S D V Q S T F T I G A W N F S S G N E V Y I D R I E F V P V E V T Y E A S Y D F E K A Q E K V 660
DB 601 T F R T V G T T P P S F L D V Q S T F T I G A W N F S S G N E V Y I D R I E F V P V E V T Y E A S Y D F E K A Q E K V 660

QY 661 T A L F T S T N P R G L K T D V K D Y H I D Q V N L V E S I S D F Y L D E K R E L F E I V K Y A K O I H I E R N M 719
DB 661 T A L F T S T N P R G L K T D V K D Y H I D Q V N L V E S L S D F Y L D E K R E L F E I V K Y A K O L H I E R N M 719

RESULT 5
US-10-428-961-42
; Sequence 42, Application US/10428961
; Publication No. US20030237111A1
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Chu, Chih-Rei
; APPLICANT: Donovan, William P.
; APPLICANT: Galmer, Amy J.
; APPLICANT: Rupaar, Mark J.
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin
; TITLE OF INVENTION: Polynucleotides, Compositions, and Methods of Use (Amended)
; FILE REFERENCE: MECO201--1
; CURRENT APPLICATION NUMBER: US/10/428,961
; CURRENT FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: 09/661,322

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QY 23 TDSLKNETDI-----ELKNNN-----EDYLRMSSEHSIDPFVSASTIQTGIG 65
DB 2 TSNRKNEEINIALSIPAVNSHSAQNLSSTDARIEDSLCIAEGNNIDPFVSASTVQTGIN 61
QY 66 IAGKILGTGVFPAGQIASLYSFIILGELWPKGSKWEIFMEHVEEIIINOKILTYARNKAL 125
DB 62 IAGRILGVLGVFPAGQIASFYSLFVGLWPRGRDPWEIFLEHVEHLIRQOVTTENTRTDAL 121
QY 126 SDRGLGDALAVYHESLESWENRNNTRARSVVKNQYIALELMFVOKLPSFAVSGEEVPL 185
DB 122 ARLOGLGNSFRAYQOSLEDWLENRDARTSRVLYTQYIALELDFLNAMPFAIRNQEVPL 181
QY 186 LPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNQVTRTRDYSCHCIKWYNTGLNN 245
DB 182 LMVYAQAANLHLLLRDASLFGSEFGLTSQELQRYRYERQVETREYSYCARWYNTGLNN 241
QY 246 LRGTNAKSWVRYNQPRKQMTLMVLVALFSPYDYLVIPIKTTTSOLTREVYTDAGTVHP 305
DB 242 LRGTNAESWLRYNQFRDLTLGLVLDLVALFSPYDTRVYPMNTSAQLTREIYTDPIGRNA 301
QY 306 NQAFASLTWYNNNAPSFAIEAARVIRSPHLLDFLEKVTIYSLSRWSNTQYMMWGGHRL 365
DB 302 PSGFASTWNNNAPSFAIEAARVIRPPHLLDFPQLTIIFSVLSRWSNTQYMMWGGHRL 361
QY 366 ESRPIGALNTSTOGSTNTSINPVTLOFTSRDVRATESLAGNLFLTOPVNGVPRVDFHW 425
DB 362 ESRTRIGSLSTWTHGNTSINPVTLOFTSRDVRATESFAGINILLTTPVNGVPRVDFHW 421
QY 426 KEPTPIASDNFYLYGACVGTQLODSENELPPTTGPQNVESYHRLSHIGLISASHVK 485
DB 422 RNPLNSLRGSLTYTGYGVGTQLODSENELPPTTGPQNVESYHRLSHIGLISASHVK 481
QY 486 ALVYSWTHRSADRTNTIPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRNTGTGFG 545
DB 482 APVYSWTHRSADRTNTISSDSITQIPLVKSFNLNSGTSVVGPGTGGDIIRTNVNGSVL 541
QY 546 DIRVNIINPPFAQRYRIRYASTTDLOFHTSINGKALINGCFNSATMNGEDLDYKTRTI 605
DB 542 SMGLFNNTSLQRYRVRYAAASQTMVLRTVVGSTTFDQGFPTMSANESLTSQSFRA 601
QY 606 GFTTTPFSFDVOSTTIGAWNFSSGNEVYIDRIEVPVVEVYEAHYDEKAEQKVTAFT 665
DB 602 EFPVGISASGSO-TAGISISNNAGRQTFPHDKIEPIPTATFEAYDYDLERAQEAVALFT 660
QY 666 STNPRGLKTDVXDYHIDQVSNLVESLSDEFYLDKRELFELVIKYAKQHIERNM 719
DB 661 NTNPRRLKGTVDYDHYDEVSNLVACLSDDEFCLDEXRELLEKVKYAKRLSDERNL 714

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## RESULT 9

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US-09-826-660-23
; Sequence 23, Application US/09826660
; Patent No. US20010026940A1
; GENERAL INFORMATION:
; APPLICANT: Cardineau, Guy A.
; APPLICANT: Stelman, Steven J.
; APPLICANT: Narva, Kenneth E.
; TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins
; FILE REFERENCE: MA-714XC2D1
; CURRENT APPLICATION NUMBER: US/09/826,660
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/178,252
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: 60/065,215
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/076,445
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 1186
; TYPE: PRT
; ORGANISM: Artificial Sequence

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; FEATURE:
; OTHER INFORMATION: Toxin encoded by synthetic B.t. gene
US-09-826-660-23

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Query Match 59.3%; Score 2219; DB 9; Length 1186;
Best Local Similarity 60.5%; Pred. No. 6.8e-177;
Matches 432; Conservative 103; Mismatches 161; Indels 18; Gaps 3;

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QY 23 TDSLKNETDI-----ELKNNN-----EDYLRMSSEHSIDPFVSASTIQTGIG 65
DB 2 TSNRKNEEINIALSIPAVNSHSAQNLSSTDARIEDSLCIAEGNNIDPFVSASTVQTGIN 61
QY 66 IAGKILGTGVFPAGQIASLYSFIILGELWPKGSKWEIFMEHVEEIIINOKILTYARNKAL 125
DB 62 IAGRILGVLGVFPAGQIASFYSLFVGLWPRGRDPWEIFLEHVEHLIRQOVTTENTRTDAL 121
QY 126 SDRGLGDALAVYHESLESWENRNNTRARSVVKNQYIALELMFVOKLPSFAVSGEEVPL 185
DB 122 ARLOGLGNSFRAYQOSLEDWLENRDARTSRVLYTQYIALELDFLNAMPFAIRNQEVPL 181
QY 186 LPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNQVTRTRDYSCHCIKWYNTGLNN 245
DB 182 LMVYAQAANLHLLLRDASLFGSEFGLTSQELQRYRYERQVETREYSYCARWYNTGLNN 241
QY 246 LRGTNAKSWVRYNQPRKQMTLMVLVALFSPYDYLVIPIKTTTSOLTREVYTDAGTVHP 305
DB 242 LRGTNAESWLRYNQFRDLTLGLVLDLVALFSPYDTRVYPMNTSAQLTREIYTDPIGRNA 301
QY 306 NQAFASLTWYNNNAPSFAIEAARVIRSPHLLDFLEKVTIYSLSRWSNTQYMMWGGHRL 365
DB 302 PSGFASTWNNNAPSFAIEAARVIRPPHLLDFPQLTIIFSVLSRWSNTQYMMWGGHRL 361
QY 366 ESRPIGALNTSTOGSTNTSINPVTLOFTSRDVRATESLAGNLFLTOPVNGVPRVDFHW 425
DB 362 ESRTRIGSLSTWTHGNTSINPVTLOFTSRDVRATESFAGINILLTTPVNGVPRVDFHW 421
QY 426 KEPTPIASDNFYLYGACVGTQLODSENELPPTTGPQNVESYHRLSHIGLISASHVK 485
DB 422 RNPLNSLRGSLTYTGYGVGTQLODSENELPPTTGPQNVESYHRLSHIGLISASHVK 481
QY 486 ALVYSWTHRSADRTNTIPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRNTGTGFG 545
DB 482 APVYSWTHRSADRTNTISSDSITQIPLVKSFNLNSGTSVVGPGTGGDIIRTNVNGSVL 541
QY 546 DIRVNIINPPFAQRYRIRYASTTDLOFHTSINGKALINGCFNSATMNGEDLDYKTRTI 605
DB 542 SMGLFNNTSLQRYRVRYAAASQTMVLRTVVGSTTFDQGFPTMSANESLTSQSFRA 601
QY 606 GFTTTPFSFDVOSTTIGAWNFSSGNEVYIDRIEVPVVEVYEAHYDEKAEQKVTAFT 665
DB 602 EFPVGISASGSO-TAGISISNNAGRQTFPHDKIEPIPTATFEAYDYDLERAQEAVALFT 660
QY 666 STNPRGLKTDVXDYHIDQVSNLVESLSDEFYLDKRELFELVIKYAKQHIERNM 719
DB 661 SNNQIGLKTVDYDHYDVRVSNLVECLSDDEFCLDEXRELSEKVKHAKRLSDERNL 714

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## RESULT 10

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US-10-428-961-38
; Sequence 38, Application US/10428961
; Publication No. US20030237111A1
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Chu, Chih-Rei
; APPLICANT: Donovan, William P.
; APPLICANT: Gilmer, Amy J.
; APPLICANT: Rupal, Mark J.
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin
; FILE REFERENCE: MECO201-1
; CURRENT APPLICATION NUMBER: US/10/428,961
; CURRENT FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: 09/661,322

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; PRIOR FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: 60/153,995
; PRIOR FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
; LENGTH: 1228
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-428-961-38

Query Match      58.0%; Score 2170.5; DB 14; Length 1228;
Best Local Similarity 60.5%; Pred. No. 8.6e-173; Indels 15; Gaps 8;
Matches 435; Conservative 98; Mismatches 171;

QY 12 LSSNAK-----VDKIATDSLKN-ETDIELK-NMNNEDYLRMSHEHSDPFSASTIQTGI 64
Db 1 LTSNRKNEIINALSIPAVSNHSTOMDLSDPARIEDSLCIAEGNNINPLVSASTVQTGI 60

QY 65 GIAGKILGTGVPPAGQIASLYSFLGELWPKGKOWEIEFMEHVEEINOKILTYARNKA 124
Db 61 NIAGRILGVLPVPPAGQIASFSLVGLWPRGRDQWEIEFLEHVEQLINQITENARNTA 120

QY 125 LSDRLGLDALAVYHESLESWENNRNTRASVVKNOYIALELMFVQKLSFAVSGEEVP 184
Db 121 LARIQGLGDSFRAYQQSLEDWLENRDARTRSVLTYQVIALELDFLNAMPLFAIRNQEVP 180

QY 185 LPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVTRDYSDHCHIKWYNTGLN 244
Db 181 LMVYAQAANLHLLLRDASLFGSEFGLTSQEIQRYYERQVEQTRDYSDYCVWYNTGLN 240

QY 245 NLRGTNKSWRYNQFQKMTLMVLVDVALPSPYDVLVYPIKTTSQLTRVYDAGTGVH 304
Db 241 SLRGTNKSWRYNQFQKMTLMVLVDVALPSPYDVLVYPIKTTSQLTRVYDAGTGVH 300

QY 305 PNQAFSTWYNNAPSFSAIEAAVIRSPHLLDFLEKVTIYSLSRWSNTQYNNMGGHR 364
Db 301 VN--MASNMWYNNAPSFSAIEAAVIRSPHLLDFLEKVTIYSLSRWSNTQYNNMGGHR 358

QY 365 LESRPIGGALNTSTOGSTNTSINPVTLOFTSRDYVTRTESLAGLNLF--LTQPVNGVPRVD 422
Db 359 IQSRPIGGALNTSTOGSTNTSINPVTLOFTSRDYVTRTESLAGLNLF--LTQPVNGVPRVD 418

QY 423 FHWKFP--TLPIASDNFYLYGAGVGTQLODSENELPPTTGPQNYESYSHRLSHIGLIS 480
Db 419 FNPRNPQNTFERGTAN--YSQPYESPGQLKQDSELTPELTERPNYESYSHRLSHIGLIS 477

QY 481 ASHKALVYSWTHRSADRTNTEPNSITQIPLVKAFLNSGAAVVRGPGFTGGDILRTN 540
Db 478 QSRVHVPVYSWTHRSADRTNTEPNSITQIPLVKAFLNSGAAVVRGPGFTGGDILRTN 537

QY 541 TGTFGDIRVNIAPPFAQRYRVRIRYASTTDLOFHTSINGKAINQGNFSAATMNGEDLDYK 600
Db 538 NGSVLSMGLNFNTSLQRYRVRIRYASTTDLOFHTSINGKAINQGNFSAATMNGEDLDYK 597

QY 601 TFRITGFTTFFSFDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDEKAEKV 660
Db 598 SFRFAEPFVGISASGSC--TAGISISNAGRQTFHFDEKIEFIPITATFEAEYDLERAQEA 656

QY 661 TALFTSTNPRGLTKDVKDHYDQVSNLVESISDEFYLDKRELFIVKYAKQIHIERNM 719
Db 657 NALFTNTNPRRLKTDVTDYHIDQVSNLVACLSDEFCLDEKRELEKVKYAKRLSDERNL 715

RESULT 11
US-10-614-524-2
; Sequence 2, Application US/10614524
; Publication No. US20040016020A1
; GENERAL INFORMATION: Greta
; APPLICANT: Arnaut, Greta
; APPLICANT: Boets, Annemie
; APPLICANT: Damme, Nicole
; APPLICANT: Mathieu, Eva

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; APPLICANT: Vanneste, Stijn
; APPLICANT: Van Rie, Jeroen
; TITLE OF INVENTION: Insecticidal proteins from Bacillus thuringiensis.
; FILE REFERENCE: NEWBTSUS2
; CURRENT APPLICATION NUMBER: US/10/614,524
; CURRENT FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: US/09/739,243
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/173387
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1228
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-614-524-2

Query Match      58.0%; Score 2170.5; DB 15; Length 1228;
Best Local Similarity 60.5%; Pred. No. 8.6e-173; Indels 15; Gaps 8;
Matches 435; Conservative 98; Mismatches 171;

QY 12 LSSNAK-----VDKIATDSLKN-ETDIELK-NMNNEDYLRMSHEHSDPFSASTIQTGI 64
Db 1 LTSNRKNEIINALSIPAVSNHSTOMDLSDPARIEDSLCIAEGNNINPLVSASTVQTGI 60

QY 65 GIAGKILGTGVPPAGQIASLYSFLGELWPKGKOWEIEFMEHVEEINOKILTYARNKA 124
Db 61 NIAGRILGVLPVPPAGQIASFSLVGLWPRGRDQWEIEFLEHVEQLINQITENARNTA 120

QY 125 LSDRLGLDALAVYHESLESWENNRNTRASVVKNOYIALELMFVQKLSFAVSGEEVP 184
Db 121 LARIQGLGDSFRAYQQSLEDWLENRDARTRSVLTYQVIALELDFLNAMPLFAIRNQEVP 180

QY 185 LPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVTRDYSDHCHIKWYNTGLN 244
Db 181 LMVYAQAANLHLLLRDASLFGSEFGLTSQEIQRYYERQVEQTRDYSDYCVWYNTGLN 240

QY 245 NLRGTNKSWRYNQFQKMTLMVLVDVALPSPYDVLVYPIKTTSQLTRVYDAGTGVH 304
Db 241 SLRGTNKSWRYNQFQKMTLMVLVDVALPSPYDVLVYPIKTTSQLTRVYDAGTGVH 300

QY 305 PNQAFSTWYNNAPSFSAIEAAVIRSPHLLDFLEKVTIYSLSRWSNTQYNNMGGHR 364
Db 301 VN--MASNMWYNNAPSFSAIEAAVIRSPHLLDFLEKVTIYSLSRWSNTQYNNMGGHR 358

QY 365 LESRPIGGALNTSTOGSTNTSINPVTLOFTSRDYVTRTESLAGLNLF--LTQPVNGVPRVD 422
Db 359 IQSRPIGGALNTSTOGSTNTSINPVTLOFTSRDYVTRTESLAGLNLF--LTQPVNGVPRVD 418

QY 423 FHWKFP--TLPIASDNFYLYGAGVGTQLODSENELPPTTGPQNYESYSHRLSHIGLIS 480
Db 419 FNPRNPQNTFERGTAN--YSQPYESPGQLKQDSELTPELTERPNYESYSHRLSHIGLIS 477

QY 481 ASHKALVYSWTHRSADRTNTEPNSITQIPLVKAFLNSGAAVVRGPGFTGGDILRTN 540
Db 478 QSRVHVPVYSWTHRSADRTNTEPNSITQIPLVKAFLNSGAAVVRGPGFTGGDILRTN 537

QY 541 TGTFGDIRVNIAPPFAQRYRVRIRYASTTDLOFHTSINGKAINQGNFSAATMNGEDLDYK 600
Db 538 NGSVLSMGLNFNTSLQRYRVRIRYASTTDLOFHTSINGKAINQGNFSAATMNGEDLDYK 597

QY 601 TFRITGFTTFFSFDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDEKAEKV 660
Db 598 SFRFAEPFVGISASGSC--TAGISISNAGRQTFHFDEKIEFIPITATFEAEYDLERAQEA 656

QY 661 TALFTSTNPRGLTKDVKDHYDQVSNLVESISDEFYLDKRELFIVKYAKQIHIERNM 719
Db 657 NALFTNTNPRRLKTDVTDYHIDQVSNLVACLSDEFCLDEKRELEKVKYAKRLSDERNL 715

RESULT 12
US-09-826-660-25

```

; Sequence 25, Application US/09826660  
; Patent No.: US20010026940A1  
; GENERAL INFORMATION:  
; APPLICANT: Cardineau, Guy A.  
; APPLICANT: Stelman, Steven J.  
; APPLICANT: Narva, Kenneth E.  
; TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins  
; FILE REFERENCE: WA-714XC2D1  
; CURRENT APPLICATION NUMBER: US/09/826,660  
; CURRENT FILING DATE: 2001-04-05  
; PRIOR APPLICATION NUMBER: 09/178,252  
; PRIOR FILING DATE: 1998-10-23  
; PRIOR APPLICATION NUMBER: 60/065,215  
; PRIOR FILING DATE: 1997-11-12  
; PRIOR APPLICATION NUMBER: 60/076,445  
; PRIOR FILING DATE: 1998-03-02  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 25  
; LENGTH: 643  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Toxin encoded by synthetic B.t. gene  
US-09-826-660-25

Query Match 53.0%; Score 1982; DB 9; Length 643;  
Best Local Similarity 59.6%; Pred. No. 2.2e-157;  
Matches 383; Conservative 94; Mismatches 148; Indels 18; Gaps 3;  
QY 23 TDSLKNETDI---ELKNNN-----EDYLRMSEHSIDPFVSASTIOTGIG 65  
DB 2 TSNRKNENEIINALSIPAVSHSAQNMISTDARIEDSLCIAEGNNIDPFVSASTVQTGIN 61  
QY 66 TAGKILGTLPVFAQIASLVSFILGELWPKGSQWEIEMHVEEIIINOKILTIVARNKAL 125  
DB 62 IAGRLGVLPVFAQIASLVSFILGELWPKGRDPEWEIFLHVHQLTRQVTEINTOTAL 121  
QY 126 SDRGLGDAIAYHSHLSLSESVENNRNTRARVKNQYIALELMFVQKLPSPAVSGEEVPL 185  
DB 122 ARLOGLGSLFRAYQOSLEDWLENRDARTSRVLYTQYIALELDELFLNAMPFAIRNQSVPL 181  
QY 186 LPIYAQAANLHLLLRDASIFGKWLGSASEISITFYNRQVETRDYSDHCHIKWYNTGLNN 245  
DB 182 LNVYAQAANLHLLLRDASIFGSEFGLTSQIORYIERQVETREYSDYCARWYNTGLNN 241  
QY 246 LRGTNAKSWRYNQRKQMTLMVLVLPVSYDTLPYPIKTSQLTREVVYDAIGTVHP 305  
DB 242 LRGTNAESWLRNQRKQMTLMVLVLPVSYDTLPYPIKTSQLTREIYTDPIGRNA 301  
QY 306 NQAFASTWYNNAPSAFAIAEAVIRSHLADLEKVTIYSLSRWNTQYNNWVGHRLL 365  
DB 302 PSGPASTWNNAPSAFAIAEAVIRSHLADLEKVTIYSLSRWNTQYNNWVGHRLL 361  
QY 366 ESRPICGALNTSTQGSTNTSINPVLQFTSRDVRATESLAGINLFLTPQVNGVRVDFHW 425  
DB 362 ESRITRGSLSSTHGNTSINPVLQFTSRDVRATESLAGINLFLTPQVNGVRVDFHW 421  
QY 426 KPTPLPIASDNPYLYGAGVGTQLODSNELPPETGQPNYESYSHRLSHLIGLISASHVK 485  
DB 422 RNPLSLRGLSLYITGYGVGTQLODSNELPPETGQPNYESYSHRLSHLIGLISASHVK 481  
QY 486 ALVYSWTHRSADRNTIIPNSITQIPLVKAFNLSSGAAVVRGPGFTGDIILRRNTIGTFG 545  
DB 482 APVYSWTHRSADRNTIIPNSITQIPLVKAFNLSSGAAVVRGPGFTGDIILRRNTIGTFG 541  
QY 546 DIRVNIINPFAQRYRVRIRYASTDLDQFHTSINGKAINQGNFSAATMARGEDLDYKTRTI 605  
DB 542 SMGLNFNNTSLQRYRVRIRYASTDLDQFHTSINGKAINQGNFSAATMARGEDLDYKTRTI 601  
QY 606 GFTTFPFSQVSTTIGAMNFFSSGNEVYIDRIEFVPEVVEVYE 648  
DB 602 EPPVGISASGSQ-TAGISISNAGRQTFHFDEKIEFIPITATLE 643

RESULT 13  
US-10-089-678-1  
; Sequence 1, Application US/10089678  
; Publication No. US20030017967A1  
; GENERAL INFORMATION:  
; APPLICANT: ASANO, Shinichiro  
; TITLE OF INVENTION: PROTEIN HAVING INSECTICIDAL ACTIVITY, DNA ENCODING THE PROTEIN, AN  
; FILE REFERENCE: Q68821  
; CURRENT APPLICATION NUMBER: US/10/089,678  
; CURRENT FILING DATE: 2002-05-02  
; PRIOR APPLICATION NUMBER: JP 2000-236140  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: PCT/JP01/06660  
; PRIOR FILING DATE: 2001-08-02  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 1  
; LENGTH: 1167  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
US-10-089-678-1

Query Match 46.4%; Score 1734.5; DB 14; Length 1167;  
Best Local Similarity 48.2%; Pred. No. 3.5e-136;  
Matches 366; Conservative 123; Mismatches 210; Indels 61; Gaps 14;  
QY 1 MKLKQPDKHQSL---SSNAKVDKIATDSLKNETDIELKNNMNNEDYLRMSEH-----SI 51  
DB 1 MKNQNEVEIILDASSISVSNSVRYPLANDQTTTLQNMVYKDYLRMSEGENPELFGNP 60  
QY 52 DPFVSASTIQTGIGTAGKILGTLPVFAQIASLVSFILGELWPKGK-SQWEIEMHVEE 110  
DB 61 EWFISSTVQTGIGVGVQVGLGALGVFAQIASFYFVGVQVLPSPSTVSVMMIMKQVED 120  
QY 111 IINOKILTIVARNKALSDRLGDAIAYHSHLSLSESVENNRNTRARVKNQYIALELMFV 170  
DB 121 LIDQKITDSVRTALAGLQGLGDLVQKSLKNWLENRNDTRARVSVVTVQYIALELDFV 180  
QY 171 QKLPSFAVSGEEVPLPIYAQAANLHLLLRDASIFGKWLGSASEISITFYNRQVETRD 230  
DB 181 AKIPSPAISSQVPEVPLSVYAQAANLHLLLRDASIFGAEWGFTPGCEISTFYDRQVTRTAQ 240  
QY 231 YSDHCHIKWYNTGLNLRGTNAKSWRYNQRKQMTLMVLVLPVSYDTLPYPIKTSQ 290  
DB 241 YSDYCVKWTNGLDKLKGTTNAASWLKYQFREEMTLVLDLVALFPNDYTRTYPIETTAQ 300  
QY 291 LTRREVYDAIGTVHPNQAFASTWYNNAPSAFAIAEAVIRSHLADLEKVTIYSLLS- 349  
DB 301 LTRREVYDPIVNRRTSGGFCRRWSLNSDISFSEVESAVIRSHPLFDILSEIEFVTRAG 360  
QY 350 -RWSNTQYNNWVGHRLESRRPIGGALNTSTQGSTNTSINPVT-----LQFTSRDVRTE 402  
DB 361 LPLNTEYLEYVWGHSHIKYK-----NTNASSALEPNYGTITSNKIKYDVLANKDIFQVR 414  
QY 403 SL-AGNLNLFLOPVNGVRVDFHWKFPPLPIASDNPYLYGAGV-----T 447  
DB 415 SLGADLANIYAO-VYGVFYASP-----TLDDKN---TGSVGVGFYKSPHHTMQVCT 463  
QY 448 QLODSNELPPETGQPNYESYSHRLSHLIGLIS-----ASHVKALVSWTHRSADR 499  
DB 464 QYNTIDEIPPE--NEPLSRGYSHRLSHITSYFSKNASSPARYGNLFPFAWTHRSADVT 521  
QY 500 NTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGDIILRRNTIGTFGDIRVNIINPFAQRY 559  
DB 522 NTVYSDKITQIPVKAHTLVSGTTWIKGPCFTGCGNLKRTSSGPLAYTSVSVKSLSQRY 581  
QY 560 RVRIRYASTDLDQFHTSINGKAINQGNFSAATMARGEDLDYKTRTIGTTPFPFSQVST 619  
DB 582 RARIRYASTNLRFLVFTISGTRIYSINNVNKNKGGDLTFTNTFDLATIGTATFTFSNYS 641

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QY 620 FTIGAMFSSGNEYVIDIRIBFVPVEVYEAZYDEKAEKVETALFTSTNPRGLTKVDKY 679
Db 642 LTUGADSFASGEVYVUKFELIPNATFEAEEDLDVAKAVGLFTSKKD-ALQTSYTDY 700
QY 680 HIDQSVNLVSLSDFFVLDKRELFELIVKAKQIHIERNM 719
Db 701 QVNOAANLVCLSDPELYNEKMLWDVAKEAKRLVQARNL 740

RESULT 14
US-10-428-961-6
; Sequence 6, Application US/10428961
; Publication No. US20030237111A1
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Chu, Chih-Rei
; APPLICANT: Donovan, William P.
; APPLICANT: Gilmer, Amy J.
; APPLICANT: Rugar, Mark J.
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin
; FILE OF INVENTION: Polynucleotides, Compositions, and Methods of Use (Amended)
; FILE REFERENCE: MECO201-1
; CURRENT APPLICATION NUMBER: US/10/428,961
; CURRENT FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: 09/681,322
; PRIOR FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: 60/153,995
; PRIOR FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 653
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-428-961-6

Query Match 45.0%; Score 1683.5; DB 14; Length 653;
Best Local Similarity 51.3%; Pred. No. 2.8e-132; Indels 47; Gaps 15;
Matches 345; Conservative 111; Mismatches 169;

QY 13 SSNAKVDKIATDSLKN---ETDIKMNKNEDYLRSEHSIDPFVSASTIQTGIGIAGK 69
Db 2 NENEIINALIPAVSNHSAQMDLSL-DAR'EDSLCIAEGNNINPLVSAVQTGINIAGR 60
QY 70 ILGTLGVPPAGQASLYSFTLGBLWPKXQWEIFMEHVEEILNOKLITVARNKALSDLR 129
Db 61 ILGLVGVPPAGQASLYSFTLGBLWPKXQWEIFMEHVEEILNOKLITVARNKALSDLR 120
QY 130 GLGDALAVYHESLESWSVENNTRARSVVKNQYIALEMFVQKLPFAVSGEEVPLPIY 189
Db 121 GLGGRYSYQQALETLDNENDARSIIILERYVALELDITTAIPLRIRNEEVPLLMVY 180
QY 190 AQANLHLLLRDASIFGKWLGSASEISTFYNRQVTRDYSDCHCKWNTGLNNLRGT 249
Db 181 AQANLHLLLRDASIFGKWLGSASEISTFYNRQVTRDYSDCHCKWNTGLNNLRGT 240
QY 250 NAKSWRYNQFRKDMTLMVLDLVALPSPYTLVYPIKTTSQLTRVYTDAGVTHPNQAF 309
Db 241 NAKSWRYNQFRKDMTLMVLDLVALPSPYTLVYPIKTTSQLTRVYTDAGVTHPNQAF 300
QY 310 ASTWYNNAPPSAIEAAVIRSPHLLDFLEKTYISLLSRWNTQVMNMGHRLSRRP 369
Db 301 ASTWYNNAPPSAIEAAVIRSPHLLDFLEKTYISLLSRWNTQVMNMGHRLSRRP 360
QY 370 IGGALNTSTOGST-NTSINPVTQF-TSRDQVYTESLAGNLFLTPQVNGVPRVDFHWKF 427
Db 361 IGGALNTSTOGST-NTSINPVTQF-TSRDQVYTESLAGNLFLTPQVNGVPRVDFHWKF 420
QY 428 PTL-----PIASDN--FYVLGAVGTQLOQSDENELPPTTQGPNYESYSHRLSHIG-- 477
Db 419 ITLRIFWKEAPLTVNRIRELGNLYLQKLNHOK-----QONDQIMNHVIDISYR 470
QY 478 LISASHVYKALVSWTHRSADRTNIENSTQIPLKAFNLSSGAAVRCPGFTGGDILR 537

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Db 471 LIIGNTLRAPVSWTHRSADRTNITGNRIQIPAVKGRFLPNG-SVSGPGFTGDDVVR 529
QY 538 -RTNIGTP---GDIVNIN-PFAQORYVRIRYASTTDLQHTSINGKALNCGNFSATMN 592
Db 530 LNRNNGNIQNRGYIEVPIQFTSTSTRYVRVRYASVTSIELNVNLGNSISFTNTLPATAA 589
QY 593 RGEDLDYKTRFTIGFTTTPFSFSDVOSTFT-----IGAWNFSGNEVVIDRIEFVPEVT 646
Db 590 SLDNLQ-----SGDFGYVEINNAFTSATGNIVGARNFSANAIEVIDRPEFIPVTAT 640
QY 647 YEAYDFEKAQE 658
Db 641 FEVEYDLERAQK 652

RESULT 15
US-10-782-141-16
; Sequence 16, Application US/10782141
; Publication No. US20040197917A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and
; FILE OF INVENTION: Methods for Its Use
; FILE REFERENCE: 045600/274143
; CURRENT APPLICATION NUMBER: US/10/782,141
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: 60/448,632
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 1157
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-782-141-16

Query Match 44.3%; Score 1657.5; DB 17; Length 1157;
Best Local Similarity 48.9%; Pred. No. 1e-129;
Matches 368; Conservative 107; Mismatches 228; Indels 49; Gaps 19;

QY 1 MKLKNPDKHQSLSSNAKVDKIATDS-----LKNEDTIELKNNKNEDYLRSEHE-----S 50
Db 1 MSPNNQNEYIIDAFTPT-SVSSDSNRYPPFANEPTDALQNNMYKDYLKXGSGENPELFGN 59
QY 51 IDPFVSASTIQTGIGIAGKILGTLGVPPAGQIASLYSFTLGBLWPKXQWEIFMEHVE 109
Db 60 PTFISSSTIQTGIGIAGKILGTLGVPPAGQIASLYSFTLGBLWPKXQWEIFMEHVE 119
QY 110 EIINQKILTYARNKALSDRLGLGDALAVYHESLESWSVENNTRARSVVKNQYIALEMF 169
Db 120 ELVDQKIEKYKDKALAEKLGKLNALDVYQOSLEDWLENRNDARTSRVSNQFIALDLNF 179
QY 170 VCKLPSFAVSGEEVPLPIYQAANLHLLLRDASIFGKWLGSASEISTFYNRQVTR 229
Db 180 VSSIFSAVSGEEVPLPIYQAANLHLLLRDASIFGKWLGSASEISTFYNRQVTR 239
QY 230 DYSRCHCKWNTGLNNLRGTNAKSWRYNQFRKDMTLMVLDLVALPSPYTLVYPIKTT 289
Db 240 EYSDYCVKWKYKDKKLGKLTSSKSWLNHQRFRREMTLLVLDLVALFPNYDTHMVEIETTA 299
QY 290 QLTREYVYDAG-TVHPNQAASITWYNNAPPSAIEAAVIRSPHLLDFLEKTYISLL 348
Db 300 QLTREYVYDAG-TVHPNQAASITWYNNAPPSAIEAAVIRSPHLLDFLEKTYISLL 356
QY 349 SR-----WSNTQVMNMGHRLSRRPSTGFCN-PWSTHSGILFYVENNVIRPPHLLDLSSEVINT-- 402
Db 357 SRGGITLNDAYINWVSGHTLKRYRTADSTVITYANYGRITSEKNSFALE--DRDIFPIN 414

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QY	403	SLAGLNLELTQPVNGVPRVDFHW-KFPTLP	IASDNFYLYGYAGVGTOLQ-----	DSENE	455	
Db	415	STVANLANYQKAYGVP	PGSWFHMVKRG	T-----SSTAYL-YSKTH	TALQGCTQVYESSDE	469
QY	456	LPPETTGQPNYESYSHRLSHI-----	GLISASHVKALVYSWTHRSAD	ETNTIE	ENSI	507
Db	470	IPLDRT-VFVAESYSHRLSHITSHSFKNG--	SAYYGSFPVFWTHTSADLNNTIYSDKI			526
QY	508	TQIPLVKAFNLSSGA	AVVRGPGFTGGDILRRTNTGTFGDIRVNINPPFAQRYR	IRYAS		567
Db	527	TQIPAVKGDMLYLG	SVVQGGFTGGDILKRTNPSILGTFAVTVNGSLSOR	YRIRYAS		586
QY	568	TTDLOFHTSINGKAINQGNF	SATMNRGEDLDYKTRIGFTTPFS	SDVQSTFTIG	AWNF	627
Db	587	TTDPEF-TLYLGD	NTIEKRNKNTMDNGASLT	YETFKFASFTIDFP	RETQDKILL	SGDF 645
QY	628	SSGNEWYIDRIEFV	PVEVTEAEYDFEKAQEKVTALFTSTNPRGLKTDV	KYHIDQV	SNL	687
Db	646	SSQEVYIDRIEF	IPVDETYEAEQDLEAAKAVNALFTNTKD-GLRPG	VTDYEVNQ	ANL	704
QY	688	VESLSDEPYLDEK	RELFEIVKYAKOIHIERNM			719
Db	705	VECLSDDLYPNEK	RLLFDAVREAKRLSGARNL			736

Search completed: October 28, 2004, 18:41:13  
 Job time : 68.6795 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 28, 2004, 17:51:02 ; Search time 86.6903 Seconds  
(without alignments)  
2975.262 Million cell updates/sec

Title: US-10-019-823B-59

Perfect score: 3742

Sequence: 1 MKLKNPDHQSLSSNAKVDK.....KRELFEIVKYAQIHIERNM 719

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:\*

1: Geneseq1950s:\*

2: Geneseq1990s:\*

3: Geneseq2000s:\*

4: Geneseq2001s:\*

5: Geneseq2002s:\*

6: Geneseq2003as:\*

7: Geneseq2003bs:\*

8: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3742	100.0	719	4	AAB66912
2	3742	100.0	719	6	AAB66912 Insectici
3	3598	96.2	719	7	AAB66912 B. thurin
4	3546	94.8	719	2	ADM74717 B. thurin
5	3520	94.1	719	4	AAB66908
6	3520	94.1	719	6	AAB66908 Insectici
7	3516	94.0	719	6	AAB66910
8	3516	94.0	719	6	AAB66910 Insectici
9	3511	93.8	719	4	AAB66911
10	3509	93.8	719	6	AAB66911 Insectici
11	3509	93.8	719	6	AAB66911 Insectici
12	3503	93.6	719	6	AAB66909
13	3503	93.6	719	6	AAB66909 Insectici
14	3499	93.5	719	2	AAR08041
15	3488.5	93.2	718	6	AAB66910
16	3482.5	93.1	718	4	AAB66907
17	3368.5	90.0	710	4	AAB66911
18	3311	88.5	719	3	ABB07073
19	3060	81.8	1217	4	AAU02092
20	2645	70.7	1208	4	AAU02093
21	2460	65.7	1230	8	ADK98484
22	2460	65.7	1230	8	ADK98489
23	2460	65.7	1230	8	ADK98481
24	2460	65.7	1230	8	ADK98491
25	2460	65.7	1230	8	ADK98487

26	2459	65.7	1229	2	AAR54074
27	2459	65.7	1229	2	AAR54074 CryET5. 2
28	2459	65.7	1229	2	AAW35259 Bacillus
29	2459	65.7	1229	2	AAW17699 CryET5. 3
30	2459	65.7	1229	2	AAW87633 CryET5. pr
31	2459	65.7	1229	8	AAK98479 B. thurin
32	2322.5	62.1	1228	2	AAR50955 Bacillus
33	2317.5	61.9	1209	4	AAU02094
34	2308.5	61.7	1227	2	AAV31990 Chimeric
35	2243	59.9	1227	2	AAW44321 Bacillus
36	2243	59.9	1227	4	AB119950
37	2234	59.7	1227	4	AAU02046 B. thurin
38	2233.5	59.7	488	2	AAW44322 Bacillus
39	2233.5	59.7	488	4	AB119947
40	2219	59.3	1186	2	AAV16796 Amino aci
41	2198.5	58.8	1221	4	AAU00421 B. thurin
42	2184.5	58.4	1221	4	AAU00420 B. thurin
43	2170.5	58.0	1228	4	AB884628 Amino aci
44	2168.5	58.0	1228	4	AAU02039 B. thurin
45	1982	53.0	643	2	AAV16797 Amino aci

## ALIGNMENTS

RESULT 1

AAB66912

ID AAB66912 standard; protein; 719 AA.

XX

AC AAB66912;

DT 12-APR-2001 (first entry)

XX Insecticidal protein cryIb1.

XX Insecticide; transgenic plant; insect-resistance.

XX Paecilomyces sp.

XX WO200100841-A1.

XX 04-JAN-2001.

XX 23-JUN-2000; 2000WO-GB002457.

XX 29-JUN-1999; 99GB-00015215.

XX 23-DEC-1999; 99GB-00030536.

XX (ZENE ) ZENECA LTD.

XX Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;

XX Vincent JL, Lee MD;

XX WPI; 2001-123015/13.

XX Novel insecticidal protein obtained from species of Paecilomyces for

XX controlling insects, and for insect-resistant transgenic plant

XX Claim 14; Page 64-66; 72pp; English.

XX The present invention relates to novel insecticidal proteins obtained

XX from Paecilomyces sp. (see AAB66901 and AAB66913). The

XX insecticidal proteins can be used to produce transgenic plants, which are

XX insect-resistant. Also, the insecticidal proteins are useful for

XX controlling insects by providing them at a locus where insects feed

XX Sequence 719 AA;

XX Query Match 100.0%; Score 3742; DB 4; Length 719;

XX Best Local Similarity 100.0%; Pred. No. 2e-300;

XX Matches 719; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLKNPDKHQSLSSNAKVDKIATDSLKNETDIELKNNMNNEDYLRMSHESIDPPVSASTI 60  
 DB 1 MKLKNPDKHQSLSSNAKVDKIATDSLKNETDIELKNNMNNEDYLRMSHESIDPPVSASTI 60  
 QY 61 QTGIGIAGKIILGTGVPFAGQIASLYSFIIGELMFKGKSQWEIFMEHVEEIIINQKILTYA 120  
 DB 61 QTGIGIAGKIILGTGVPFAGQIASLYSFIIGELMFKGKSQWEIFMEHVEEIIINQKILTYA 120  
 QY 121 RNKALSDRLGGLDALAVHSHESLVENNRNTRRSVVKQYIAELMFKVQLPSFAVSG 180  
 DB 121 RNKALSDRLGGLDALAVHSHESLVENNRNTRRSVVKQYIAELMFKVQLPSFAVSG 180  
 QY 181 BEVPLPIYAQAANLHLLLRDASIFGKMWGLSASEISTFYNRQVTRDYSDHCIKWYN 240  
 DB 181 BEVPLPIYAQAANLHLLLRDASIFGKMWGLSASEISTFYNRQVTRDYSDHCIKWYN 240  
 QY 241 TGLNNLRGTNAKSWRYNQFRKDMTLMVLDLVALFPSPYDTLVYPIKTSQLTREVVYDAI 300  
 DB 241 TGLNNLRGTNAKSWRYNQFRKDMTLMVLDLVALFPSPYDTLVYPIKTSQLTREVVYDAI 300  
 QY 301 GTVHPNQAFSTTWYNNNAPSFAIEAAVIRSPHLLDFLEKVTIYSLSRWSNTQYNNMW 360  
 DB 301 GTVHPNQAFSTTWYNNNAPSFAIEAAVIRSPHLLDFLEKVTIYSLSRWSNTQYNNMW 360  
 QY 361 GGHRLSRPIGGALNTSTQGSTNTSINPVTLOFTSRDVRTESLAGNLFUTQPVNGVPR 420  
 DB 361 GGHRLSRPIGGALNTSTQGSTNTSINPVTLOFTSRDVRTESLAGNLFUTQPVNGVPR 420  
 QY 421 VDFHMKFPTLPASDNFYVLGAGVGTQDSENELPETTGQPNYESYSHRLSHIGLIS 480  
 DB 421 VDFHMKFPTLPASDNFYVLGAGVGTQDSENELPETTGQPNYESYSHRLSHIGLIS 480  
 QY 481 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
 DB 481 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
 QY 541 TGTFGDIRVNIINPPFAQRYRVRIRYASTTDLOFHTSINGKAINQGNFSATMNRGDDLYK 600  
 DB 541 TGTFGDIRVNIINPPFAQRYRVRIRYASTTDLOFHTSINGKAINQGNFSATMNRGDDLYK 600  
 QY 601 TPTTIGFTTPSFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660  
 DB 601 TPTTIGFTTPSFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660  
 QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQIHIERNM 719  
 DB 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQIHIERNM 719

RESULT 2  
 AAE36276  
 ID: AAE36276 standard; protein; 719 AA.  
 XX AAE36276;  
 AC AAE36276;  
 XX 26-JUN-2003 (first entry)  
 DT B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIb1.  
 XX Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.  
 XX Bacillus thuringiensis.  
 XX WO200298911-A2.  
 XX 12-DEC-2002.  
 XX 30-MAY-2002; 2002WO-GB002666.  
 XX 07-JUN-2001; 2001GB-00013900.  
 XX (SYGN ) SYNGENTA LTD.  
 XX

PI Vincent JL, Viner R;  
 XX WPI; 2003-175137/17.  
 XX New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.  
 PT Claim 12; Page 56-58; 67pp; English.  
 XX The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects.  
 CC Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is CC Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention  
 XX Sequence 719 AA;  
 SQ  
 Query Match 100.0%; Score 3742; DB 6; Length 719;  
 Best Local Similarity 100.0%; Pred. No. 2e-300;  
 Matches 719; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MKLKNPDKHQSLSSNAKVDKIATDSLKNETDIELKNNMNNEDYLRMSHESIDPPVSASTI 60  
 DB 1 MKLKNPDKHQSLSSNAKVDKIATDSLKNETDIELKNNMNNEDYLRMSHESIDPPVSASTI 60  
 QY 61 QTGIGIAGKIILGTGVPFAGQIASLYSFIIGELMFKGKSQWEIFMEHVEEIIINQKILTYA 120  
 DB 61 QTGIGIAGKIILGTGVPFAGQIASLYSFIIGELMFKGKSQWEIFMEHVEEIIINQKILTYA 120  
 QY 121 RNKALSDRLGGLDALAVHSHESLVENNRNTRRSVVKQYIAELMFKVQLPSFAVSG 180  
 DB 121 RNKALSDRLGGLDALAVHSHESLVENNRNTRRSVVKQYIAELMFKVQLPSFAVSG 180  
 QY 181 BEVPLPIYAQAANLHLLLRDASIFGKMWGLSASEISTFYNRQVTRDYSDHCIKWYN 240  
 DB 181 BEVPLPIYAQAANLHLLLRDASIFGKMWGLSASEISTFYNRQVTRDYSDHCIKWYN 240  
 QY 241 TGLNNLRGTNAKSWRYNQFRKDMTLMVLDLVALFPSPYDTLVYPIKTSQLTREVVYDAI 300  
 DB 241 TGLNNLRGTNAKSWRYNQFRKDMTLMVLDLVALFPSPYDTLVYPIKTSQLTREVVYDAI 300  
 QY 301 GTVHPNQAFSTTWYNNNAPSFAIEAAVIRSPHLLDFLEKVTIYSLSRWSNTQYNNMW 360  
 DB 301 GTVHPNQAFSTTWYNNNAPSFAIEAAVIRSPHLLDFLEKVTIYSLSRWSNTQYNNMW 360  
 QY 361 GGHRLSRPIGGALNTSTQGSTNTSINPVTLOFTSRDVRTESLAGNLFUTQPVNGVPR 420  
 DB 361 GGHRLSRPIGGALNTSTQGSTNTSINPVTLOFTSRDVRTESLAGNLFUTQPVNGVPR 420  
 QY 421 VDFHMKFPTLPASDNFYVLGAGVGTQDSENELPETTGQPNYESYSHRLSHIGLIS 480  
 DB 421 VDFHMKFPTLPASDNFYVLGAGVGTQDSENELPETTGQPNYESYSHRLSHIGLIS 480  
 QY 481 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
 DB 481 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
 QY 541 TGTFGDIRVNIINPPFAQRYRVRIRYASTTDLOFHTSINGKAINQGNFSATMNRGDDLYK 600  
 DB 541 TGTFGDIRVNIINPPFAQRYRVRIRYASTTDLOFHTSINGKAINQGNFSATMNRGDDLYK 600  
 QY 601 TPTTIGFTTPSFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660  
 DB 601 TPTTIGFTTPSFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660  
 QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQIHIERNM 719  
 DB 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQIHIERNM 719



CC strain which produces at least three different types of crystal proteins  
 CC and is therefore claimed to be capable of killing insects from at least  
 CC three orders, thus providing a suitable alternative for broad-spectrum  
 CC agricultural pest control. The isolated crystal proteins, for e.g. CryII  
 CC protein, can also be applied to control pests (alone or with e.g. other  
 CC insecticidal proteins) and is useful to control pests (alone or with e.g. other  
 CC insecticidal proteins) and is useful to produce antibodies to isolate  
 CC similar proteins from other strains/organisms. The invention also  
 CC provides a BtC-18 toxin protein which is active against rootworms. The  
 CC Cry encoding nucleic acids are claimed to be useful for expressing the  
 CC Cry proteins in plants, to produce pest-resistant transgenic plants and  
 CC plant products, or in micro-organisms, which can be applied to protect  
 CC agricultural crops. They are also useful to isolate nucleic acids  
 CC encoding potentially pesticidal proteins from other strains/organisms by  
 CC hybridisation  
 XX  
 SQ

Query Match 94.8%; Score 3546; DB 2; Length 719;  
 Best Local Similarity 95.0%; Pred. No. 3.4e-284;  
 Matches 683; Conservative 11; Mismatches 25; Indels 0; Gaps 0;  
 QY 1 MKLKNPDKHQSSNAKVDKIATDSLKNEDYLRMSEHESIDPFVSASTI 60  
 DB 1 MKLKNPDKHQSSNAKVDKIATDSLKNEDYLRMSEHESIDPFVSASTI 60  
 QY 61 QTGIGIAGKILGTGVPFAGQIASLYSPILGELMPKGSQWEIEMFVHEEIIINQKILTYA 120  
 DB 61 QTGIGIAGKILGTGVPFAGQIASLYSPILGELMPKGSQWEIEMFVHEEIIINQKILTYA 120  
 QY 121 RNKALSDRLGDLAVYHESLESVENNTRARSVVKNQYIALELMFVQKLPSPFVSG 180  
 DB 121 RNKALSDRLGDLAVYHESLESVENNTRARSVVKNQYIALELMFVQKLPSPFVSG 180  
 QY 181 BEVPLLPPIYAQAANLHLLLDASIFGKWSGLSEISTFYNNQVETRDYSDHCIKWYN 240  
 DB 181 BEVPLLPPIYAQAANLHLLLDASIFGKWSGLSEISTFYNNQVETRDYSDHCIKWYN 240  
 QY 241 TGLNNLRGTNAKSWRYNQFPRDKMTLMDLVALFPSPYDVLVPIKTTLSQLTREVIYDAI 300  
 DB 241 TGLNNLRGTNAKSWRYNQFPRDKMTLMDLVALFPSPYDVLVPIKTTLSQLTREVIYDAI 300  
 QY 301 GTVHPNQAFSTTWNNNAPSFSAIEAAVIRSPHLLDFLEKVTIYSLLSRWSNTQYNNMW 360  
 DB 301 GTVHPNQAFSTTWNNNAPSFSAIEAAVIRSPHLLDFLEKVTIYSLLSRWSNTQYNNMW 360  
 QY 361 GCHRLSEPIGALNTSQGTNTSINPVTLOFTSRDYRTESLAGLNLFLTQPVNGVPR 420  
 DB 361 GCHRLSEPIGALNTSQGTNTSINPVTLOFTSRDYRTESLAGLNLFLTQPVNGVPR 420  
 QY 421 VDFHWKFTPLIADNFYLYGAGVGTQLODSENELPETTGQPNVESYSHRLSHIGLIS 480  
 DB 421 VDFHWKFTPLIADNFYLYGAGVGTQLODSENELPETTGQPNVESYSHRLSHIGLIS 480  
 QY 481 ASHKALVYSWTHRSADNTIENSITQIPLVKAFNLSSGAAVVRGPGTGGDILRTN 540  
 DB 481 GSHVKALVSWTHRSADNTIENSITQIPLVKAFNLSSGAAVVRGPGTGGHILRTK 540  
 QY 541 TGTFGDIRVNIPTPAQRYRIRYASTDLOFTTSINGKAINQGNFSATMNRGEDLDYK 600  
 DB 541 SGTFGHIRVNIPTPAQRYRIRYASTDLOFTTSINGKAINQGNFSATMNRGEDLDYK 600  
 QY 601 TFRIGFTTSPFSDVQSTFTIGAWNPFSSGNEVYIDRIEVPVETVYEAEDYDEKQEKV 660  
 DB 601 TFRIGFTTSPFSDVQSTFTIGAWNPFSSGNEVYIDRIEVPVETVYEAEDYDEKQEKV 660  
 QY 661 TALEFTSTNPRGLKTDVQDYHIDQVSNLVESLSDYLDEKRELFEIVKYAKQIHIERNM 719  
 DB 661 TALEFTSTNPRGLKTDVQDYHIDQVSNLVESLSDYLDEKRELFEIVKYAKQIHIERNM 719  
 RESULT 5  
 AAB66908  
 ID AAB66908 standard; protein; 719 AA.

XX AAB66908;  
 AC 12-APR-2001 (first entry)  
 DT Insecticidal protein cryIIa2.  
 DE Insecticide; transgenic plant; insect-resistance.  
 KW Paecilomyces sp.  
 OS WO200100841-A1.  
 PN 04-JAN-2001.  
 PD 23-JUN-2000; 2000WO-GB002457.  
 PF 29-JUN-1999; 99GB-00015215.  
 PR 23-DEC-1999; 99GB-00030536.  
 XX (ZENE ) ZENECA LTD.  
 PA Griffin J, Carille AJ, Cayley PJ, Mackay EA, Warner SAJ;  
 PI Vincent JL, Lee MD;  
 XX WPI; 2001-123015/13.  
 DR Novel insecticidal protein obtained from species of Paecilomyces for  
 XX controlling insects, and for insect-resistant transgenic plant  
 PT production.  
 PS Claim 14; Page 55-57; 72pp; English.  
 XX The present invention relates to novel insecticidal proteins obtained  
 CC from Paecilomyces sp. (see AAB66908 to AAB66913). The  
 CC insecticidal proteins can be used to produce transgenic plants, which are  
 CC insect-resistant. Also, the insecticidal proteins are useful for  
 CC controlling insects by providing them at a locus where insects feed  
 XX  
 SQ Sequence 719 AA;

Query Match 94.1%; Score 3520; DB 4; Length 719;  
 Best Local Similarity 92.9%; Pred. No. 4.8e-282;  
 Matches 668; Conservative 31; Mismatches 20; Indels 0; Gaps 0;  
 QY 1 MKLKNPDKHQSSNAKVDKIATDSLKNEDYLRMSEHESIDPFVSASTI 60  
 DB 1 MKLKNPDKHQSSNAKVDKIATDSLKNEDYLRMSEHESIDPFVSASTI 60  
 QY 61 QTGIGIAGKILGTGVPFAGQIASLYSPILGELMPKGSQWEIEMFVHEEIIINQKILTYA 120  
 DB 61 QTGIGIAGKILGTGVPFAGQIASLYSPILGELMPKGSQWEIEMFVHEEIIINQKILTYA 120  
 QY 121 RNKALSDRLGDLAVYHESLESVENNTRARSVVKNQYIALELMFVQKLPSPFVSG 180  
 DB 121 RNKALSDRLGDLAVYHESLESVENNTRARSVVKNQYIALELMFVQKLPSPFVSG 180  
 QY 181 BEVPLLPPIYAQAANLHLLLDASIFGKWSGLSEISTFYNNQVETRDYSDHCIKWYN 240  
 DB 181 BEVPLLPPIYAQAANLHLLLDASIFGKWSGLSEISTFYNNQVETRDYSDHCIKWYN 240  
 QY 241 TGLNNLRGTNAKSWRYNQFPRDKMTLMDLVALFPSPYDVLVPIKTTLSQLTREVIYDAI 300  
 DB 241 TGLNNLRGTNAKSWRYNQFPRDKMTLMDLVALFPSPYDVLVPIKTTLSQLTREVIYDAI 300  
 QY 301 GTVHPNQAFSTTWNNNAPSFSAIEAAVIRSPHLLDFLEKVTIYSLLSRWSNTQYNNMW 360  
 DB 301 GTVHPNQAFSTTWNNNAPSFSAIEAAVIRSPHLLDFLEKVTIYSLLSRWSNTQYNNMW 360  
 QY 361 GCHRLSEPIGALNTSQGTNTSINPVTLOFTSRDYRTESLAGLNLFLTQPVNGVPR 420  
 DB 361 GCHRLSEPIGALNTSQGTNTSINPVTLOFTSRDYRTESLAGLNLFLTQPVNGVPR 420



QY 421 VDFHWKFPPTLPASDNFYLYGAGVGTQLODSNELPPETGQPNYESYSHRLSHIGLIS 480  
DB 421 VDFHWKFPPTLPASDNFYLYGAGVGTQLODSNELPPETGQPNYESYSHRLSHIGLIS 480  
QY 481 ASHVXKALVSWTHRSADRTNITIPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540  
DB 481 ASHVXKALVSWTHRSADRTNITIPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540  
QY 541 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDLDYK 600  
DB 541 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDLDYK 600  
QY 601 TFRITGFTTFFSDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVYEAEDFEKAQEKV 660  
DB 601 TFRVGTFTTFFFLDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVYEAEDFEKAQEKV 660  
QY 661 TALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDEFYLDKRELFEIVKAKQIHIERNM 719  
DB 661 TALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDEFYLDKRELFEIVKAKQIHIERNM 719

RESULT 6  
AAE36272  
ID AAE36272 standard; protein; 719 AA.  
XX AAE36272;  
AC  
XX  
XX  
DT 26-JUN-2003 (first entry)  
XX  
DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa2.  
XX  
XX Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.  
XX  
XX Bacillus thuringiensis.  
XX  
XX WO200298911-A2.  
XX  
PD 12-DEC-2002.  
XX  
XX 30-MAY-2002; 2002WO-GB002666.  
XX  
XX 07-JUN-2001; 2001GB-00013900.  
XX  
XX (SYGN ) SYNGENTA LTD.  
XX  
XX Vincent JL, Viner R;  
XX  
XX WPI; 2003-175137/17.  
XX  
PT New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.  
XX  
XX  
PS Claim 12; Page 44-47; 67pp; English.  
XX  
XX The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects. Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention  
XX  
XX Sequence 719 AA;  
SQ

Query Match 94.1%; Score 3520; DB 6; Length 719;  
Best Local Similarity 92.9%; Pred. No. 4.8e-282;  
Matches 668; Conservative 31; Mismatches 20; Indels 0; Gaps 0;  
QY 1 MGLKNPKHQSLSSNAKVDKIATDSLKNETDIELKMNEDYLEMSEHSIDDPFVSASTI 60  
DB 1 MGLKNQDKHQSFSSNAKVDKIATDSLKNETDIELQINHEDCLNSEYENVEPFVSASTI 60

QY 61 QTGIGIACKILGTLPAGQIASLYSPILGELWPKGKSOMEIFMEHVVEEIIINQKILTYA 120  
DB 61 QTGIGIACKILGTLPAGQIASLYSPILGELWPKGKSOMEIFMEHVVEEIIINQKISTYA 120  
QY 121 RNKALSDURGIGDALAVVHESLESWENNRNTRARSVVKQYIALELMFVOKLPSFAVSG 180  
DB 121 RNKALTDLKGLGDALAVVHDSLESWVGNRNTRARSVVKQYIALELMFVOKLPSFAVSG 180  
QY 181 BEVPLLPIYAQAANLHLLLRDASIFGKEMGLSASEISTFYNNROVERTRDYSDHCIKWYN 240  
DB 181 BEVPLLPIYAQAANLHLLLRDASIFGKEMGLSASEISTFYNNROVERAGDYSDHCVKWS 240  
QY 241 TGLNNLRGTNAKSWRYNQFRKDMTLMVLDLVALPSPYDITLVPIKTTTSQITREYITDAI 300  
DB 241 TGLNNLRGTNAESWRYNQFRDMTLMVLDLVALPSPYDITLVPIKTTAQITREYITDAI 300  
QY 301 GTVHENQAFASWTWNNNAPSFALEAAVIRSPHLLDFLEKVITVYLSLSRSNTQYMMW 360  
DB 301 GTVHPHPGFTSTTWNNNAPSFALEAAVIRSPHLLDFLEKVITVYLSLSRSNTQYMMW 360  
QY 361 GGHRLSERPIGGALNTSTQGSTNTSINPVTLOFTSRDVIYRTESLAGLNLFLTQPVNGVPR 420  
DB 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVIYRTESLAGLNLFLTQPVNGVPR 420  
QY 421 VDFHWKFPPTLPASDNFYLYGAGVGTQLODSNELPPETGQPNYESYSHRLSHIGLIS 480  
DB 421 VDFHWKFPVTHPTIASDNFYLYGAGVGTQLODSNELPPETGQPNYESYSHRLSHIGLIS 480  
QY 481 ASHVXKALVSWTHRSADRTNITIPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540  
DB 481 ASHVXKALVSWTHRSADRTNITIPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540  
QY 541 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDLDYK 600  
DB 541 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDLDYK 600  
QY 601 TFRITGFTTFFSDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVYEAEDFEKAQEKV 660  
DB 601 TFRVGTFTTFFFLDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVYEAEDFEKAQEKV 660  
QY 661 TALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDEFYLDKRELFEIVKAKQIHIERNM 719  
DB 661 TALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDEFYLDKRELFEIVKAKQIHIERNM 719

RESULT 7  
AAB66910  
ID AAB66910 standard; protein; 719 AA.  
XX AAB66910;  
AC  
XX  
DT 12-APR-2001 (first entry)  
XX  
XX Insecticidal protein cryIIa4.  
DE  
XX Insecticide; transgenic plant; insect-resistance.  
KW  
XX Paecilomyces sp.  
OS  
XX WO200100841-A1.  
PN  
XX  
PD 04-JAN-2001.  
XX  
XX 23-JUN-2000; 2000WO-GB002457.  
PF  
XX 29-JUN-1999; 99GB-00015215.  
PR 23-DEC-1999; 99GB-00030536.  
XX  
XX (ZENE ) ZENECA LTD.  
XX  
XX Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;  
PI Vincent JL, Lee MD;

XX WPI; 2001-123015/13.  
 XX Novel insecticidal protein obtained from species of Paecilomyces for  
 PT controlling insects, and for insect-resistant transgenic plant  
 PT production.  
 XX Claim 14; Page 60-62; 72pp; English.  
 XX The present invention relates to novel insecticidal proteins obtained  
 CC from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The  
 CC insecticidal proteins can be used to produce transgenic plants, which are  
 CC insect-resistant. Also, the insecticidal proteins are useful for  
 CC controlling insects by providing them at a locus where insects feed  
 XX  
 XX Sequence 719 AA;

Query Match 94.0%; Score 3516; DB 4; Length 719;  
 Best Local Similarity 92.8%; Pred. No. 1e-281;  
 Matches 667; Conservative 31; Mismatches 21; Indels 0; Gaps 0;

QY 1 MKLKNPDHQSLSNAKVDKIATDSLKNEDYLRMSHESIDPPVSASTI 60  
 DB 1 MKLKNQDQHQSLSNAKVDKIATDSLKNEDYLRMSHESIDPPVSASTI 60  
 QY 61 QTGIGIAGKILGTGVPFAGQVASYFILGELWPKGKQWEIFMEHVEEIIINQKISTYA 120  
 DB 61 QTGIGIAGKILGTGVPFAGQVASYFILGELWPKGKQWEIFMEHVEEIIINQKISTYA 120  
 QY 121 RNKALSDRLGLDALAVVHESLESVENNTRASVVKNOYIALELMFVKLPSFAVSG 180  
 DB 121 RNKALTDLKLGLDALAVVHDSLESVGNRNTRASVVKNOYIALELMFVKLPSFAVSG 180  
 QY 181 BEVPLLPYIAQAANLHLLRLDASIFGKWLGSASEISTFYNRQVTRDYSHCIKWYN 240  
 DB 181 BEVPLLPYIAQAANLHLLRLDASIFGKWLGSASEISTFYNRQVTRDYSHCIKWYN 240  
 QY 241 TGLNLRGTNAKSWRYNQFRDMTLMVLDLVALFPSSYDTLVYPIKTTQSUTREVTYDAI 300  
 DB 241 TGLNLRGTNAESWRYNQFRDMTLMVLDLVALFPSSYDTLVYPIKTTQSUTREVTYDAI 300  
 QY 301 GTVHPNQAFSTTWYNNAPSFSAEAAVIRSPHLLDLEKVTIYSLSRWSNTQYNNMW 360  
 DB 301 GTVHPSPFTSTWYNNAPSFSAEAAVIRSPHLLDLEKVTIYSLSRWSNTQYNNMW 360  
 QY 361 GGHRLSPIGGALNTSTCGSTNTSINPVTILOFTSRDVRTESLAGLNLFTQPVNGVPR 420  
 DB 361 GGHRLSPIGGALNTSTCGSTNTSINPVTILOFTSRDVRTESLAGLNLFTQPVNGVPR 420  
 QY 421 VDFHWKFTPIASDNFYLYGAVGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 DB 421 VDFHWKFTPIASDNFYLYGAVGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 QY 481 ASHVKALVYVTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 540  
 DB 481 ASHVKALVYVTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 540  
 QY 541 TGTGDIRVNIAPPQAYRVRIRYASTTDLOFTHSINGKAINQGNFSATNMGEDLDYK 600  
 DB 541 TGTGDIRVNIAPPQAYRVRIRYASTTDLOFTHSINGKAINQGNFSATNMGEDLDYK 600  
 QY 601 TFRIGFTTPSPDSVOSTFTIGAWNFSNGENVYIDRIEFPVPEVTYEAEDPEKAEKV 660  
 DB 601 TFRIGFTTPSPDSVOSTFTIGAWNFSNGENVYIDRIEFPVPEVTYEAEDPEKAEKV 660  
 QY 661 TALTSTNPRGLKTDVXDYHIDQVSNLVESLSDSEFYLDKRELFEIVKYAKQHLIERNM 719  
 DB 661 TALTSTNPRGLKTDVXDYHIDQVSNLVESLSDSEFYLDKRELFEIVKYAKQHLIERNM 719

RESULT 8  
 AAB66274  
 ID AAB66274 standard; protein; 719 AA.

XX AAB66274;  
 XX 26-JUN-2003 (first entry)  
 DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa4.  
 XX Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.  
 XX Bacillus thuringiensis.  
 OS WO200298911-A2.  
 XX 12-DEC-2002.  
 XX 30-MAY-2002; 2002WO-GB002666.  
 XX 07-JUN-2001; 2001GB-00013900.  
 XX (SYGN) SYNGENTA LTD.  
 XX Vincent JL, Viner R;  
 XX WPI; 2003-175137/17.  
 XX New insecticidal protein comprising an X-glycine motif at the amino-  
 PT terminus, useful as an active ingredient of a pesticide.  
 XX Claim 12; Page 50-53; 67pp; English.  
 XX The invention relates to insecticidal protein comprising an X-glycine  
 CC motif at the amino-terminus. Polynucleotide or DNA constructs of the  
 CC invention are useful for producing plants or plant parts that are  
 CC resistant to insects. The protein or synergistic combination is useful as  
 CC an active ingredient of a pesticide or for controlling insects.  
 CC Antibodies raised to the insecticidal proteins can be used to identify  
 CC other proteins with insecticidal activity. The present sequence is  
 CC Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This  
 CC sequence is used in the invention  
 XX  
 XX Sequence 719 AA;

Query Match 94.0%; Score 3516; DB 6; Length 719;  
 Best Local Similarity 92.8%; Pred. No. 1e-281;  
 Matches 667; Conservative 31; Mismatches 21; Indels 0; Gaps 0;

QY 1 MKLKNPDHQSLSNAKVDKIATDSLKNEDYLRMSHESIDPPVSASTI 60  
 DB 1 MKLKNQDQHQSLSNAKVDKIATDSLKNEDYLRMSHESIDPPVSASTI 60  
 QY 61 QTGIGIAGKILGTGVPFAGQVASYFILGELWPKGKQWEIFMEHVEEIIINQKISTYA 120  
 DB 61 QTGIGIAGKILGTGVPFAGQVASYFILGELWPKGKQWEIFMEHVEEIIINQKISTYA 120  
 QY 121 RNKALSDRLGLDALAVVHESLESVENNTRASVVKNOYIALELMFVKLPSFAVSG 180  
 DB 121 RNKALTDLKLGLDALAVVHDSLESVGNRNTRASVVKNOYIALELMFVKLPSFAVSG 180  
 QY 181 BEVPLLPYIAQAANLHLLRLDASIFGKWLGSASEISTFYNRQVTRDYSHCIKWYN 240  
 DB 181 BEVPLLPYIAQAANLHLLRLDASIFGKWLGSASEISTFYNRQVTRDYSHCIKWYN 240  
 QY 241 TGLNLRGTNAKSWRYNQFRDMTLMVLDLVALFPSSYDTLVYPIKTTQSUTREVTYDAI 300  
 DB 241 TGLNLRGTNAESWRYNQFRDMTLMVLDLVALFPSSYDTLVYPIKTTQSUTREVTYDAI 300  
 QY 301 GTVHPNQAFSTTWYNNAPSFSAEAAVIRSPHLLDLEKVTIYSLSRWSNTQYNNMW 360  
 DB 301 GTVHPSPFTSTWYNNAPSFSAEAAVIRSPHLLDLEKVTIYSLSRWSNTQYNNMW 360  
 QY 361 GGHRLSPIGGALNTSTCGSTNTSINPVTILOFTSRDVRTESLAGLNLFTQPVNGVPR 420  
 DB 361 GGHRLSPIGGALNTSTCGSTNTSINPVTILOFTSRDVRTESLAGLNLFTQPVNGVPR 420

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QY 421 VDFHWKFPPLPIASDNFYLYGVAGVGTQLQDSNELPPTTGPVNYESYSHLSHIGLIS 480
Db 421 VDFHWKFPVTHPIASDNFYLYGVGIGTQLQDSNELPPTTGPVNYESYSHLSHIGLIS 480
QY 481 ASHVKALVSWTHRSADRNTIIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRN 540
Db 481 ASHVKALVSWTHRSADRNTIIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRN 540
QY 541 TGTFGDIRVNIINPPFAQRVVRIRYASTTDLQFHTSINGKAINQGNFSATMRGEDLDYK 600
Db 541 TGTFGDIRVNIINPPFAQRVVRIRYASTTDLQFHTSINGKAINQGNFSATMRGEDLDYK 600
QY 601 TERTIGFTTFFSDVQSTFTIGAMFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660
Db 601 TERTIGFTTFFSFLDQSTFTIGAMFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660
QY 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVESLSEFYLDEKRELFVYKAKQIHIERNM 719
Db 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVESLSEFYLDEKRELFVYKAKQIHIERNM 719

RESULT 9
AAU02095
ID AAU02095 standard; protein; 719 AA.
XX
AC AAU02095;
XX
DT 07-SEP-2001 (first entry)
XX
DE Bacillus thuringiensis partial mutant CryIIa.
XX
KW Crystal protein; CryIIa; CryIa; moth; butterfly; Colorado potato beetle;
mutant; mutein.
XX
OS Bacillus thuringiensis.
XX
PH Key Location/Qualifiers
FT Peptide 1..19
FT Protein /label= Signal_peptide
FT Protein 20..719
FT Protein /label= Mature_CryIIa
XX
PN EPI099760-A1.
XX
PD 16-MAY-2001.
XX
PF 09-NOV-1999; 99EP-00203723.
XX
PR 09-NOV-1999; 99EP-00203723.
XX
PA (CPRO-) CPRO-DLO CENT PLANTENVERDELINGS REPROD.
XX
PI De Maagd RA, Bosch HJ;
XX
PS WPI; 2001-337141/36.
XX
DR N-PSDB; AAS04855.
XX
PT New hybrid Bacillus thuringiensis hybrid toxins comprising structural
FT domains derived from at least 2 different crystal proteins; such as
FT CryIIa and CryIIa, and having insecticidal activity, useful for combating
FT insects.
XX
PS Example; Page 30-32; 43pp; English.
XX
CC The sequence is B. thuringiensis (Bt) crystal protein CryIIa, the DNA
CC encoding which was mutated to allow cloning of domain III or domains I
CC and II, to make the hybrid protoxins of the invention. The hybrid toxins
CC of the invention, having structural domains I, II and III in this order
CC starting from the N-terminal derived from at least 2 different crystal
CC proteins, are useful for protecting plants against pest insects, e.g.
CC moths, butterflies and Colorado potato beetle or for combating insects
XX
```

SQ Sequence 719 AA;

Query Match 93.8%; Score 3511; DB 4; Length 719;  
Best Local Similarity 92.8%; Pred. No. 2.7e-281;  
Matches 667; Conservative 31; Mismatches 21; Indels 0; Gaps 0;

```
QY 1 MKLKMPDKHQSLSNAKVDKIATSLKNETDIEIKNNANNEDYLRMSEHESIDPFSASTI 60
Db 1 MKLKMQDKHQSLSNAKVDKIATSLKNETDIEIKNNANNEDYLRMSEHESIDPFSASTI 60
QY 61 QTGGIAGKILGTGLVPPAGQIASLYGFIILGELWPKGKOWEIMFHEHVEEIIINOKIITYA 120
Db 61 QTGGIAGKILGTGLVPPAGQIASLYGFIILGELWPKGKOWEIMFHEHVEEIIINOKIITYA 120
QY 121 RNKALSDURGLGDALAVVHSHESLWENNRNTRARSVKNQYIIALELFPVKLSFAVSG 180
Db 121 RNKALTDLKGLGDALAVVHSHESLWENNRNTRARSVKNQYIIALELFPVKLSFAVSG 180
QY 181 EEVPLLPYIAQAANLHLLLRDASIFGKEWGLSASEISTFYNROVERTRDYSHCIKWYN 240
Db 181 EEVPLLPYIAQAANLHLLLRDASIFGKEWGLSASEISTFYNROVERTRDYSHCIKWYN 240
QY 241 TGLNNLRCTNAKSVRYNQPRKDMTLMVLDVALFPPSYDTLVYPIKTTQSOLTREYITDAI 300
Db 241 TGLNNLRCTNAESVRYNQPRKDMTLMVLDVALFPPSYDTLVYPIKTTQSOLTREYITDAI 300
QY 301 GTVHPNOAFSTWYNNNAPSFAIEAAVIRSPHLLDFLEKVTIYSLLSRWSNTOYMMNW 360
Db 301 GTVHPHPSFTSTWYNNNAPSFAIEAAVIRSPHLLDFLEKVTIYSLLSRWSNTOYMMNW 360
QY 361 GGHRLSERPIGALNTSTQSGTNTSINPVTLOFTSRDYRTESLAGLNLFTQPVNGVPR 420
Db 361 GGHKLEFRTIGTLNISTQSGTNTSINPVTLPFTSRDYRTESLAGLNLFTQPVNGVPR 420
QY 421 VDFHWKFPPLPIASDNFYLYGVAGVGTQLQDSNELPPTTGPVNYESYSHLSHIGLIS 480
Db 421 VDFHWKFPVTHPIASDNFYLYGVGIGTQLQDSNELPPTTGPVNYESYSHLSHIGLIS 480
QY 481 ASHVKALVSWTHRSADRNTIIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRN 540
Db 481 ASHVKALVSWTHRSADRNTIIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRN 540
QY 541 TGTFGDIRVNIINPPFAQRVVRIRYASTTDLQFHTSINGKAINQGNFSATMRGEDLDYK 600
Db 541 TGTFGDIRVNIINPPFAQRVVRIRYASTTDLQFHTSINGKAINQGNFSATMRGEDLDYK 600
QY 601 TERTIGFTTFFSDVQSTFTIGAMFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660
Db 601 TERTIGFTTFFSFLDQSTFTIGAMFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660
QY 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVESLSEFYLDEKRELFVYKAKQIHIERNM 719
Db 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVESLSEFYLDEKRELFVYKAKQIHIERNM 719
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RESULT 10  
AAB66911  
ID AAB66911 standard; protein; 719 AA.

XX AAB66911;  
XX AAB66911;  
DT 12-APR-2001 (first entry)

XX Insecticidal protein cryIIa5.  
XX Insecticide; transgenic plant; insect-resistance.  
XX Paecilomyces sp.

XX WO200100841-A1.  
XX 04-JAN-2001.  
XX

23-JUN-2000; 2000WO-GB002457.  
 29-JUN-1999; 99GB-00015215.  
 23-DEC-1999; 99GB-00030536.  
 (ZENE) ZENECA LTD.  
 Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;  
 Vincent JL, Lee MD;  
 WPI; 2001-123015/13.  
 Novel insecticidal protein obtained from species of Paecilomyces for  
 controlling insects, and for insect-resistant transgenic plant  
 production.  
 Claim 14; Page 62-64; 72pp; English.  
 The present invention relates to novel insecticidal proteins obtained  
 from Paecilomyces sp. (see AAB66899 to AAB6901 and AAB6913). The  
 insecticidal proteins can be used to produce transgenic plants, which are  
 insect-resistant. Also, the insecticidal proteins are useful for  
 controlling insects by providing them at a locus where insects feed  
 Sequence 719 AA;

Query Match 93.8%; Score 3509; DB 4; Length 719;  
 Best Local Similarity 92.5%; Fred. No. 3.9e-281;  
 Matches 665; Conservative 33; Mismatches 21; Indels 0; Gaps 0;

QY 1 MKLKNPDKHQSLSNAKVDKIATDSLNKNETDIELKNMNNEDYLRMSHESIDPVSASTI 60  
 DB 1 MKLKNQDQHQSFSSNAKVDKISTDSLNKNETDIELQNHEDCLKNSEYENVEPVSASTI 60  
 QY 61 QTGIGIAGKILGTGVPFAGQIASLYSIFILGELPKGKSQWEIFMEHVEEIIINOKILTYA 120  
 DB 61 QTGIGIAGKILGTGVPFAGQIASLYSIFILGELPKGKSQWEIFMEHVEEIIINOKILTYA 120  
 QY 121 RNKALSDLRGIDGALAVYHESLESWENNRNTRARSVVKNQYIALELMFVKQLPSFAVSG 180  
 DB 121 RNKALTDLKGLGDALAVYHDSLESWGNRNTRARSVRSQYIALELMFVKQLPSFAVSG 180  
 QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKWLSEISTFVNROVERTRDYSHCICKWYN 240  
 DB 181 EEPVLLPIYAQAANLHLLLRDASIFGKWLSEISTFVNROVERTRDYSHCICKWYS 240  
 QY 241 TGLNLRGTNAKSWRYNQFRKDMTLMVLDLVALFPSPYDTLVPIKTTSQLTRVYTDAL 300  
 DB 241 TGLANLRGTNAESWRYNQFRDMTLMVLDLVALFPSPYDTLVPIKTTSQLTRVYTDAL 300  
 QY 301 GTVHPNQAFSTTWNKNAPSFAIEAAVIRSPHLLDFLEKVTIYSLSSWSNTQYNNMW 360  
 DB 301 GTVHPHPSFTTWNKNAPSFAIEAAVIRSPHLLDFLEQVTIYSLSSWSNTQYNNMW 360  
 QY 361 GGHRLSEPIGALNTSTQGSTNTSINPVTLPFTSRDVTYTESLAGNLFLOPVGVR 420  
 DB 361 GGHLEPFTIGTLNISTQGSTNTSINPVTLPFTSRDVTYTESLAGNLFLOPVGVR 420  
 QY 421 VDFHWKPTFLIASDNFYLYAGVGTQLODSENELPETTGQPNYESYSHRLSHGLIS 480  
 DB 421 VDFHWKFTTHFIASDNFYYPGAGIGTQLODSENELPETTGQPNYESYSHRLSHGLIS 480  
 QY 481 ASHVKALVSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRPGFTGCDILRTN 540  
 DB 481 ASHVKALVSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRPGFTGCDILRTN 540  
 QY 541 TGTFGDIRVNIINPFAQRYRVEYASTDLOFTSINGKAINQGNFSATMNGEDLDYK 600  
 DB 541 TGTFGDIRVNIINPFAQRYRVEYASTDLOFTSINGKAINQGNFSATMNGEDLDYK 600  
 QY 601 TFRITGFTTSPFSFVQSTFTIGAWNFSSGNEVYIDRIEFVPEVITYEAYDFEKAQEKV 660  
 DB 601 TFRIVGFTTSPFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVITYEAYDFEKAQEKV 660

QY 661 TALFTSTNPRGLTKVDYKHIDQVSNLVESLSDEPYLDEKRELFEIVKYAKOIHIERNM 719  
 DB 661 TALFTSTNPRGLTKVDYKHIDQVSNLVESLSDEPYLDEKRELFEIVKYANELHIERNM 719

## RESULT 11

AAE36275  
 ID AAE36275 standard; protein; 719 AA.

XX AAE36275;  
 AC AAE36275;

XX 26-JUN-2003 (first entry)

DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa5.

XX Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.

XX Bacillus thuringiensis.

OS WO200298911-A2.

PN 12-DEC-2002.

XX 30-MAY-2002; 2002WO-GB002666.

XX 07-JUN-2001; 2001GB-00013900.

XX (SYGN) SYNGENTA LTD.

XX Vincent JL, Viner R;

XX WPI; 2003-175137/17.

XX New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.

XX Claim 12; Page 53-56; 67pp; English.

XX The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects. Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention

XX Sequence 719 AA;

Query Match 93.8%; Score 3509; DB 6; Length 719;

Best Local Similarity 92.5%; Fred. No. 3.9e-281; Mismatches 21; Indels 0; Gaps 0;

Matches 665; Conservative 33; Mismatches 21; Indels 0; Gaps 0;

QY 1 MKLKNPDKHQSLSNAKVDKIATDSLNKNETDIELKNMNNEDYLRMSHESIDPVSASTI 60

DB 1 MKLKNQDQHQSFSSNAKVDKISTDSLNKNETDIELQNHEDCLKNSEYENVEPVSASTI 60

QY 61 QTGIGIAGKILGTGVPFAGQIASLYSIFILGELPKGKSQWEIFMEHVEEIIINOKILTYA 120

DB 61 QTGIGIAGKILGTGVPFAGQIASLYSIFILGELPKGKSQWEIFMEHVEEIIINOKILTYA 120

QY 121 RNKALSDLRGIDGALAVYHESLESWENNRNTRARSVVKNQYIALELMFVKQLPSFAVSG 180

DB 121 RNKALTDLKGLGDALAVYHDSLESWGNRNTRARSVRSQYIALELMFVKQLPSFAVSG 180

QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKWLSEISTFVNROVERTRDYSHCICKWYN 240

DB 181 EEPVLLPIYAQAANLHLLLRDASIFGKWLSEISTFVNROVERTRDYSHCICKWYS 240

QY 241 TGLNLRGTNAKSWRYNQFRKDMTLMVLDLVALFPSPYDTLVPIKTTSQLTRVYTDAL 300

Db 241 TGLNLRGRTNAESWVRYNQFRDRTLMLVDLVALFPSTQMPYIKTTAQLTREVTDAI 300  
 QY 301 GTVHPNOAFSTWYNNNAPSFAIEAAVIRSPHLLDFLEKVTIYSLSRWSNTQYNNMW 360  
 Db 301 GTVHPNPFSTWYNNNAPSFAIEAAVIRSPHLLDFLEKVTIYSLSRWSNTQYNNMW 360  
 QY 361 GGHRLSRPFGGALNTSGSTNTSINPVTLOFTSRDVRTESLAGLNLFLTPQVNGVPR 420  
 Db 361 GGHRLSRPFGGALNTSGSTNTSINPVTLOFTSRDVRTESLAGLNLFLTPQVNGVPR 420  
 QY 421 VDFHWKPTPIASDNFVYLYGACVGTQLODSENELPPEFTGPNYESYSHRLSHGLIS 480  
 Db 421 VDFHWKPTPIASDNFVYLYGACVGTQLODSENELPPEFTGPNYESYSHRLSHGLIS 480  
 QY 481 ASHVKALVSWTHRSADRNTIENPSTIQIPLVKAFNLSSGAAVVRGPGTGGDILRRTN 540  
 Db 481 ASHVKALVSWTHRSADRNTIENPSTIQIPLVKAFNLSSGAAVVRGPGTGGDILRRTN 540  
 QY 541 TGFEGDIRVINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLDYK 600  
 Db 541 TGFEGDIRVINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLDYK 600  
 QY 601 TFRITGTTTSPFSDVOSTTIGAWNFSSGNEVYIDRIEFVPEVYEAEDYDEKAQEKV 660  
 Db 601 TFRIVGTTTSPFLDVOSTTIGAWNFSSGNEVYIDRIEFVPEVYEAEDYDEKAQEKV 660  
 QY 661 TALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719  
 Db 661 TALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719

RESULT 12  
 AAB66909  
 ID AAB66909 standard; protein; 719 AA.  
 AC AAB66909;  
 DT 12-APR-2001 (first entry)  
 DE Insecticidal protein cryIIa3.  
 KW Insecticide; transgenic plant; insect-resistance.  
 OS Paecilomyces sp.  
 PN WO200100841-A1.  
 PD 04-JAN-2001.  
 PF 23-JUN-2000; 2000WO-GB002457.  
 PR 29-JUN-1999; 99GB-00015215.  
 PR 23-DEC-1999; 99GB-00030536.  
 XX (ZENE ) ZENECA LTD.  
 XX Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;  
 PI Vincent JL, Lee MD;  
 XX WPI; 2001-123015/13.  
 XX Novel insecticidal protein obtained from species of Paecilomyces for  
 FT controlling insects, and for insect-resistant transgenic plant  
 PT production.  
 XX Claim 14; Page 57-59; 72pp; English.  
 XX The present invention relates to novel insecticidal proteins obtained  
 CC from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The  
 CC insecticidal proteins can be used to produce transgenic plants, which are  
 CC insect-resistant. Also, the insecticidal proteins are useful for  
 CC controlling insects by providing them at a locus where insects feed

SQ Sequence 719 AA;  
 Query Match 93.6%; Score 3503; DB 4; Length 719;  
 Best Local Similarity 92.5%; Pred No. 1.2e-280;  
 Matches 665; Conservative 32; Mismatches 22; Indels 0; Gaps 0;  
 QY 1 MKLKNPDKHQSSNAKVDKATDLSLKNETDIELKANNEDYLRMSEHESIDPFVSASTI 60  
 Db 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMSYENVEPFFVSASTI 60  
 QY 61 QTGIGIAGKILGTCLGVPFAGQIASIYSLFLGELPKGKSOMEIFMEHVEEIIINQKILTVA 120  
 Db 61 QTGIGIAGKILGTCLGVPFAGQVASIYSLFLGELPKGKNQWEIFMEHVEEIIINQKISYA 120  
 QY 121 RNKALSDRLGLDALAVYHESLESWVENRNNTRASVVKNQYIALELMFVKQLPFAVSG 180  
 Db 121 RNKALTDLKGLDALAVYHDSLESWVGNRNNTRASVVKQSIVIALELMFVKQLPFAVSG 180  
 QY 181 REVPLPIPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNQVERTRDYSDCIKWYN 240  
 Db 181 REVPLPIPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSYHCWKWYS 240  
 QY 241 TGLNLRGTNAKSWVRYNQFRDRTLMLVDLVALFPSTQMPYIKTTAQLTREVTDAI 300  
 Db 241 TGLNLRGTNAESWVRYNQFRDRTLMLVDLVALFPSTQMPYIKTTAQLTREVTDAI 300  
 QY 301 GTVHPNOAFSTWYNNNAPSFAIEAAVIRSPHLLDFLEKVTIYSLSRWSNTQYNNMW 360  
 Db 301 GTVHPNPFSTWYNNNAPSFAIEAAVIRSPHLLDFLEKVTIYSLSRWSNTQYNNMW 360  
 QY 361 GGHRLSRPFGGALNTSGSTNTSINPVTLOFTSRDVRTESLAGLNLFLTPQVNGVPR 420  
 Db 361 GGHRLSRPFGGALNTSGSTNTSINPVTLOFTSRDVRTESLAGLNLFLTPQVNGVPR 420  
 QY 421 VDFHWKPTPIASDNFVYLYGACVGTQLODSENELPPEFTGPNYESYSHRLSHGLIS 480  
 Db 421 VDFHWKPTPIASDNFVYLYGACVGTQLODSENELPPEFTGPNYESYSHRLSHGLIS 480  
 QY 481 ASHVKALVSWTHRSADRNTIENPSTIQIPLVKAFNLSSGAAVVRGPGTGGDILRRTN 540  
 Db 481 ASHVKALVSWTHRSADRNTIENPSTIQIPLVKAFNLSSGAAVVRGPGTGGDILRRTN 540  
 QY 541 TGFEGDIRVINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLDYK 600  
 Db 541 TGFEGDIRVINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLDYK 600  
 QY 601 TFRITGTTTSPFSDVOSTTIGAWNFSSGNEVYIDRIEFVPEVYEAEDYDEKAQEKV 660  
 Db 601 TFRIVGTTTSPFLDVOSTTIGAWNFSSGNEVYIDRIEFVPEVYEAEDYDEKAQEKV 660  
 QY 661 TALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQIHIERNM 719  
 Db 661 TALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719

RESULT 13  
 AAB66273  
 ID AAB66273 standard; protein; 719 AA.  
 AC AAB66273;  
 DT 26-JUN-2003 (first entry)  
 DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa3.  
 XX Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.  
 XX Bacillus thuringiensis.  
 XX WO200298911-A2.  
 PD 12-DEC-2002.  
 XX

30-MAY-2002; 2002WO-CB002666.  
 07-JUN-2001; 2001GB-00013900.  
 (SYGN ) SYNGENTA LTD.  
 Vincent JL, Viner R;  
 WPI; 2003-175137/17.  
 New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.  
 Claim 12; Page 47-50; 67pp; English.  
 The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects.  
 Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention

Query Match 93.6%; Score 3503; DB 6; Length 719;  
 Best Local Similarity 92.5%; Pred. No. 1.2e-280;  
 Matches 665; Conservative 32; Mismatches 22; Indels 0; Gaps 0;

1 MKLKNPDHQSSNAKVDKIATDSLKNETDIELKMNEDYLRMSHESIDPFVSASTI 60  
 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKSEYENVEPVSASTI 60  
 61 QTGIGIAGKILGTGVPPAGQIASLYSIFILGELMPKGSOWEIFMEHVEEIIINQILTYA 120  
 61 QTGIGIAGKILGTGVPPAGQIASLYSIFILGELMPKGSOWEIFMEHVEEIIINQILTYA 120  
 121 RNKALSDLRLGDLALAVYHDSLESVWENNRNTRASVVKVKSQVIALLELMFVKLPFAVSG 180  
 121 RNKALSDLRLGDLALAVYHDSLESVWENNRNTRASVVKVKSQVIALLELMFVKLPFAVSG 180  
 181 EEPVLLPIVAQAANLHLLLRDASIFGKWLGSASEISTFYNRQVTRDYSDCIKWYN 240  
 181 EEPVLLPIVAQAANLHLLLRDASIFGKWLGSASEISTFYNRQVTRDYSDCIKWYN 240  
 241 TGLNLRGTNAKSWRYNQPRKDMTLMVLDLVALFPSTDTLVYPIKITSQLTREVTYDAI 300  
 241 TGLNLRGTNAKSWRYNQPRKDMTLMVLDLVALFPSTDTLVYPIKITSQLTREVTYDAI 300  
 301 GTVHPNQAFSTWYNNAPSFSAEAAVIVSPHLLDFLEKVTIYSLLSRMSNTQYNNMW 360  
 301 GTVHPNQAFSTWYNNAPSFSAEAAVIVSPHLLDFLEKVTIYSLLSRMSNTQYNNMW 360  
 361 GGHRLSPRIGALNTSGSTNTSINPVLQFTSRDYRTESLAGNLFITQPVNGVPR 420  
 361 GGHRLSPRIGALNTSGSTNTSINPVLQFTSRDYRTESLAGNLFITQPVNGVPR 420  
 421 VDFHWKFTPIASDNFYVLGAGVGTQDSENELPPEATGQPNYSYSHRLSHIGLIS 480  
 421 VDFHWKFTPIASDNFYVLGAGVGTQDSENELPPEATGQPNYSYSHRLSHIGLIS 480  
 481 ASHVKALYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 540  
 481 ASHVKALYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 540  
 541 TGTGDIRVNPFAQRYVRIRYASTDLOFTHSINGKAINOGNFSATNWRGCDLYK 600  
 541 TGTGDIRVNPFAQRYVRIRYASTDLOFTHSINGKAINOGNFSATNWRGCDLYK 600  
 601 TFRITGFTTFSDFSDQSTFTTIGAMNFGSGNEVIDRIEFVPEVVTYEAEDYDPEKAQEKV 660

601 TFRITGFTTFSDFSDQSTFTTIGAMNFGSGNEVIDRIEFVPEVVTYEAEDYDPEKAQEKV 660  
 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESSLDEFLDEKRELFEIVKYAKOIHIERNM 719  
 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESSLDEFLDEKRELFEIVKYAKOIHIERNM 719

RESULT 14  
 AAR08041  
 ID AAR08041 standard; protein; 719 AA.  
 XX AC AAR08041;  
 XX DT 24-OCT-2003 (revised)  
 DT 25-MAR-2003 (revised)  
 DT 27-FEB-1991 (first entry)  
 XX 81 kD endotoxin deduced from DNA carried on pJH12.  
 DE Crystal; insecticide; toxin; delta endotoxin.  
 XX Bacillus thuringiensis; JHCC 4353 and 4835.  
 OS WO9013651-A.  
 XX 15-NOV-1990.  
 XX 09-MAY-1989; 89GB-00010624.  
 XX 09-MAY-1989; 89GB-00010624.  
 XX (ICIL ) IMPERIAL CHEM IND PLC.  
 PA Blenk RG, Ely S, Tailor RH, Tippet JM;  
 PI WPI; 1990-361486/48.  
 DR N-PSDB; AAQ06636.  
 XX Bacillus thuringiensis strains - used for producing an endotoxin for protecting plants against insects, partic. Lepidoptera and Coleoptera.  
 PS Claim 5; Fig 5-10; 66pp; English.  
 XX The sequence carried on pJH12 which was isolated from B. thuringiensis strains JHCC4835 and JHCC 4353 (NCIB 40091 and 40090 resp.). The DNA can be used to produce transformants E. coli strain MC1202/pJH12 (NCIB 40278, or bacteriophage EMBL4 vector (NCIB 40279) or E. coli strain BL21/pJH11 (NCIB 40275). The delta-endotoxin produced by the transformants can be used in formulations for combating Lepidoptera and Coleoptera pests.  
 CC (Updated on 25-MAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to standardise OS field)

Query Match 93.5%; Score 3499; DB 2; Length 719;  
 Best Local Similarity 92.5%; Pred. No. 2.7e-280;  
 Matches 665; Conservative 31; Mismatches 23; Indels 0; Gaps 0;

1 MKLKNPDHQSSNAKVDKIATDSLKNETDIELKMNEDYLRMSHESIDPFVSASTI 60  
 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKSEYENVEPVSASTI 60  
 61 QTGIGIAGKILGTGVPPAGQIASLYSIFILGELMPKGSOWEIFMEHVEEIIINQILTYA 120  
 61 QTGIGIAGKILGTGVPPAGQIASLYSIFILGELMPKGSOWEIFMEHVEEIIINQILTYA 120  
 121 RNKALSDLRLGDLALAVYHDSLESVWENNRNTRASVVKVKSQVIALLELMFVKLPFAVSG 180  
 121 RNKALSDLRLGDLALAVYHDSLESVWENNRNTRASVVKVKSQVIALLELMFVKLPFAVSG 180  
 181 EEPVLLPIVAQAANLHLLLRDASIFGKWLGSASEISTFYNRQVTRDYSDCIKWYN 240  
 181 EEPVLLPIVAQAANLHLLLRDASIFGKWLGSASEISTFYNRQVTRDYSDCIKWYN 240

QY 241 TGLNLRGTWAKSVRYNQPRKDMTLMVLDLVALFPYSYDITLVPIKTTSQLTREVYTDAL 300  
 DB 241 TGLNLRGTWAKSVRYNQPRKDMTLMVLDLVALFPYSYDITLVPIKTTSQLTREVYTDAL 300  
 QY 301 GTVHPNOAPASTTWNWNNAPSFSAIEAAVIRSPHLLDFLEKVTIYSLLSWSNTQYNNMW 360  
 DB 301 GTVHPNPFSTSTWNNNAPSFSAIEAAVIRSPHLLDFLEKVTIYSLLSWSNTQYNNMW 360  
 QY 361 GGHLESPRTGGALNTSTQSTNTSINPVTLOFTSRDVTSTESLAGLNLFLOPVNGVPR 420  
 DB 361 GGHLESPRTGGALNTSTQSTNTSINPVTLOFTSRDVTSTESLAGLNLFLOPVNGVPR 420  
 QY 421 VDFHWKFTPLPIASDNFYLYGAGVGTQLODSENELPEPTTGPNYESYSHRLSHIGLIS 480  
 DB 421 VDFHWKFTPLPIASDNFYLYGAGVGTQLODSENELPEPTTGPNYESYSHRLSHIGLIS 480  
 QY 481 ASHKALVYSWTHRSADRTNTEPNSITQPLVKAFNLSSGAAVVRGPGTGGDILRRTN 540  
 DB 481 ASHKALVYSWTHRSADRTNTEPNSITQPLVKAFNLSSGAAVVRGPGTGGDILRRTN 540  
 QY 541 TGTFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKALNQGNSATMNRGEDIYK 600  
 DB 541 TGTFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKALNQGNSATMNRGEDIYK 600  
 QY 601 TFRIGTTPPSFDVOSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDPEKAQEKV 660  
 DB 601 TFRIGTTPPSFDVOSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDPEKAQEKV 660  
 QY 661 TALFTSTNPRGLKTDVKDHYDQVNLVESLSDEFYLDKRELFEIVKYAKQHIERNM 719  
 DB 661 TALFTSTNPRGLKTDVKDHYDQVNLVESLSDEFYLDKRELFEIVKYAKQHIERNM 719

RESULT 15  
 ID AAE36271 standard; protein; 718 AA.  
 XX AC AAE36271;  
 XX DT 26-JUN-2003 (first entry)  
 XX DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa1.  
 XX KW Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.  
 XX OS Bacillus thuringiensis.  
 XX PN WO200298911-A2.  
 XX PD 12-DEC-2002.  
 XX PF 30-MAY-2002; 2002WO-GB002666.  
 XX PR 07-JUN-2001; 2001GB-00013900.  
 XX PA (SYGN ) SYNGENTA LTD.  
 XX PI Vincent JL, Viner R;  
 XX DR WPI; 2003-175137/17.  
 XX PT New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.  
 XX PS Claim 12; Page 42-44; 67pp; English.

CC The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects. Antibodies raised to the insecticidal proteins can be used to identify

CC other proteins with insecticidal activity. The present sequence is  
 CC Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This  
 CC sequence is used in the invention  
 XX  
 SQ Sequence 718 AA;

Query Match 93.2%; Score 3488.5; DB 6; Length 718;  
 Best Local Similarity 92.5%; Pred. No. 28-279;  
 Matches 665; Conservative 31; Mismatches 22; Indels 1; Gaps 1;

QY 1 MKLKPDKHOSISSNAKVDKIATDSIKNETDTELKMNEDYLRMSEHSDIPFVSASTI 60  
 DB 1 MKLKPDKHOSISSNAKVDKIATDSIKNETDTELKMNEDYLRMSEHSDIPFVSASTI 60  
 QY 61 QTGIGIAGKILGTGVPPFAGQIASYSLFGLBPKGKQWEIFMEHVEEIIINQKILTA 120  
 DB 61 QTGIGIAGKILGTGVPPFAGQIASYSLFGLBPKGKQWEIFMEHVEEIIINQKILTA 120  
 QY 121 RNKALSDLEGLDGLAVYHESLESVENENNTNRASVVKNOYIALELMFVKLPSPFVSG 180  
 DB 121 RNKALSDLEGLDGLAVYHESLESVENENNTNRASVVKNOYIALELMFVKLPSPFVSG 180  
 QY 181 EEPVLLPIYAOAANLHLLLRDASIFGKEMGLSSASEISTFYNRQVTRDYSDHCIKWYN 240  
 DB 181 EEPVLLPIYAOAANLHLLLRDASIFGKEMGLSSASEISTFYNRQVTRDYSDHCIKWYN 240  
 QY 241 TGLNLRGTWAKSVRYNQPRKDMTLMVLDLVALFPYSYDITLVPIKTTSQLTREVYTDAL 300  
 DB 241 TGLNLRGTWAKSVRYNQPRKDMTLMVLDLVALFPYSYDITLVPIKTTSQLTREVYTDAL 300  
 QY 301 GTVHPNOAPASTTWNWNNAPSFSAIEAAVIRSPHLLDFLEKVTIYSLLSWSNTQYNNMW 360  
 DB 301 GTVHPNPFSTSTWNNNAPSFSAIEAAVIRSPHLLDFLEKVTIYSLLSWSNTQYNNMW 360  
 QY 361 GGHLESPRTGGALNTSTQSTNTSINPVTLOFTSRDVTSTESLAGLNLFLOPVNGVPR 420  
 DB 361 GGHLESPRTGGALNTSTQSTNTSINPVTLOFTSRDVTSTESLAGLNLFLOPVNGVPR 420  
 QY 421 VDFHWKFTPLPIASDNFYLYGAGVGTQLODSENELPEPTTGPNYESYSHRLSHIGLIS 480  
 DB 421 VDFHWKFTPLPIASDNFYLYGAGVGTQLODSENELPEPTTGPNYESYSHRLSHIGLIS 480  
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 DB 481 ASHKALVYSWTHRSADRTNTEPNSITQPLVKAFNLSSGAAVVRGPGTGGDILRRTN 540  
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 DB 541 TGTFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKALNQGNSATMNRGEDIYK 600  
 QY 601 TFRIGTTPPSFDVOSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDPEKAQEKV 660  
 DB 601 TFRIGTTPPSFDVOSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDPEKAQEKV 660  
 QY 661 TALFTSTNPRGLKTDVKDHYDQVNLVESLSDEFYLDKRELFEIVKYAKQHIERNM 719  
 DB 661 TALFTSTNPRGLKTDVKDHYDQVNLVESLSDEFYLDKRELFEIVKYAKQHIERNM 719

Search completed: October 28, 2004, 18:20:08  
 Job time : 89.6903 secs





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OM protein - protein search, using sw model

Run on: October 28, 2004, 18:06:07 ; Search time 22.3343 Seconds  
(without alignments)  
2134.948 Million cell updates/sec

Title: US-10-019-823B-59  
Perfect score: 3742  
Sequence: 1 MKLKNPKHQSLSSNAKVDK.....KRELFEIVKYAKOIHIERNM 719

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*  
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2: /cgn2\_6/ptodata/1/iaa/5B.COMB.pep.\*  
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4: /cgn2\_6/ptodata/1/iaa/6B.COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PTUS.COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query	Length	ID	Description
1	3546	94.8	719	2	US-09-003-217-2
2	3541	94.6	719	3	US-03-218-942-2
3	3516	94.0	719	3	US-08-286-870A-8
4	3388.5	90.0	710	4	US-08-661-322A-42
5	3160	84.4	648	3	US-08-286-870A-4
6	2573	68.8	535	3	US-08-286-870A-6
7	2459	65.7	1229	1	US-08-100-709-4
8	2459	65.7	1229	1	US-08-176-865-4
9	2459	65.7	1229	1	US-08-474-038-4
10	2459	65.7	1229	2	US-08-779-046-4
11	2459	65.7	1229	2	US-08-881-340-4
12	2314.5	61.9	1207	1	US-07-951-715A-7
13	2314.5	61.9	1207	2	US-08-459-448A-7
14	2314.5	61.9	1207	3	US-08-459-595A-7
15	2314.5	61.9	1207	3	US-08-459-504B-7
16	2314.5	61.9	1207	3	US-08-459-444-7
17	2314.5	61.9	1207	3	US-08-053-549-8
18	2314.5	61.9	1207	3	US-08-547-422-7
19	2314.5	61.9	1207	4	US-08-988-462-7
20	2308.5	61.7	1227	3	US-08-053-549-2
21	2243	59.9	1227	1	US-08-448-170-8
22	2243	59.9	1227	3	US-08-961-803-9
23	2234	59.7	1227	4	US-08-661-322A-63
24	2233.5	59.7	488	1	US-08-448-170-10
25	2233.5	59.7	488	3	US-08-961-803-10
26	2219	59.3	1186	3	US-09-178-252-23
27	2219	59.3	1186	4	US-09-826-660-23

28	2168.5	58.0	1228	4	US-09-661-322A-38	Sequence 38, Appl
29	1982	53.0	643	3	US-09-178-252-25	Sequence 25, Appl
30	1982	53.0	643	4	US-09-826-660-25	Sequence 25, Appl
31	1813	48.5	380	5	PCT-US91-02560-4	Sequence 4, Appl
32	1683.5	45.0	653	4	US-09-661-322A-6	Sequence 6, Appl
33	1657.5	44.3	1157	1	US-07-876-280-30	Sequence 30, Appl
34	1657.5	44.3	1157	1	US-07-812-180A-2	Sequence 2, Appl
35	1657.5	44.3	1157	1	US-08-315-468-2	Sequence 2, Appl
36	1657.5	44.3	1157	3	US-07-941-650A-2	Sequence 2, Appl
37	1519.5	40.6	1176	1	US-08-257-999-2	Sequence 2, Appl
38	1507	40.3	1157	2	US-08-532-547-5	Sequence 5, Appl
39	1507	40.3	1157	2	US-08-379-656B-5	Sequence 5, Appl
40	1507	40.3	1157	3	US-08-455-838-5	Sequence 5, Appl
41	1507	40.3	1157	3	US-09-019-809-5	Sequence 5, Appl
42	1507	40.3	1157	4	US-09-471-177-5	Sequence 5, Appl
43	1507	40.3	1157	4	US-09-220-806-5	Sequence 5, Appl
44	1506.5	40.3	1168	1	US-08-291-368-4	Sequence 4, Appl
45	1506.5	40.3	1168	2	US-08-962-190-4	Sequence 4, Appl

## ALIGNMENTS

RESULT 1  
US-09-003-217-2  
; Sequence 2, Application US/09003217  
; Patent No. 5986177  
; GENERAL INFORMATION:  
; APPLICANT: Osman, Yehia A.  
; APPLICANT: Mackour, Magdy A.  
; APPLICANT: Bulla, Lee A.  
; TITLE OF INVENTION: BACILLUS THURINGIENSIS ISOLATES WITH  
; TITLE OF INVENTION: BROAD SPECTRUM ACTIVITY  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: W. Murray Spruill (Alston & Bird, LLP)  
; STREET: 3605 Glenwood Ave. Suite 310  
; CITY: Raleigh  
; STATE: NC  
; COUNTRY: US  
; ZIP: 27622  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APLICATION NUMBER: US/09/003,217  
; FILING DATE:  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Spruill, W. Murray  
; REGISTRATION NUMBER: 32,943  
; REFERENCE/DOCKET NUMBER: 5718-3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 919 420 2202  
; TELEFAX: 919 881 3175  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 719 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-003-217-2

Query Match 94.8%; Score 3546; DB 2; Length 719;  
Best Local Similarity 95.0%; Pred. No. 5.6e-318;  
Matches 683; Conservative 11; Mismatches 25; Indels 0; Gaps 0;

OY 1 MKLKNPKHQSLSSNAKVDKIATDSIKNETDIELKNMKNEDYLRMSEHSDPFVSASTI 60  
DB 1 MKLKNPKHQSLSSNAKVDKIATDSIKNETDIELKNMKNEDYLRMSEHSDPFVSASTI 60

QY 61 QTGIGIAGKILGTGVPAGQIASLYSPTLGBLWPKGKSOWEIMFHVBEIINOKILTYA 120  
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 Db 121 RNKALSDLRGLGDALAVHESLESVENNRNTRASVVKNOYIALELMFVQKLPSPFAVSG 180  
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 Db 181 EYVPLPIYAQAANLHLLLRDASIFGKXWGLSASEISTFYNRQVTRDRYSDHCIKWYN 240  
 QY 241 TGLNNLRGNTAKSWRYNQFRKDMTLMVLDLVALPSPSYDTLVPIKTTSQLTREVYTDAI 300  
 Db 241 TGLNNLRGNTAKSWRYNQFRKDMTLMVLDLVALPSPSYDTLVPIKTTSQLTREVYTDAI 300  
 QY 301 GTVHPNQAFASFTWYNNNAPSFAIEAAVIRSPHLLDFLEKVTIYSLSRWSNTQYNNMW 360  
 Db 301 GTVHPNQAFASFTWYNNNAPSFAIEAAVIRSPHLLDFLEKVTIYSLSRWSNTQYNNMW 360  
 QY 361 GGHRESRPIGGALNTSTOGSNTSINPVTLQFTSRDVRVRESLAGLNLFLTQPVNGVPR 420  
 Db 361 GGHRESRPIGGALNTSTOGSNTSINPVTLQFTSRDVRVRESLAGLNLFLTQPVNGVPR 420  
 QY 421 VDFHWKFTPLPIASDNFYLYGAGVGTQLQDSENELPPTTQPNYESYSHRSLSHIGLIS 480  
 Db 421 VDFHWKFTPLPIASDNFYLYGAGVGTQLQDSENELPPTTQPNYESYSHRSLSHIGLIS 480  
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 QY 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVSLSDEFYLDKRELFEIVKAKQIHIERNM 719  
 Db 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVSLSDEFYLDKRELFEIVKAKQIHIERNM 719

## RESULT 2

US-09-218-942-2  
 ; Sequence 2, Application US/09218942  
 ; Patent No. 6232439  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Osman, Yehia  
 ; TITLE OF INVENTION: Bacillus Thuringiensis Isolates with Broad Spectrum  
 ; FILE OF INVENTION: Activity  
 ; FILE REFERENCE: Crv11  
 ; CURRENT APPLICATION NUMBER: US/09/218,942  
 ; EARLIER FILING DATE: 1998-12-22  
 ; EARLIER APPLICATION NUMBER: 60/035,361  
 ; EARLIER FILING DATE: 1997-01-10  
 ; EARLIER APPLICATION NUMBER: 09/003,217  
 ; EARLIER FILING DATE: 1998-01-06  
 ; NUMBER OF SEQ ID NOS: 2  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 2  
 ; LENGTH: 719  
 ; TYPE: PRT  
 ; ORGANISM: Bacillus thuringiensis  
 US-09-218-942-2

Query Match 94.6%; Score 3541; DB 3; Length 719;  
 Best Local Similarity 95.0%; Pred. No. 1.5e-317;  
 Matches 683; Conservative 11; Mismatches 25; Indels 0; Gaps 0;

QY 1 MKLKNPDKHQSLSSNAKVDKIATDSLKNETDIELKMNNDYLRMSEHSDPFSASTI 60

Db 1 MKLKNPDKHQSLSSNAKVDKIATDSLKNETDIELKMNNDYLRMSEHSDPFSASTI 60  
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 Db 61 QTGIGIAGKILGTGVPAGQIASLYSPTLGBLWPKGKSOWEIMFHVBEIINOKILTYA 120  
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 Db 361 GGHRESRPIGGALNTSTOGSNTSINPVTLQFTSRDVRVRESLAGLNLFLTQPVNGVPR 420  
 QY 421 VDFHWKFTPLPIASDNFYLYGAGVGTQLQDSENELPPTTQPNYESYSHRSLSHIGLIS 480  
 Db 421 VDFHWKFTPLPIASDNFYLYGAGVGTQLQDSENELPPTTQPNYESYSHRSLSHIGLIS 480  
 QY 481 ASHVKALVSWTHRSADRNTIPEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILARTN 540  
 Db 481 ASHVKALVSWTHRSADRNTIPEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILARTN 540  
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 Db 541 TGTGDIRVNIINPPPAQRVVRVIRVASTTDLQFHTSINGKAINQGNFSAATNRGDEDLYK 600  
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 Db 601 TPTTGTTPPFSQVSTFTTICANFNSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEKV 660  
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 Db 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVSLSDEFYLDKRELFEIVKAKQIHIERNM 719

## RESULT 3

US-08-286-870A-8  
 ; Sequence 8, Application US/08286870A  
 ; Patent No. 6063605  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ELY, S  
 ; APPLICANT: TAILOR, RH  
 ; APPLICANT: TIPPETT, JM  
 ; APPLICANT: BLENK, RG  
 ; TITLE OF INVENTION: BACTERIAL GENES  
 ; NUMBER OF SEQUENCES: 10  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: CUSHMAN DABY & CUSHMAN  
 ; ADDRESSEE: Intellectual Property Group of  
 ; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP  
 ; STREET: 1100 New York Avenue, N.W.  
 ; CITY: Washington  
 ; STATE: DC  
 ; COUNTRY: USA  
 ; ZIP: 20005-3918  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/286,870A  
; FILING DATE: 05-AUG-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/520228  
; FILING DATE: 09-MAY-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 8910624.9  
; FILING DATE: 09-MAY-1989  
; ATTORNEY/AGENT INFORMATION:  
; NAME: PAUL N. KOKULIS  
; REGISTRATION NUMBER: 16,773  
; REFERENCE/DOCKET NUMBER: 70608/220720  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 861-3000  
; TELEFAX: (202) 822-0944  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 719 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-286-870A-8

Query Match 94.0%; Score 3516; DB 3; Length 719;  
Best Local Similarity 92.8%; Pred. No. 2.9e-315;  
Matches 667; Conservative 32; Mismatches 20; Indels 0; Gaps 0;  
  
Qy 1 MKLKPDKHQSLSNAKVDKIATDSLKNETDIELKNNEDYLRMSHESIDPFVSASTI 60  
Db 1 MKLKPDKHQSLSNAKVDKIATDSLKNETDIELKNNEDYLRMSHESIDPFVSASTI 60  
  
Qy 61 QTGIGIAGKILGTGVPPAGQIASLYSFTILGELMPKGSQWEIPEHVEEIIINOKILTYA 120  
Db 61 QTGIGIAGKILGTGVPPAGQIASLYSFTILGELMPKGSQWEIPEHVEEIIINOKILTYA 120  
  
Qy 121 RNKALSDLRGDGLAVVHESLESVWENRNNTARSVVXQYIALELMFVKQLPSFAVSG 180  
Db 121 RNKALSDLRGDGLAVVHESLESVWENRNNTARSVVXQYIALELMFVKQLPSFAVSG 180  
  
Qy 181 BEVPLLPITYAQAANLHLLLRDASIFGKEWGLSASEISTFYNQVETRDYSDHCIKWYN 240  
Db 181 BEVPLLPITYAQAANLHLLLRDASIFGKEWGLSASEISTFYNQVETRDYSDHCIKWYN 240  
  
Qy 241 TGLNNLRGTNAKSWRYNQFRDMTLMVLDLVALFPSPYDTLVYPIKTTTSOLTREVYTDAI 300  
Db 241 TGLNNLRGTNAKSWRYNQFRDMTLMVLDLVALFPSPYDTLVYPIKTTTSOLTREVYTDAI 300  
  
Qy 301 GTVHPNQAFSTTWNNNAPSFAIEAAVIRSPHLLDFLEKVTIYSLSRWSNTQYNNMW 360  
Db 301 GTVHPNQAFSTTWNNNAPSFAIEAAVIRSPHLLDFLEKVTIYSLSRWSNTQYNNMW 360  
  
Qy 361 GGHRLSPGIGALNTSTQGSTNTSINPVTLOFTSRDVYRTESLAGNLFLTPQVNGVPR 420  
Db 361 GGHRLSPGIGALNTSTQGSTNTSINPVTLOFTSRDVYRTESLAGNLFLTPQVNGVPR 420  
  
Qy 421 VDFHWKFTPLPIASDNFFYLGAGVGTQLQDSENELPPEATQPNYESYSHRLSHIGLIS 480  
Db 421 VDFHWKFTPLPIASDNFFYLGAGVGTQLQDSENELPPEATQPNYESYSHRLSHIGLIS 480  
  
Qy 481 ASHKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRTN 540  
Db 481 ASHKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRTN 540  
  
Qy 541 TGTGDIRVNIINPPFAQRYRIRYASTDLOFHTSINGKAINQGNFSATMNRGEDLDYK 600  
Db 541 TGTGDIRVNIINPPFAQRYRIRYASTDLOFHTSINGKAINQGNFSATMNRGEDLDYK 600  
  
Qy 601 TFRIGTTPPSFSDVQSTFTIGAWNPFSSGNEVYIDRIEFVPEVVEYAEYDFPKAQEKV 660  
Db 601 TFRIGTTPPSFSDVQSTFTIGAWNPFSSGNEVYIDRIEFVPEVVEYAEYDFPKAQEKV 660  
  
Qy 661 TFRVGFVTPPSFSDVQSTFTIGAWNPFSSGNEVYIDRIEFVPEVVEYAEYDFPKAQEKV 660  
Db 661 TFRVGFVTPPSFSDVQSTFTIGAWNPFSSGNEVYIDRIEFVPEVVEYAEYDFPKAQEKV 660

Qy 661 TALFTSTNPRGLKTDVQYHIDQVSNLVESLSDBFYLDKRELFEIVKAKQIHIERNM 719  
Db 661 TALFTSTNPRGLKTDVQYHIDQVSNLVESLSDBFYLDKRELFEIVKAKQIHIERNM 719  
  
RESULT 4  
US-09-661-322A-42  
; Sequence 42, Application US/09661322A  
; Patent No. 6593293  
; GENERAL INFORMATION:  
; APPLICANT: Baum, James A.  
; APPLICANT: Chu, Chih-Rei  
; APPLICANT: Donovan, William P.  
; APPLICANT: Gilmer, Amy J.  
; APPLICANT: Rupal, Mark J.  
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Compos  
; FILE REFERENCE: MECO201  
; CURRENT APPLICATION NUMBER: US/09/661,322A  
; CURRENT FILING DATE: 2000-09-13  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 42  
; LENGTH: 710  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (200)..(200)  
; OTHER INFORMATION: No. 6593293-Coding  
US-09-661-322A-42

Query Match 90.0%; Score 3368.5; DB 4; Length 710;  
Best Local Similarity 89.2%; Pred. No. 1.2e-301;  
Matches 641; Conservative 32; Mismatches 37; Indels 9; Gaps 1;  
  
Qy 1 MKLKPDKHQSLSNAKVDKIATDSLKNETDIELKNNEDYLRMSHESIDPFVSASTI 60  
Db 1 MKLKPDKHQSLSNAKVDKIATDSLKNETDIELKNNEDYLRMSHESIDPFVSASTI 60  
  
Qy 61 QTGIGIAGKILGTGVPPAGQIASLYSFTILGELMPKGSQWEIPEHVEEIIINOKILTYA 120  
Db 61 QTGIGIAGKILGTGVPPAGQIASLYSFTILGELMPKGSQWEIPEHVEEIIINOKILTYA 120  
  
Qy 121 RNKALSDLRGDGLAVVHESLESVWENRNNTARSVVXQYIALELMFVKQLPSFAVSG 180  
Db 121 RNKALSDLRGDGLAVVHESLESVWENRNNTARSVVXQYIALELMFVKQLPSFAVSG 180  
  
Qy 181 BEVPLLPITYAQAANLHLLLRDASIFGKEWGLSASEISTFYNQVETRDYSDHCIKWYN 240  
Db 181 BEVPLLPITYAQAANLHLLLRDASIFGKEWGLSASEISTFYNQVETRDYSDHCIKWYN 240  
  
Qy 241 TGLNNLRGTNAKSWRYNQFRDMTLMVLDLVALFPSPYDTLVYPIKTTTSOLTREVYTDAI 300  
Db 241 TGLNNLRGTNAKSWRYNQFRDMTLMVLDLVALFPSPYDTLVYPIKTTTSOLTREVYTDAI 300  
  
Qy 301 GTVHPNQAFSTTWNNNAPSFAIEAAVIRSPHLLDFLEKVTIYSLSRWSNTQYNNMW 360  
Db 301 GTVHPNQAFSTTWNNNAPSFAIEAAVIRSPHLLDFLEKVTIYSLSRWSNTQYNNMW 360  
  
Qy 361 GGHRLSPGIGALNTSTQGSTNTSINPVTLOFTSRDVYRTESLAGNLFLTPQVNGVPR 420  
Db 361 GGHRLSPGIGALNTSTQGSTNTSINPVTLOFTSRDVYRTESLAGNLFLTPQVNGVPR 420  
  
Qy 421 VDFHWKFTPLPIASDNFFYLGAGVGTQLQDSENELPPEATQPNYESYSHRLSHIGLIS 480  
Db 421 VDFHWKFTPLPIASDNFFYLGAGVGTQLQDSENELPPEATQPNYESYSHRLSHIGLIS 480  
  
Qy 481 ASHKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRTN 540  
Db 481 ASHKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRTN 540  
  
Qy 541 TGTGDIRVNIINPPFAQRYRIRYASTDLOFHTSINGKAINQGNFSATMNRGEDLDYK 600  
Db 541 TGTGDIRVNIINPPFAQRYRIRYASTDLOFHTSINGKAINQGNFSATMNRGEDLDYK 600

Db 532 TGTGDIRVNPPFAQRVRIRVASTDLOFHTSINGKALNQNFSAWNRGDDLDYK 591  
QY 601 TFRITGTFPPFSVDQSTFTTIGANFSSGNEVYIDRIEFVFPVETVYEAEDYDFEKAQEKY 660  
Db 592 TERTVGTFPPFSVDQSTFTTIGANFSSGNEVYIDRIEFVFPVETVYEAEDYDFEKAQEEV 651  
QY 661 TALFTSTPRGKTDVQYHDOVNLVESLSDEYLDKEKLEBEIVKYAKOIHENM 719  
Db 652 TALFTSTPRGKTDVQYHDOVNLVESLSDEYLDKEKLEBEIVKYAKOIHENM 710

RESULT 5  
US-08-286-870A-4  
; Sequence 4, Application US/08286870A  
; Patent No. 6063605  
; GENERAL INFORMATION:  
; APPLICANT: ELY, S  
; APPLICANT: TAILOR, RH  
; APPLICANT: TIPPETT, JM  
; APPLICANT: BLENK, RG  
; TITLE OF INVENTION: BACTERIAL GENES  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CUSHMAN DABBY & CUSHMAN  
; ADDRESSEE: Intellectual Property Group of  
; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP  
; STREET: 1100 New York Avenue, N.W.  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3918  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/286.870A  
; FILING DATE: 05-AUG-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/520228  
; FILING DATE: 09-MAY-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 8910624.9  
; FILING DATE: 09-MAY-1989  
; ATTORNEY/AGENT INFORMATION:  
; NAME: PAUL N. KOKULIS  
; REGISTRATION NUMBER: 16,773  
; REFERENCE/DOCKET NUMBER: 70608/220720  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 861-3000  
; TELEFAX: (202) 822-0944  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 648 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-286-870A-4

Query Match 84.4%; Score 3160; DB 3; Length 648;  
Best Local Similarity 92.3%; Pred. No. 1.7e-282;  
Matches 598; Conservative 30; Mismatches 20; Indels 0; Gaps 0;

QY 1 MKLKNPKHQSLSSNAKYDKIATDSLKNETDIELKNNMNDYLRMSHESIDPVSASTI 60  
Db 1 MKLKNQDKHQSFSSNAKYDKISTDSLKNETDIELQNIHEDCLKMSYEYENPEVFSASTI 60  
QY 61 OTGIGIAGKILGTIGVPPAGQIASLYSPILGELWPKGKSQWEIFMEHVEETINQILTYA 120  
Db 61 QTGIGIAGKILGTIGVPPAGQIASLYSPILGELWPKGKNQWEIFMEHVEETINQISTYA 120

QY 121 RNKALSRLRGDGLALAVYHESLESWVENNTRASVVKNOYIALELMFVKLPSPFVSG 180  
Db 121 RNKALTDGLRGDGLALAVYHDSLESWVGNRRNTRASVVKSQYIALELMFVKLPSPFVSG 180  
QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNNRQVERTRDYSHCIKWYN 240  
Db 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNNRQVERAGDYSHCVKWYS 240  
QY 241 TGLNNLRGTNAKSWRYNQFRDMILMWLDLVALPSSDYTLVYPIKTTISLTREYVYDAI 300  
Db 241 TGLNNLRGTNAESWRYNQFRDMILMWLDLVALPSSDYTYQMPYPIKTTAQLTREYVYDAI 300  
QY 301 GTVHPNCAFASTTWYNNAPSFSAIEAAVIRPHLLDFLEKVTIYSLSRWNTQYMMNW 360  
Db 301 GTVHPHPSFTSTWYNNAPSFSAIEAAVVRPHLLDFLEQVTIYSLSRWNTQYMMNW 360  
QY 361 GGHRLSRPIGGALNTSTOGSTNWSINPVTLQFTGRDYYRTESLAGLNLFLTQPVNGVPR 420  
Db 361 GGHKLEFRITGGTANISITQGSTNWSINPVTLPTSTRDYYRTESLAGLNLFLTQPVNGVPR 420  
QY 421 VDFHMKFPPTLPJASDNFYVYLGAVGTQLQDSNELPPETGQPNYESYSHRLSHIGLIS 480  
Db 421 VDFHMKFVTHPIASDNFYVYVYAGIGTQLQDSNELPPEATQPNYESYSHRLSHIGLIS 480  
QY 481 ASHVKALVYSWTHRSADRTNTTIEPNSITQIPLVKAFNLSGGAUVVRGPGFTGGDILRRTN 540  
Db 481 ASHVKALVYSWTHRSADRTNTTIEPNSITQIPLVKAFNLSGGAUVVRGPGFTGGDILRRTN 540  
QY 541 TGTFGDIRVNINPPFAQRVRIRVASTDLOFHTSINGKALNQNFSAWNRGDDLDYK 600  
Db 541 TGTFGDIRVNINPPFAQRVRIRVASTDLOFHTSINGKALNQNFSAWNRGDDLDYK 600  
QY 601 TFRITGTFPPFSVDQSTFTTIGANFSSGNEVYIDRIEFVFPVETVY 648  
Db 601 TFRITGTFPPFSVDQSTFTTIGANFSSGNEVYIDRIEFVFPVETVY 648

RESULT 6  
US-08-286-870A-6  
; Sequence 6, Application US/08286870A  
; Patent No. 6063605  
; GENERAL INFORMATION:  
; APPLICANT: ELY, S  
; APPLICANT: TAILOR, RH  
; APPLICANT: TIPPETT, JM  
; APPLICANT: BLENK, RG  
; TITLE OF INVENTION: BACTERIAL GENES  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CUSHMAN DABBY & CUSHMAN  
; ADDRESSEE: Intellectual Property Group of  
; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP  
; STREET: 1100 New York Avenue, N.W.  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3918  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/286.870A  
; FILING DATE: 05-AUG-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/520228  
; FILING DATE: 09-MAY-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 8910624.9  
; FILING DATE: 09-MAY-1989

```
; ATTORNEY/AGENT INFORMATION:
; NAME: PAUL N. KOKULIS
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 70608/220720
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 535 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-286-870A-6

Query Match      68.8%; Score 2573; DB 3; Length 535;
Best Local Similarity 91.0%; Pred. No. 1.9e-228;
Matches 487; Conservative 29; Mismatches 19; Indels 0; Gaps 0;

QY 1 MRLKXPKHOSLSNAKVADIATSLKNETDIELKNNEDYLRMSHEHIDPFVASTI 60
DB 1 MRLKXPKHOSLSNAKVADIATSLKNETDIELKNNEDYLRMSHEHIDPFVASTI 60
QY 61 QTGIGIAGKILGTGVFAGQIASLYSFI LGELWPKGKQWEIFMEHVEEIIINQKILTYA 120
DB 61 QTGIGIAGKILGTGVFAGQIASLYSFI LGELWPKGKQWEIFMEHVEEIIINQKILTYA 120
QY 121 RNKALSDLRGLGDALAVYHESLESWENRNNTRARSVVKQYIALELMFVKLPSPAVSG 180
DB 121 RNKALSDLRGLGDALAVYHESLESWENRNNTRARSVVKQYIALELMFVKLPSPAVSG 180
QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVTRDYSCHIKWYN 240
DB 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVTRDYSCHIKWYN 240
QY 241 TGLNLRGTNAKSVRYNQFRKQMTLMVLDLVALFPSYDTPVPIKTTSQLTREVYTDAL 300
DB 241 TGLNLRGTNAKSVRYNQFRKQMTLMVLDLVALFPSYDTPVPIKTTSQLTREVYTDAL 300
QY 301 GTVHPNQAFSTWYNNNAPFSAIEAAVIRSPHLLDFLEKVIYSLLSWSNTQYMMNW 360
DB 301 GTVHPNQAFSTWYNNNAPFSAIEAAVIRSPHLLDFLEKVIYSLLSWSNTQYMMNW 360
QY 361 GGHLESRPITGALNTSTQSTNTSINPVTLOFTSRDVRVYTESLAGNLFLTPQVNGVPR 420
DB 361 GGHLESRPITGALNTSTQSTNTSINPVTLOFTSRDVRVYTESLAGNLFLTPQVNGVPR 420
QY 421 VDFHWKPEPTPIASDNFYLYGAGVGTQLODSENELPPTGQPNYESYSHRLSHGLIS 480
DB 421 VDFHWKPEPTPIASDNFYLYGAGVGTQLODSENELPPTGQPNYESYSHRLSHGLIS 480
QY 481 ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDI 535
DB 481 ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDI 535

RESULT 7
US-08-100-709-4
; Sequence 4, Application US/08100709
; Patent No. 5322687
; GENERAL INFORMATION:
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yiping
; APPLICANT: Jany, Christine S.
; APPLICANT: Gonzalez Jr., Jose M.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS CRYE4 AND CRYE5
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
; ADDRESSEE: Nadel
; STREET: 1601 Market Street, 36th Floor
; CITY: Philadelphia
```

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; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/100,709
; FILING DATE: 19930729
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Egolf, Christopher
; REGISTRATION NUMBER: 27633
; REFERENCE/DOCKET NUMBER: 7205-49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-757-1590
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1229 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-100-709-4

Query Match      65.7%; Score 2459; DB 1; Length 1229;
Best Local Similarity 64.8%; Pred. No. 2.5e-217;
Matches 470; Conservative 91; Mismatches 128; Indels 36; Gaps 5;

QY 3 LKNPKHOSLSNAKVADIATSLKNETDIELKNNEDYLRMSHEHIDPFVASTIQT 62
DB 20 VSNPSTQVNLSPDARI-----EDSLCAEVNNDIPFVASTVQT 58
QY 63 GIGIAGKILGTGVFAGQIASLYSFI LGELWPKGKQWEIFMEHVEEIIINQKILTYARN 122
DB 59 GINIAGRILGVLCVFPAGQIASLYSFI LGELWPKGKQWEIFMEHVEEIIINQKILTYARN 118
QY 123 KALSRLGLGDALAVYHESLESWENRNNTRARSVVKQYIALELMFVKLPSPAVSGEE 182
DB 119 TAALEGLGRGYSYQQALETWLDNRNDARSRIILERYVALELDITTAIPLFRIRNEE 178
QY 183 VPLLPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVTRDYSCHIKWYNTG 242
DB 179 VPLLPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVTRDYSCHIKWYNTG 238
QY 243 LNNLRGTNAKSVRYNQFRKQMTLMVLDLVALFPSYDTPVPIKTTSQLTREVYTDALGT 302
DB 239 LNNLRGTNAKSVRYNQFRKQMTLMVLDLVALFPSYDTPVPIKTTSQLTREVYTDALGT 298
QY 303 VHPNQAFSTWYNNNAPFSAIEAAVIRSPHLLDFLEKVIYSLLSWSNTQYMMNWGG 362
DB 299 TNAPSQFSTWYNNNAPFSAIEAAVIRSPHLLDFLEKVIYSLLSWSNTQYMMNWGG 358
QY 363 HRLNRPITGALNTSTQSTNTSINPVTLOFTSRDVRVYTESLAGNLFLTPQVNGVPRV 421
DB 359 HRLNRPITGALNTSTQSTNTSINPVTLOFTSRDVRVYTESLAGNLFLTPQVNGVPRV 418
QY 422 DFHWKPEPTPIASDNFYLYG-----YAGVGTQLODSENELPPTGQPNYESYSHRLS 474
DB 419 RENF-----INPQNIYERGATTSYQYGVGIQVDFSETBELPPTTERPNYESYSHRLS 472
QY 475 HGLISASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGD 534
DB 473 HGLISASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGD 532
QY 535 ILRRNTGTGDIRVNIINPPFPAQRVVRIRVASTTDLQFHTSINGKAINQGNFSATMNRG 594
DB 533 ILRRNTGTGDIRVNIINPPFPAQRVVRIRVASTTDLQFHTSINGKAINQGNFSATMNRG 592
QY 595 EDLDYKTRTGTGFTTTPFSFSDVQSTFTIGANFSSGNEWYIDRIEFPVVEYIEYDFE 654
DB 593 DNLEYSRPTAGFTTTPFSFSDVQSTFTIGANFSSGNEWYIDRIEFPVVEYIEYDFE 651
```



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; FILING DATE: 29-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Egolf, Christopher
; REGISTRATION NUMBER: 27633
; REFERENCE/DOCKET NUMBER: 7205-49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-757-1590
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1229 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-474-038-4

Query Match      65.7%; Score 2459; DB 1; Length 1229;
Best Local Similarity 64.8%; Pred. No. 2.5e-217;
Matches 470; Conservative 91; Mismatches 128; Indels 36; Gaps 5;

QY 3 LKPKDKEQHSLSNAKVDKIATSDLSKNETDIELKMNVEDYLRMEHESIDPFVSASTIQT 62
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 20 VSNPSTQWNLSPDARI-----EDSLCAEVANNIDPFVSASIVQT 58

QY 63 GIGIAGKILGTGLVPPFAGQIASLYSFILGELWPKGKSCWEIFMHHVEEINQKILT YARN 122
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 59 GINIAGRIILGVLGVFFAGQLASFYSFLVGLWPGSRDFEWFIFLHVHQLIRQQVTENRN 118

QY 123 KALSDIRGLGDALAVYHESLESWEVENNNTFARSWKNOXIALFLMFVKQLPSPAVSGEE 182
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 119 TATARLEGLGRGYSYQOALETWLDNRNDARSIIILERVVALELDTTTAIPFRINEE 178

QY 183 VPLLPIYQAANLHLILLRDAISIPGKWKGLSASISITFYNRQVVERTRDYSDHCIKWYNTG 242
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 179 VPLLWVYAQANLHLILLRDAISIPGSEWGMASSDVQYQEQIRYTEYSNHCVQWYNTG 238

QY 243 LNLNRGNAXSWRYNQFRKDMTLMVLDIVALPESYDTLVYPIKTTSQLTRVYVTDIAIGT 302
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 239 LNLNRGNASWIRYNGFRDLTLGVLDLVALPFSYDTRTPYINTSAQLTREIYTDPIGR 298

QY 303 VHPNQAFATWYNNNAPSFAIEAAVIRSPHLDLFLEKVTIYSLLSRWENTQVMNWGG 362
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 299 TNAPSGFATWNNFNNAAPSFAIEAAIFRPPHLLDPEQLTIYSASSRWSTQHMNYWVG 358

QY 363 HRLESRPDICALNTSTOGST-NTSINPVTLOFTSRDVTYRTESLAGLNLFTQPVNGVPRV 421
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 359 HRLNFRPIGTLNTSTOGLTNNTSINPVTLOFTSRDVTYRTESNAGTNILFTTPVNGVPWA 418

QY 422 DFHWKPFETLPASDNFYILG-----YAGVGTQLQDSENELPPTTGGQNYESYSHRLS 474
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 419 RFNF-----INQNIYERGATTYSQYQGVGLFDSELTPELPTTERFNYESYSHRLS 472

QY 475 HIGLISASHVKALVYSWTHRSADRTNIENSITDPLVAFNLSSGAAYVRGPGFTGGD 534
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 473 HIGLIIGTLRAPVYSWTHRSADRTNITGNRTIQIPLVKALNLHSGVTVVGPGFTGGD 532

QY 535 ILRNTNIGTGGDIRVNIIPPQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRG 594
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 533 ILRNTNIGTGGDIRLNIINVLPSQRYRVRIRYASTTDLQFTRNGTIVNIGNSRTMNRG 592

QY 595 EDLDYKTRFRIQHTTTPSPSDVOSTFTTIGAWNPFSSGNEVVIDRIEFVVPVETVVEAYDFE 654
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 593 DNLFXRSFRTAGSTPTPNFNLAQSTFTFLGAQSFEN-QEVYIDRVFVPAEVTPEABYDLE 651

QY 655 KAEKVTALTFTSNPRGLKTDVMDYHIDQVSNLVESSIDSEFYLDKREKLEFIVKYAKQIH 714
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 652 RAQKAVNALFTSNPRGLKTDVTDYHIDQVSNMVACLSDSEFYLDKREKLEFIVKYAKRLS 711

QY 715 IERNM 719
   : : : : :
Db 712 DERNL 716
   : : : : :

```

## RESULT 10

US-08-779-046-4  
; Sequence 4, Application US/08779046  
; Patent No. 5854053  
; GENERAL INFORMATION:  
; APPLICANT: Donovan, William P.  
; APPLICANT: Tan, Yuping  
; APPLICANT: Jany, Christine S. M.  
; APPLICANT: Gonzalez Jr., Jose M.  
; TITLE OF INVENTION: BACILLUS THURINGIENSIS cYET4 AND cYET5  
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.  
; ADDRESS: Nadel  
; STREET: 1601 Market Street, 36th Floor  
; CITY: Philadelphia  
; STATE: Pennsylvania  
; COUNTRY: U.S.A.  
; ZIP: 19103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/779,046  
; FILING DATE: 06-JAN-1997  
; CLASSIFICATION: 435  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: 08/100,709  
; FILING DATE: 29-JUL-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Egolf, Christopher  
; REGISTRATION NUMBER: 27633  
; REFERENCE/DOCKET NUMBER: 7205-49  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 215-757-1590  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1229 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-779-046-4

Query Match	65.7%;	Score 2459;	DB 2;	Length 1229;
Best Local Similarity	64.8%;	Pred. No. 2.5e-217;		
Matches	470;	Conservative 91;	Mismatches 128;	Indels 36; Gaps 5;
QY	3	LKNPDKQHSLSSNAKVDKIATDSLAKNETDIELKNNNEDYLRMGSEHSIDPFGASVQT	62	
Db	20	VSNPSTQMQLSPDKRI-----EDSLCVAEAVNNIDPFGASVQT	58	
QY	63	GIGIAGKIILGTGVFPFAGQIASLYFIILGELWPKGSQWEIFMEHVEEIIINQKITLTARN	122	
Db	59	GINIAGRIILGLVGPFAQQLASFYSFLVGELWPSGRDPWEIFLEHVQLIRQQVTENRN	118	
QY	123	KALSDURGLGDALAVHYESLSWSVENRNNTRARSVKVNQYTALBELFMVKQLPSFAVGEE	182	
Db	119	TAIARLEGLGGRYSYQQALETWLDRNRDARSIIILERYVALEDITTAILEPRINEE	178	
QY	183	VPLLPITYAAANLHLLLRDASIICKEKWGLSASEISFTYNQVERTRDYSDHCIKWNTG	242	
Db	179	VPLMVIYAANLHLLLRDALSGFSEGWMASSDVNQYYEQIKRYTBEYSHNCVOWNTG	238	
QY	243	LNNLRGTNAKSVMRYNQFRKMOTMLVLDLVALFPSYDTLVYPPIKTTSOLTREVYTDAGT	302	
Db	239	LNNLRGTNAESWLRYNQFRRLTLGLVDLVALFSYDTRTYPINTSAQLTHEIYDDTIGR	298	
QY	303	VHPNQAFASTTWNNAPSFSAIEAIVTRSPLLDFLEKVTIYSLLRGSWNTOYNNMWGG	362	
Db	299	TNAPSGFASTWNNFNPPASFSAIEAIIIRPPPHLLDFPEQLTIYSGASRWGSTCHMYTVWG	358	





APPLICANT: Launis, Karen L.  
APPLICANT: Rothstein, Steven J.  
APPLICANT: Bowman, Cindy G.  
APPLICANT: Dawson, John L.  
APPLICANT: Dunder, Erik M.  
APPLICANT: Pace, Gary M.  
APPLICANT: Suttie, Janet L.  
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE  
NUMBER OF SEQUENCES: 94  
CORRESPONDENCE ADDRESS:  
ADDRESS: CIBA-GEIGY Corporation  
STREET: 7 Skyline Drive  
CITY: Hawthorne  
STATE: New York  
COUNTRY: USA  
ZIP: 10532  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30B  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/951.715A  
FILING DATE: 25-SEP-1992  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/772,027  
FILING DATE: 04-OCT-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Spruill, W. Murray  
REGISTRATION NUMBER: 32,943  
REFERENCE/DOCKET NUMBER: S-18805/A/CGC 1577/CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919)541-8615  
TELEFAX: (919)541-8689  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1207 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-951-715A-7

Query Match 61.9%; Score 2314.5; DB 1; Length 1207;  
Best Local Similarity 65.4%; Pred. No. 5.3e-204;  
Matches 447; Conservative 77; Mismatches 154; Indels 5; Gaps 3;  
Qy 40 EDYLRMSEHSIDPFVSASTIGTIGTAGKILGTGVFPAGQIASLYSPILGELWPKGS 99  
Db 10 EDSLCIAEGNNIDPFVSASTVGTGINTAGRIILGVLGVPFAGQIASFYLVLGELWPKGRD 69  
Qy 100 QWEIFMEHVEEINQKILTVARNKALSDRLGLDALAVYHESLESWYENNNTRARSVVK 159  
Db 70 QWEIFLBEHVEQLNQITENARNALTARLQGLGDSFRAYQOQSLDMLNDRDARTSVLY 129  
Qy 160 NQYIALMLFVQKLPSFVSGVEVPLPIYQAANLHLLLRDASTFGKELWGLSASEIST 219  
Db 130 TXYLELDELFLNAPLFAIRNQEVPLLMVYQAANLHLLLRDASTFGSEFGLTSQEIQR 189  
Qy 220 FYNQVQERTDYSCHIKWNTGLNLRGNNAKSWRYNQFRKDMTLWLVDLVALPSPYD 279  
Db 190 YQEQVQERTDYSYCVENWTGLNSURGNVNAKSWRYNQFRDLTLGLVDLVALPSPYD 249  
Qy 280 TLVYPIKTSQLTREVYTDAGTVHPNQAFSTWYNNAPSFSAIEAAVIRSFHLLDFL 339  
Db 250 TRTYPIKTSQLTREVYTDAGTVN--NASHMWNYNNAFSAIEAAVIRSFHLLDFL 307  
Qy 340 EKVYISLLGRWSNQYMMWGGHRLSRPISGGLANTSTOGSTNTSINPVTLQFTSRDYY 399  
Db 308 EQLTIFASGRWSNTRMTYWRGHTTQSRPIGGGLNTSTHGATNTSINPVTLFASGRDY 367  
Qy 400 RTESLAGLNLF--LTQPVNGVPRVDFHWKFP--TLPIASDNFYILGVAGVGTQLQDSENEL 456

Db 368 RTESYAGVLLWGIYLEPIHGVPTRFNTFNPQNSDRGTANYSQPYESGLQKQDSETEL 427  
Qy 457 PPTETGQPNYESYSHRLSHIGLISASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAF 516  
Db 428 PPTETGQPNYESYSHRLSHIGLISASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAF 487  
Qy 517 NLSGSAVVRGPGFTGGDILRRTNTGTGDIRVNNPFPQAQRYRVRIRYASTDLCQFTS 576  
Db 488 ELPOGTTVVVRGPGFTGGDILRRTNTGGFPIRVTVNGPLTQRYRIGFRYASTVDFDFVS 547  
Qy 577 INGKALNCGNSATMNRGDELDYKFRITGFTTTFESFSDVOSTFTIGAWNFSNGEVID 636  
Db 548 RGTTVNPRFLRTMNSGDELKYGNEVRAFTTPTFTQIQDIIRTSIQGLSGNEVID 607  
Qy 637 RIEFVPEVTVYEAAYDFEKAQSKVTALFTSTNPRGLKTDVYDHYDQVSNLVESLSDFFY 696  
Db 608 KIEIIPVTATFEAYDLERAQAVNALFTNTNPRKLKTDVTDHYDQVSNLVACLSDEFC 667  
Qy 697 LDEKBELEIVKYAKOIHENNM 719  
Db 668 LDEKBELEKVKYARLSDERNL 690

## RESULT 13

US-08-459-448A-7  
Sequence 7, Application US/08459448A  
Patent No. 5859336  
GENERAL INFORMATION:  
APPLICANT: Koziel, Michael G.  
APPLICANT: Desai, Nalini M.  
APPLICANT: Lewis, Kelly S.  
APPLICANT: Kramer, Vance C.  
APPLICANT: Warren, Gregory W.  
APPLICANT: Evola, Stephen V.  
APPLICANT: Crossland, Lyle D.  
APPLICANT: Wright, Martha S.  
APPLICANT: Merlin, Ellis J.  
APPLICANT: Launis, Karen L.  
APPLICANT: Rothstein, Steven J.  
APPLICANT: Bowman, Cindy G.  
APPLICANT: Dawson, John L.  
APPLICANT: Dunder, Erik M.  
APPLICANT: Pace, Gary M.  
APPLICANT: Suttie, Janet L.  
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE  
NUMBER OF SEQUENCES: 94  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 5859336artis Corporation  
STREET: Patent & Trademark Dept., 520 White Plains  
STREET: Rd., POB 2005  
CITY: Tarrytown  
STATE: New York  
COUNTRY: USA  
ZIP: 10591-9005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/459.448A  
FILING DATE: 02-JUN-1995  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/951,715  
FILING DATE: 25-SEP-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/772,027  
FILING DATE: 04-OCT-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Pace, Gary M.

```

; REGISTRATION NUMBER: 40403
; REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8582
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1207 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-459-595A-7

Query Match 61.9%; Score 2314.5; DB 2; Length 1207;
Best Local Similarity 65.4%; Pred. No. 5.3e-204;
Matches 447; Conservative 77; Mismatches 154; Indels 5; Gaps 3;

QY 40 EDYLRMSHESIDPPVSASTTGTGIGIAGKILGVLGVPFAGQIASLVSFILGELWPKGKS 99
Db 10 EDSLCTAEGNNIDPPVSASTVGTGINIAGRIAGLVGVPFAGQIASLVSFILGELWPKGRD 69
QY 100 QWEIFMEHVEEIIQKILTYARNKALSDLRGLGDALAVYHESLESWENNRNTRARSVK 159
Db 70 QWEIFLEHVEQLINQIITENARNTALRQLGSDSFAYQQSLEDWLENRDDARTSRVLY 129
QY 160 NOYIALELMFVQKLPFAVSGEEVPLPIYQAANLHLLLRDASIFGKEWGLSASEIST 219
Db 130 TQYIALELDPLNAMPFAIRNQEVPLLMVYAQAANLHLLLRDASLFGSEFGLTSQETOR 189
QY 220 FYNQOVERTRDYSCHICKWYNTGLNNRGTNAKSWRVYVNRQKDMTLMVLVDLVALF 279
Db 190 YVERQVERTRDYSCHICKWYNTGLNNRGTNAKSWRVYVNRQKDMTLMVLVDLVALF 249
QY 280 TLVYPIKITSQUTREVYDAITGVHPNQAFATTTWYNNNAPSFAIEAAVIRSPHLLD 339
Db 250 TRTYPINTSAQLTREVYDAITGVHPNQAFATTTWYNNNAPSFAIEAAVIRSPHLLD 307
QY 340 EKVTIYLLSRWSNTQYNNMCGHLESPRPGALNTSTQSTNTSINPVTIQTSDVY 399
Db 308 EQLTIFSASSRWSNTRHMYTGRHTIQSRPIGGGLNTSTHGTATNTSINPVTIQTSDVY 367
QY 400 RTESLAGNLFLQTPVNGVPRVDFHWKFP-TLPIASDNFYILGAGVGTQLODSENEL 456
Db 368 RYESAGVLLGIIIEPIHGVTVFNTNQNISDRGTANYSPQYESPGIQLXSETEL 427
QY 457 PPTTGQPNYESYSHRLSHIGLISASHKALVYSWTHRSADRTNTIENPNSITQIPVKAF 516
Db 428 PPTTERPNYESYSHRLSHIGLISASHKALVYSWTHRSADRTNTIENPNSITQIPVKAS 487
QY 517 NLSGAAVVRGFGTGGDILRTNTGTGDIRVNNPPFAQRYRVRVYASTTDLQHTS 576
Db 488 ELPGQTVVRGFGTGGDILRTNTGTGDIRVNNPPFAQRYRVRVYASTTDLQHTS 547
QY 577 INKAINQGNFATWNRGEBDYKTRFTIGTTPPSFDSQSTFTTIGAMNFSSENEVID 636
Db 548 RGGTTVNNFRFRTWNSGDELKYGNFVRAFTTPTFTQIQIIRTSIQGLSGNVEYVID 607
QY 637 RIEFVPEVTVYAEYDFEKAQSKVTALETSTNPRGLKTDVYKHDDQVSNLVESSLDEFY 696
Db 608 KIEIIPVATFPAEYDLERAQAVNALFTNPRKLKTDVYKHDDQVSNLVESSLDEFY 667
QY 697 LDEKRELEIYKAKQIHIERNM 719
Db 668 LDEKRELEKVKYAKRLSDERNL 690

RESULT 14
US-08-459-595A-7
; Sequence 7, Application US/08459595A
; Patent No. 6018104
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.

```

Db 190 YVERQVTRDYSYCVWYNTGNSLRGTNAASWVRYNQFRDLTLGLVDLVALPSPSYD 249  
QY 280 TLVPIKTTTSOLTREVYTDALGTVHPNOAFSTWYNNAPSPSAIEAAVIRSPHLLDPL 339  
Db 250 TRTYPINTSAQLTREVYTDALGTAGVN--MASMWNWYNNAPSPSAIEAAVIRSPHLLDPL 307  
QY 340 EKVTIYLLSRWNTQYNNMGGHRLSRPIGGALNTSTOGSTNTSINPVTLOFTSRDYY 399  
Db 308 EQLTIFSSASSRWSNTRHMTYWRGHTIQSRPIGGGLNTSTHGATNTSINPVTLPASRDYV 367  
QY 400 RTESLAGLNL--LTQPVNGVRVDFHWKFP--TLPIASDNFYLYGAGVGTQQLQDSNEL 456  
Db 368 RTESYAGVLLWGIYLEPIHGVTFRVFNTPONISDRGTANYSPYSPGLQKDSDEL 427  
QY 457 PPTTGPQNYESYSHRLSHIGLISASHVKALVSWTHRSADRTNTPNSITQIPLVKAF 516  
Db 428 PPTTERPNYESYSHRLSHIGLILQSRVNVVSWTHRSADRTNTPNRTQIIPMKAS 487  
QY 517 NLSGAAVVRGPGTGGDILRTNTGFDIRVNINPFAQRYVRIRYASTTDLQPHTS 576  
Db 488 ELPGQTTVVRGPGTGGDILRTNTGFGPIRVTVNGELTQRYRIGRYASTVDFDFVS 547  
QY 577 INKAINQGNFSATNRGEDIYKTFRTIGTTPFSFSDVQSTFTIGAMNFSNGEYVID 636  
Db 548 RGGTVANNFRFLRTMNSGDELKYGNFVRRAFTTFTTQIQDIIRTSIQGLSGNGEYVID 607  
QY 637 RIEFVPEVITYEAEYDFEKAQEKVTALTSTNPRGLKTDVKDHYDQVSNLVESLSEDFY 696  
Db 608 KIEIIPVTATPEAYDRLERAQEAVALFTNPRRLKTDVTDHYDQVSNLVACLSDSEFC 667  
QY 697 LDEKRELFEIVKYAKQIHERNM 719  
Db 668 LDEKRELLEKVKYAKRLSDERNL 690

## RESULT 15

US-08-459-504B-7  
; Sequence 7, Application US/08459504B  
; Patent No. 6075185  
; GENERAL INFORMATION:  
; APPLICANT: Koziel, Michael G.  
; APPLICANT: Desai, Nalini M.  
; APPLICANT: Lewis, Kelly S.  
; APPLICANT: Kramer, Vance C.  
; APPLICANT: Warren, Gregory W.  
; APPLICANT: Evola, Stephen V.  
; APPLICANT: Crossland, Lytle D.  
; APPLICANT: Wright, Martha S.  
; APPLICANT: Merlin, Ellis J.  
; APPLICANT: Launis, Karen L.  
; APPLICANT: Rothstein, Steven J.  
; APPLICANT: Bowman, Cindy G.  
; APPLICANT: Dawson, John L.  
; APPLICANT: Dunder, Erik M.  
; APPLICANT: Pace, Gary M.  
; APPLICANT: Suttie, Janet L.  
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE  
; NUMBER OF SEQUENCES: 94  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: No. 6075185artis Corporation  
; STREET: 3054 Cornwallis Road  
; CITY: Research Triangle Park  
; STATE: NC  
; COUNTRY: USA  
; ZIP: 27709  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/459,504B

; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION NUMBER: US 08/459,595  
; FILING DATE: 02-JUN-1995  
; APPLICATION NUMBER: US 07/951,715  
; FILING DATE: 25-SEP-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/772,027  
; FILING DATE: 04-OCT-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meigs, J. Timothy  
; REGISTRATION NUMBER: 38,241  
; REFERENCE/DOCKET NUMBER: CGC1577/CIP/DIV  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (919)541-8587  
; TELEFAX: (919)541-8689  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1207 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-459-504B-7  
Query Match 61.9%; Score 2314.5; DB 3; Length 1207;  
Best Local Similarity 65.4%; Pred. No. 5.3e-204;  
Matches 447; Conservative 77; Mismatches 154; Indels 5; Gaps 3;  
QY 40 EDYLRMSHESIDPFVSASTIQTGIGIAGKILGTGVFPAGQIASLYSPILGELWPKGKS 99  
Db 10 EDSLCTAEGNIDPFVSASTVGTGINIAGRIILGVLPFAGOLASFYFLVGLCELWPRGD 69  
QY 100 QWEIEMHVEEIIINOKILTYARKALSDLRGLGDALAVYHESLESWVENNNTRARSVVK 159  
Db 70 QWEIEMHVEEIIINOKITENAEATLARLQSGDSFRAYQQSLDLEWNRDARTSRVLY 129  
QY 160 NOVIALELMFVOKLPSEFVSGEEVPLPIYAQAANLHLLLRDASIFGKEMGLSASEIST 219  
Db 130 TQVIALELDLFNAMPLFAIRNOEVELLMYQAQANLHLLLRDASLFSFEGFOLTQEQTR 189  
QY 220 FYNQVQTRDYSYDHCIKWYNTGLNNLRGTNAKSWVRYNQFRKQMTMLVLDLVALPSPSYD 279  
Db 190 YVERQVTRDYSYCVWYNTGNSLRGTNAASWVRYNQFRDLTLGLVDLVALPSPSYD 249  
QY 280 TLVPIKTTTSOLTREVYTDALGTVHPNOAFSTWYNNAPSPSAIEAAVIRSPHLLDPL 339  
Db 250 TRTYPINTSAQLTREVYTDALGTAGVN--MASMWNWYNNAPSPSAIEAAVIRSPHLLDPL 307  
QY 340 EKVTIYLLSRWNTQYNNMGGHRLSRPIGGALNTSTOGSTNTSINPVTLOFTSRDYY 399  
Db 308 EQLTIFSSASSRWSNTRHMTYWRGHTIQSRPIGGGLNTSTHGATNTSINPVTLPASRDYV 367  
QY 400 RTESLAGLNL--LTQPVNGVRVDFHWKFP--TLPIASDNFYLYGAGVGTQQLQDSNEL 456  
Db 368 RTESYAGVLLWGIYLEPIHGVTFRVFNTPONISDRGTANYSPYSPGLQKDSDEL 427  
QY 457 PPTTGPQNYESYSHRLSHIGLISASHVKALVSWTHRSADRTNTPNSITQIPLVKAF 516  
Db 428 PPTTERPNYESYSHRLSHIGLILQSRVNVVSWTHRSADRTNTPNRTQIIPMKAS 487  
QY 517 NLSGAAVVRGPGTGGDILRTNTGFDIRVNINPFAQRYVRIRYASTTDLQPHTS 576  
Db 488 ELPGQTTVVRGPGTGGDILRTNTGFGPIRVTVNGELTQRYRIGRYASTVDFDFVS 547  
QY 577 INKAINQGNFSATNRGEDIYKTFRTIGTTPFSFSDVQSTFTIGAMNFSNGEYVID 636  
Db 548 RGGTVANNFRFLRTMNSGDELKYGNFVRRAFTTFTTQIQDIIRTSIQGLSGNGEYVID 607  
QY 637 RIEFVPEVITYEAEYDFEKAQEKVTALTSTNPRGLKTDVKDHYDQVSNLVESLSEDFY 696  
Db 608 KIEIIPVTATPEAYDRLERAQEAVALFTNPRRLKTDVTDHYDQVSNLVACLSDSEFC 667

Qy 697 LDEKRELF EIVKYAQIHIERNM 719  
||| ||| ||| ||| : ||| :  
Db 668 LDEKRELL EKVYAKRLSDERNL 690

Search completed: October 28, 2004, 18:34:24  
Job time : 25.3343 secs